

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 11:49:23 ; Search time 1874.39 Seconds  
(without alignments)  
8908.057 Million cell updates/sec

Title: US-09-856-320A-1\_COPY\_272\_958

Perfect score: 687

Sequence: 1 atcatcaagggttcgagtg.....aggagacgatgaagaacaat 687

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues 45562784

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estmu:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vr1:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	671.4	97.7	1294	11	BC015551 Homo sapi
2	631.6	91.9	678	12	B1763040 603047836
3	627.6	91.4	853	10	BG720793 602692015
4	618	90.0	841	12	B1818697 603037514

5	601.6	87.6	1072	12	BK559782	BK559782	AGENCOURT
6	583.2	84.9	1074	12	BK555917	BK555917	AGENCOURT
7	529.4	77.1	708	10	BG697071	BG697071	602660281
8	514.2	74.8	1295	11	AK009360	AK009360	Mus muscu
9	514.2	74.8	1295	11	AK009720	AK009720	Mus muscu
10	502.2	73.1	1269	11	AK009659	AK009659	Mus muscu
11	470.4	68.5	939	10	BG747134	BG747134	602704354
12	431.8	62.9	973	10	BE867930	BE867930	601443517
13	428.4	62.4	761	12	BM982377	BM982377	UI-CF-EN1
14	379.8	55.3	528	14	BK528424	BK528424	R2PD Mus
15	378	55.0	747	13	BX109836	BX109836	BX109836
16	367	53.4	539	12	BM837078	BM837078	K-EST0113
17	359.8	52.4	467	9	AA073833	AA073833	mJ99h09.y
18	359.8	52.4	467	9	A1893370	A1893370	mJ99h09.y
19	342.8	49.9	368	9	AA412318	AA412318	zt97c06.x
20	340	49.5	673	13	BE684799	BE684799	UI-CF-EN1
21	316.6	46.1	394	10	BE150851	BE150851	RC4-HM027
22	312	45.4	809	10	BF679282	BF679282	602153475
23	305.4	44.5	451	14	W60374	W60374	z6d2p01.x
24	287	41.8	654	13	B0676834	B0676834	UI-CF-DU1
25	286.4	41.7	526	10	BE898804	BE898804	601681783
26	284.8	41.5	966	14	BY709314	BY709314	BY709314
27	283.6	41.3	579	12	BI046611	BI046611	MR3-FND20
28	269.2	39.2	484	14	CB270157	CB270157	1009064.H
29	262.4	38.2	696	12	BM020073	BM020073	603648624
30	247.6	35.0	1048	11	AK004807	AK004807	Mus muscu
31	241.6	35.2	879	10	BE677072	BE677072	602086616
32	230.6	33.6	644	10	BE219655	BE219655	hvc6010.x
33	225.2	32.8	645	9	AW511566	AW511566	xu60a02.x
34	224.2	32.6	880	14	CB202840	CB202840	AGENCOURT
35	224.2	32.6	898	14	CB204935	CB204935	AGENCOURT
36	222.6	32.4	582	9	AW243944	AW243944	xo91b07.x
37	217.6	31.7	560	10	BF476474	BF476474	naa25d06.
38	213.4	31.1	852	14	CB587168	CB587168	AGENCOURT
39	205.2	29.9	826	14	CB574882	CB574882	AGENCOURT
40	194	28.2	824	13	B0592722	B0592722	AGENCOURT
41	194	28.2	897	13	B0502087	B0502087	Mus muscu
42	193.8	28.2	585	11	AK009451	AK009451	Mus muscu
43	193.8	28.2	585	11	AK019102	AK019102	Mus muscu
44	193.4	28.2	765	13	BX079152	BX079152	BX079152
45	193.4	28.2	849	13	BX078383	BX078383	BX078383

## ALIGNMENTS

RESULT 1  
LOCUS BC015551 1294 bp mRNA HTC 29-OCT-2001  
DEFINITION Homo sapiens, kallikrein 11, clone IMAGE:3847565, mRNA.  
ACCESSION BC015551  
VERSION BC015551.1 GI:15930236  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1294)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

REMARK  
COMMENT NIH-MGC Project URL: <http://mhc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNT)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www.shgc.stanford.edu>





QY 290 CGCCAGTCTCATACCTGGGCTGTGGACCCCTCACCCCTCTCTACGCTGTGTACTG 349  
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Db 245 CGCCAGTCTCATACCTGGGCTGTGGACCCCTCACCCCTCTCTACGCTGTGTACTG 304  
350 CTGGCAGCAGTGTCTCATTTCCGGTGGGGGACAGCTCCAGGCCAGTTAGCCGTC 409  
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Db 305 CTGGCAGCAGTGTCTCATTTCCGGTGGGGGACAGCTCCAGGCCAGTTAGCCGTC 364  
410 CTCACACCTTGCATGGGCCCAATCATCATCATTTGAGCAGCAGAGTGTGAGAACGCT 469  
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Db 365 CTCACACCTTGCATGGGCCCAATCATCATCATTTGAGCAGCAGAGTGTGAGAACGCT 424  
QY 470 ACCCGGCGACATACAGACACCATGTGTGTGCGCAGCTGACAGAAAGGGGGCAGAGCT 529  
425 ACCCGGCGACATACAGACACCATGTGTGTGCGCAGCTGACAGAAAGGGGGCAGAGCT 484  
530 CCTGCAGAGGTGACTCCGGGGGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 589  
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Db 485 CCTGCAGAGGTGACTCCGGGGGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 544  
QY 590 CCTGGGGCCAGAGATCCGTGTGCGATCAACCCGAAAGCCTGTGTGTGTGTGTGTGTGTGCA 649  
545 CCTGGGGCCAGAGATCCGTGTGCGATCAACCCGAAAGCCTGTGTGTGTGTGTGTGTGTGCA 604  
QY 650 AATATGTGTGATGATCCAGAGACGATGAAGAACAAT 687  
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Db 605 AATATGTGTGATGATCCAGAGACGATGAAGAACAAT 642

RESULT 3  
Bg720793 853 bp mRNA linear EST 08-MAY-2001  
LOCUS Bg720793  
DEFINITION 602692015F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:4824387 5',  
mRNA sequence.  
ACCESSION Bg720793  
VERSION Bg720793.1 GI:139999980  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
TITLE NIH-MGC http://mgi.ncl.nih.gov/.

JOURNAL  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki  
Toshiyuki and Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMNL at:  
http://image.llnl.gov  
Plate: LMNL0735 row: n column: 04  
High quality sequence stop: 826.  
Location/Qualifiers

FEATURES  
source  
1..853  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4824387"  
/lab\_host="DH10B"  
/clone\_id="NIH\_MGC\_97"  
/note="Organ: testis; Vector: pBluescriptR (modified  
pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcgag  
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTT-3',  
size-selected for average insert size 2.2 kb and  
normalized to R0F 5. This is a primary library enriched  
for full-length clones and constructed using the  
Cap-trapper method (Carninci, in preparation). Library  
constructed by M. Brownstein (NHGRI/NHGRI, National

BASE COUNT 180 a 285 c 227 g 161 t  
ORIGIN  
Query Match 91.4%; Score 627.6; DB 10; Length 853;  
Best Local Similarity 99.1%; Fred. No. 7e-115;  
Matches 652; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 1 ATCATCAAGGGGTTTCAGTGCAGAGCTGACCTCCAGCCCTGGAGAGCAGCCCTGTTGAG 60  
Db 196 ATCATCAAGGGGTTTCAGTGCAGAGCTGACCTCCAGCCCTGGAGAGCAGCCCTGTTGAG 255  
QY 61 AAGAGGGGCTACTGTGTGTGGGCGACGCTATCGCCCAAGATGGCTCTGACAGCAGCC 120  
Db 256 AAGAGGGGCTACTGTGTGTGGGCGACGCTATCGCCCAAGATGGCTCTGACAGCAGCC 315  
QY 121 CACAGCCCAAGCCCGCTACATGTTACCTGGGGGAGCACAACCTCCACAAGAGAGAG 180  
Db 316 CACTGCTCAAGCCCGCTACATGTTACCTGGGGGAGCACAACCTCCACAAGAGAGAG 375  
QY 181 GCGTGTGAGAGACCCGAGACAGCCAGCTGATCTCCACCCCGGCTTCAACAGCAGC 240  
Db 376 GCGTGTGAGAGACCCGAGACAGCCAGCTGATCTCCACCCCGGCTTCAACAGCAGC 435  
QY 241 CTCCCAACAAGAACACACCGCAATGACATGCTGTGTGAAGATGGCATGCCAGTCTCC 300  
Db 436 CTCCCAACAAGAACACACCGCAATGACATGCTGTGTGAAGATGGCATGCCAGTCTCC 495  
QY 301 ATCAACCTGGGCTGTGGACCCCTCACTCTCTCAGCTGTGTGTGTGTGTGTGTGTGTGT 360  
Db 496 ATCAACCTGGGCTGTGGACCCCTCACTCTCTCAGCTGTGTGTGTGTGTGTGTGTGTGT 555  
QY 361 TGCCCTCAATTTCCGGCTGGGGGAGAGACGTCAGCCCGAGTTACGCTCTCAACACTTG 420  
Db 556 TGCCCTCAATTTCCGGCTGGGGGAGAGACGTCAGCCCGAGTTACGCTCTCAACACTTG 615  
QY 421 CGATCGCGCAACATACCATCATTTGAGCAGCAGAGTGTGAAGAGCCCTACCCCGGCAAC 480  
Db 616 CGATCGCGCAACATACCATCATTTGAGCAGCAGAGTGTGAAGAGCCCTACCCCGGCAAC 675  
QY 481 ATCAACAGACACCAATGCTGTGTGCGACAGCTGTGAAGAGAGGGGCAAGAGCTCTGCAAGGT 540  
Db 676 ATCAACAGACACCAATGCTGTGTGCGACAGCTGTGAAGAGAGGGGCAAGAGCTCTGCAAGGT 734  
QY 541 GACTCCGGGGGCCCTGTGTGTC-TGTAAACAGCTCTTCAAGCAATATCTCTGGGGCCA 599  
Db 735 GACTCCGGGGGCCCTGTGTGTC-TGTAAACAGCTCTTCAAGCAATATCTCTGGGGCCA 794  
QY 600 GGATCCGTTGCGATCAACCCGAAAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 657  
Db 795 GGATCCGTTGCGATCAACCCGAAAGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 852

RESULT 4  
B1818697 841 bp mRNA linear EST 04-OCT-2001  
LOCUS B1818697  
DEFINITION 603037514F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5178746 5',  
mRNA sequence.  
ACCESSION B1818697  
VERSION B1818697.1 GI:15930247  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
TITLE NIH-MGC http://mgi.ncl.nih.gov/.

JOURNAL  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.jnl.gov>  
 Plate: LLM1445 row: k column: 03  
 High quality sequence stop: 784.

## FEATURES

source

1. 841

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5178746"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_115"

/note="Organ: pooled brain, lung, testis; Vector:

pCMV-SPORT6; Site:1; NotI; Site:2; EcoRV (destroyed); RNA

source anonymous pool of 6 male brains, age range 23-27; 1

male lung, age 27; and 1 male testis, age 69. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.8 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

021. Note: this is a NIH\_MGC Library."

021. Note: this is a NIH\_MGC Library."

BASE COUNT

180 a 288 c 206 g 167 t

ORIGIN

Query Match

Best local Similarity 99.3%; Pred. No. 1.2e-132; Length 841;

Matches 673; Conservative 0; Mismatches 0; Indels 5; Gaps 5;

15 CGAGTCAAGCCTCACTCCAG-CCCTGGCAGCAGCCCTGTCGAGAAGCAGGCTAC 73

1 CGAGTCAAGCCTCACTCCAGTCCAGGAGCAGCAGCCCTGTCGAGAAGCAGGCTAC 60

74 TCTGTGGGGGAGCGCTCATCGCCCGCAGATGGCTCTGTGACAGAGCCCACTGCTTAAGC 133

61 TCTGTGGGGGAGCGCTCATCGCCCGCAGATGGCTCTGTGACAGAGCCCACTGCTTAAGC 120

134 CCCGCTACATAGTTCACCTGCGGAGCAGACACCTCCAGAGAGAGGAGGCTGTGACAGA 193

121 CCCGCTACATAGTTCACCTGCGGAGCAGACACCTCCAGAGAGAGGAGGCTGTGACAGA 180

194 CCC-GGACAGCAGTGTCTTCCGCCACCCCGGCTTCACACAGCCTCCCAACAA 252

181 CCGTGGACAGCAGTGTCTTCCGCCACCCCGGCTTCACACAGCCTCCCAACAA 240

253 GACACCGGAGATGATCATGCTGTGAAGATGAGCATGCCAGTCTCC-ATCAGCTGGGC 311

241 GACACCGGAGATGATCATGCTGTGAAGATGAGCATGCCAGTCTCC-ATCAGCTGGGC 300

312 TGTGGGACCCCTCAACCTCTCTCTCAAGCTGTGTCACTGTGGACAGCAGTGCCTCATTTTC 371

301 TGTGGGACCCCTCAACCTCTCTCTCTCAAGCTGTGTCACTGTGGACAGCAGTGCCTCATTTTC 360

372 CGGCTGGGGGAGCAGCTCCAGCCCGCAGTTCAGCCTGCTTCACACCTTGCGATGGCCAA 431

361 CGGCTGGGGGAGCAGCTCCAGCCCGCAGTTCAGCCTGCTTCACACCTTGCGATGGCCAA 420

432 CATCACCATCATTTGAGCAGCAGAGTGTGAGAAAGCTTCACCCGGGAGATCAACAGAC 491

421 CATCACCATCATTTGAGCAGCAGAGTGTGAGAAAGCTTCACCCGGGAGATCAACAGAC 480

492 CATGTGTGTGCGAGCGTCCAGGA-AGGGGGCAAGAGACTCTGCCAGGTGACTCGGGG 550

481 CATGTGTGTGCGAGCGTCCAGGA-AGGGGGCAAGAGACTCTGCCAGGTGACTCGGGG 540

551 GCGCTCTGTGTGTAACAGTCTTTCAA-GGCATTATCTCTGGGGCAGGATCCGTGT 609

541 GCGCTCTGTGTGTAACAGTCTTTCAA-GGCATTATCTCTGGGGCAGGATCCGTGT 600

610 GCGATCACCCGGAAGCGCTGTGTACAGCAAGATGTGCAATATGTGAGACTGTGACAG 669

Db 601 GCGATCACCCGGAAGCGCTGTGTACAGCAAGATGTGCAATATGTGAGACTGTGACAG 660

QY 670 GAGACGATGAAGAACAT 687

Db 661 GAGACGATGAAGAACAT 678

## RESULT 5

BM559782

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cga@pds-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.jnl.gov>

Plate: LLM12765 row: 1 column: 11

High quality sequence stop: 684.

## FEATURES

source

1. 1072

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5744410"

/tissue\_type="medulla"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_119"

/note="Organ: brain; Vector: pCMV-SPORT6; Site:1; NotI;

Site:2; EcoRV (destroyed); RNA source normal medulla from

anonymous male age 27. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.3 kb, insert size range

0.9-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 013. Note:

this is a NIH\_MGC Library."

this is a NIH\_MGC Library."

BASE COUNT

238 a 340 c 307 g 185 t 2 others

Query Match

Best local Similarity 87.6%; Score 601.6; DB 12; Length 1072;

Matches 637; Conservative 0; Mismatches 21; Indels 4; Gaps 2;

QY 1 ATCATTAAGGGGTTCAGAGTCAAGCTTCACTCCAGCCTTGCGAGCAGCCTGTTCCAG 60

Db 275 ATCATTAAGGGGTTCAGAGTCAAGCTTCACTCCAGCCTTGCGAGCAGCCTGTTCCAG 334

QY 61 AAGACCGGCTACTGTGTGGGGGAGCGTCATCGCCCGCAGATGGCTCTGACAGCAGCC 120

Db 335 AAGACCGGCTACTGTGTGGGGGAGCGTCATCGCCCGCAGATGGCTCTGACAGCAGCC 394

QY 121 CACTGCTCAAGCCCGCTACATAGTTCACTGTGGGAGCAGACAACTCCAGAGAGAGAG 180

Db 395 CACTGCTCAAGCCCGCTACATAGTTCACTGTGGGAGCAGACAACTCCAGAGAGAGAG 454

QY 181 GCGTGTGACAGACCCGGAAGCGCAGCTAGTCTTCCCGCAGCCCGGCTTCAACACAGC 240

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Db      455 GCGTGTGAGCAGACCCGGACAGACCACTAGTCTTCCGCCACCCGGCTTCAACAACAGC 514
OY      241 CTCCCAACAAAGAACACACCGCAATGACATCATGTGTGAAGATGGCATCGCACTTCC 300
Db      515 CTCCCAACAAAGAACACACCGCAATGACATCATGTGTGAAGATGGCATCGCACTTCC 574
OY      301 ATCAGCTGGGCTGTGCGACCCCTCAACCTCTCTCAGCTGTGTCTGCTGGACACAC 360
Db      575 ATCAGCTGTGCTGTGCGACCCCTCAACCTCTCTCAGCTGTGTCTGCTGGACACAC 634
OY      361 TGCCTCATTTCCGGGTGGGGAGACAGCTCCAGCCCGCATTCAGCTGCTCAGACCTTG 420
Db      635 TGCCTCATTTCCGGGTGGGGAGACAGCTCCAGCCCGCATTCAGCTGCTCAGACCTTG 694
OY      421 CGATGCGGCAACATCACCATTGAGACACAGAAAGTGTGAAGAGCCCTACCCGGACAC 480
Db      695 CGATGCGGCAACATCACCATTGAGACACAGAAAGTGTGAAGAGCCCTACCCGGACAC 754
OY      481 ATCAGAGACACCATGTGTGTGCCAGCGTGCAGAGAAAGGGGCAAGGACTCTGCCAGGT 540
Db      755 ATCAGAGACACCATGTGTGTGCCAGCGTGCAGAGAAAGGGGCAAGGACTCTGCCAGGT 814
OY      541 GACTCCGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 599
Db      815 GACTCCGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 874
OY      600 GACTCCGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 656
Db      875 GACTCCGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 934
OY      657 GG 658
Db      935 GG 936

RESULT 6
LOCUS   BM559617 1074 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT 6565456 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5744314
5', mRNA sequence.
ACCESSION BM559617
VERSION   BM559617.1 GI:18803348
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1074)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
          Email: cgabs-remail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNLN at:
          http://image.lnl.gov
          Plate: LHAM12765 row: h column: 11
          High quality sequence stop: 689.
          Location/Qualifiers
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              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:5744314"
              /tissue_type="medulla"
              /lab_host="DH10B"
              /clone_id="NIH_MGC_119"
              /note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI;

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          Site_2: EcoRV (destroyed); RNA source normal medulla from
          anonymous male age 27. Library is oligo-dT primed and
          directionally cloned (EcoRV site is destroyed upon
          cloning). Average insert size 1.3 kb, insert size range
          0.9-3 kb. Library is normalized and enriched for
          full-length clones and was constructed by C. Gruber
          (Invitrogen). Research Genetics tracking code 013. Note:
          this is a NIH-MGC Library."

BASE COUNT  238 a 339 c 311 g 184 t 2 others
ORIGIN

Query Match      84.9%; Score 583.2; DB 12; Length 1074;
Best Local Similarity 97.8%; Pred. No. 1,4e-124;
Matches 632; Conservative 0; Mismatches 10; Indels 4; Gaps 4;

OY      1 ATCATCAAGGGGTTGAGTGCAGAGCTCAGCTCCAGCCCTGGACAGACCCCTGTTCCAG 60
Db      274 ATCATCAAGGGGTTGAGTGCAGAGCTCAGCTCCAGCCCTGGACAGACCCCTGTTCCAG 333
OY      61 AAGAGCGGCTACTCTGTGGGCGAGGCTCATCGCCCGCAGATGGCTCTGACAGACGCC 120
Db      334 AAGAGCGGCTACTCTGTGGGCGAGGCTCATCGCCCGCAGATGGCTCTGACAGACGCC 393
OY      121 CACTGCTCAAGCCCGCTTACATAGTACCTGCGGCGACACACCTCCAGAAAGAGAG 180
Db      394 CACTGCTCAAGCCCGCTTACATAGTACCTGCGGCGACACACCTCCAGAAAGAGAG 453
OY      181 GCGTGTGAGCAGACCCCGGACAGCCAGCTAGTCTTCCCGACCCCGGCTTCAACAACAGC 240
Db      454 GCGTGTGAGCAGACCCCGGACAGCCAGCTAGTCTTCCCGACCCCGGCTTCAACAACAGC 513
OY      241 CTCCCAACAAAGAACACACCGCAATGACATCATGTGTGAAGATGGCATCGCACTTCC 300
Db      514 CTCCCAACAAAGAACACACCGCAATGACATCATGTGTGAAGATGGCATCGCACTTCC 573
OY      301 ATCAGCTGGGCTGTGCGACCCCTCACCTCTCTCAGCTGTGTGTGTGTGTGTGTGTGT 360
Db      574 ATCAGCTGGGCTGTGCGACCCCTCACCTCTCTCAGCTGTGTGTGTGTGTGTGTGTGT 633
OY      361 TGCCTCATTTCCGGGTGGGGAGACAGCTCCAGCCCGCATTCAGCTGTGTGTGTGTGTGT 420
Db      634 TGCCTCATTTCCGGGTGGGGAGACAGCTCCAGCCCGCATTCAGCTGTGTGTGTGTGT 693
OY      421 CGATGCGGCAACATCACCATTGAGACAGCAAGATGTGAGAGCCCTACCCGGACAC 480
Db      694 CGATGCGGCAACATCACCATTGAGACAGCAAGATGTGAGAGCCCTACCCGGACAC 753
OY      481 ATCAGAGACACCATGTGTGTGCCAGCGTGCAGAGAAAGGGGCAAGGACTCTGCCAGGT 540
Db      754 ATCAGAGACACCATGTGTGTGCCAGCGTGCAGAGAAAGGGGCAAGGACTCTGCCAGGT 813
OY      541 GACTGCC-GGGGGCCCTGTGCTGTGAACCACTCTTCAAGCAATTATCTCT-GGGGCC 598
Db      814 GACTGCCGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 873
OY      599 AGGATCCGT-GTGGATACCCGAA-6CCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 642
Db      874 AGNATCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 919

RESULT 7
LOCUS   BG697071 708 bp mRNA linear EST 07-MAY-2001
DEFINITION 60260281P1 NCI_GCAP_Skn3 Homo sapiens cDNA clone IMAGE:4803356 5',
mRNA sequence.
ACCESSION BG697071
VERSION   BG697071.1 GI:13962880
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 708)

```

AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC).
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.

## FEATURES

### source

BASE COUNT	147 a	262 c	183 g	116 t
ORIGIN				

Query Match	77.18;	Score 529.4;	DB 10;	Length 708;
Best Local Similarity	99.88;	Pred. NO. 3.4e-112;		
Matches 530; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

OY 1 ATCATCAAGGGGTTGAGTGCAGAGCCTCACTCCAGACCCTGGAGGACAGCCCTGTTCGAG 60  
 Db 178 ATCATCAAGGGTTGAGTGCAGAGCCTCACTCCAGACCCTGGAGGACAGCCCTGTTCGAG 237  
 OY 61 AAGACGGGGCTACTCTGTGGGGGCGAGCGTCATCGCCCCAGATGGCTCTGTGACGAGCC 120  
 Db 238 AAGAGCGGGCTACTCTGTGGGGGCGAGCGTCATCGCCCCAGATGGCTCTGTGACGAGCC 297  
 OY 121 CACTGCTTCAGAGCCCCGGCTACATAGTTCACGTGGGGGACACAACTCCAGAAAGGAGAG 180  
 Db 238 CACTGCTTCAGAGCCCCGGCTACATAGTTCACGTGGGGGACACAACTCCAGAAAGGAGAG 357  
 OY 181 GGCTGTGAGCAGAGCCCGGACAGCCACTGATGTCCTTCCACCACCCGGCTTCAACAACAG 240  
 Db 358 GGCTGTGAGCAGAGCCCGGACAGCCACTGATGTCCTTCCACCACCCGGCTTCAACAACAG 417  
 OY 241 CTCGCCAACAAAGACACCCGGCAATATACATGATGCTGTGAATAATGGCATACGCACTCTC 300  
 Db 418 CTCGCCAACAAAGACACCCGGCAATATACATGATGCTGTGAATAATGGCATACGCACTCTC 477  
 OY 301 ATCACCCTGGGCTGTGCGAACCCTCACTCTCTTACGCTGTGTCACTCTGTGACACAG 360  
 Db 478 ATCACCCTGGGCTGTGCGAACCCTCACTCTCTTACGCTGTGTCACTCTGTGACACAG 537  
 OY 361 TGCCCATTTTCCGGTGTGGGGGACAGCTCCAGCCCCCAATTAAGCTGCTTACACCTTG 420  
 Db 538 TGCCCATTTTCCGGTGTGGGGGACAGCTCCAGCCCCCAATTAAGCTGCTTACACCTTG 597  
 OY 421 CGATGCGGCAACATACCATCATCTTATAGCACCAAGATGTGAAGACGCTTACCCCGGCAAC 480  
 Db 598 CGATGCGGCAACATACCATCATCTTATAGCACCAAGATGTGAAGACGCTTACCCCGGCAAC 657  
 OY 481 ATCACAGACACCATGTGTGTGTGCCAGCTGTCAGGAAGGGGGCAAGGACTTC 531  
 Db 658 ATCACAGACACCATGTGTGTGTGCCAGCTGTCAGGAAGGGGGCAAGGACTTAC 708

RESULT 8			
AK009360			
LOCUS	1295 bp	mRNA	1 linear
AK009360			HTC 05-DEC-200

DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM
------------	--

REFERENCE	1
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636







Db		825	GACCTGTGAGAGCCCCCGTGGTGTCATCCAGCATCTCTTCAAGCATTACTCTTGGGGTAG	884
Oy		601	GATCCGCTGTGCATCACCCGAAGCCTGTGTACACAGAAAGTCTGCCAATATGTGGAC	660
Db		885	GACCATGTGCGCGTCACCAAGAAGCCTGTGTATACAAAAGTCTGCAATTAATTNAAC	944
Oy		661	TGATCCAGGAGCAGATGATAACAAT	687
Db		945	TGATCCAGCAGGTTATGAGCAACAAT	971
RESULT 10				
LOCUS	AK009659	1369 bp	mRNA	linear HTC 05-DEC-2002
DEFINITION	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310037E23 product:protease, serine, 20, full insert sequence.			
VERSION	AK009659.1	GI:12844589		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL MEDLINE PUBMED	Genome Res. 10 (10), 1617-1630 (2000)			
REFERENCE	11042159			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisake, N., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M., Yoshida, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.			
JOURNAL MEDLINE PUBMED	RIKEN integrated sequence analysis (RISA) system - 384-format sequencing pipeline with 384 multiplexed sequencer			
REFERENCE	Genome Res. 10 (11), 1757-1771 (2000)			
AUTHORS	20530913 11076861			
TITLE	4			
JOURNAL MEDLINE PUBMED	Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aitawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaoka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Peocle, G., Quackenbush, J., Schriml, L.M., Staab, F., Suzuki, R., Tomita, M., Wagner, E., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Caranci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Humé, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzatelli, U., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyokawa, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohzuki, S., and Hayashizaki, Y.			
REFERENCE	Functional annotation of a full-length mouse cDNA collection			

JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 1269)
AUTHORS	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Canham,I.P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hirooka,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Koude,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishik,K., Nomura,K., Numasaki,R., Ohno,M., Okazaki,Y., Orido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	Please visit our web site ( <a href="http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/</a> ) for further details.
FEATURES	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAAGAGAGACATCCAGCATCAGACCTCTTTTCTTTTTTCTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the rhesus adapter of sequence [5' GAAGAGAGATTCGCAGTAATTAAATTAATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.
SOURCE	location/Qualifiers 1..1269 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:2310037E23" /db_xref="MGI:1894042" /dn_xref="taxon:10090" /cloned="2310037E23" /sex="male" /tissue_type="tongue" /collection="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 119..948 /note="protease, serine, 20 (MGD MGI:1929977) putative" /db_xref="MGI:1929977" 1251..1256 /note="putative" 1269 /note="putative" BASE COUNT 307 a 363 c 304 g 295 t ORIGIN  Query Match 73.1%; Score 502.2; DB 11; Length 1269; Best Local Similarity 84.1%; Pred No. 8.2e-106; Matches 578; Conservative 0; Mismatches 108; Indels 1; Gaps 1

Db 260 ATCATCAAGGGTTATGATGACAGGCTCACTACACCAAGGAGGTGGCCCTTTTCAG 319  
61 AAGACGGGCTACTGTGTGGGGGACGCGATGATGCCCCAGATGCTCTGACAGGAC 120  
320 AAGACAGGGCTTCTGTGTGGGGCAACCTTCATGCCCCCAATGCTCTGACAGGAC 379  
121 CACTGCTCAAGCCCGCTACATATGTTACCTGGGGCAGCACAACTCCAGAGAGAG 180  
380 CACTGCGGAGCCCATTAAGCTGATCTCTGTTGAGAGCAATCTAGAGAGAGACAG 439  
181 GGCTGACAGACCCGGACAGGCACTGATGCTTCTCCCAACCCCGGCTTCAACAGAC 240  
440 GGCTGAGAC-GAGGGGATGAGGCACTGATGCTTCTCCCAACCCCGGCTTCAACAGAC 498  
241 CTCGCCCAAGAAAGACCGGCAATGATGATGCTGTTGAGAGATGCTGCGCAGCTCC 300  
499 CTCGCCCAAGAAAGACCGGCAATGATGATGCTGTTGAGAGATGCTGCGCAGCTCC 558  
301 ATCACTGGGCTGTGGACCCCTCACTCTCTCTCACTGCTGCTGCTGCTGCTGCTGCT 360  
559 TTTACCCGAGCTGTGACGACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 618  
361 TGCCCTATTTCCGGCTGGGGGACAGCTGACAGCCCGGCTGCTGCTGCTGCTGCTGCT 420  
619 TGCTCTATTTCTGATGAGGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 678  
421 CGATGGCCAGATCACTACATCATTTGAGCAGCAGAAAGTGTAGAAAGCTTACCCGCAAC 480  
679 CGATGGCCAGATCACTACATCATTTGAGCAGCAGAAAGTGTAGAAAGCTTACCCGCAAC 738  
481 ATCAAGACAGACCATGT 540  
739 ATCAAGACAGACCATGT 798  
541 GACTCGGGGGGCTGT 600  
799 GACTCGGGGGGCTGT 858  
601 GATCGCTGT 660  
859 GATCGCTGT 918  
661 TGATCGGAGAGAGCATGAGAAACAT 687  
919 TGATCGGAGAGAGCATGAGAAACAT 945

RESULT 11  
Bg747134 639 bp mRNA 1linear EST 15-MAY-2001  
DEFINITION 602704354F1 NIH\_MGC\_15 Homo sapiens cDNA clone IMAGE:485733 5',  
Bg747134  
ACCESSION Bg747134  
VERSION Bg747134.1 GI:14057787  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 639)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

Plate: L1CM1710 row: k column: 14  
High quality sequence stop: 638.  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4857733"  
/tissue\_type="adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1lb="NIH\_MGC\_15"  
/note="Organ: colon; Vector: pORF7; Site:1: XhoI; Site:2:  
EcoRI; cDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(5). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 128 a 241 c 162 g 108 t

ORIGIN  
Query Match 68.5%; Score 470.4; DB 10; Length 639;  
Best Local Similarity 99.8%; Pred. No. 1.5e-98;  
Matches 471; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATCATCAAGGGGTTGATGACAGGCTCACTACCTCCAGCCCTGCGAGGAGCCCTGTCGAG 60  
168 ATCATCAAGGGGTTGATGACAGGCTCACTACCTCCAGCCCTGCGAGGAGCCCTGTCGAG 227  
61 AAGACGGGCTACTGTGTGGGGGACGCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
228 AAGACGGGCTACTGTGTGGGGGACGCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 287  
121 CACTGCTCAAGCCCGCTACATATGTTACCTGAGGAGCAGACAACTCCAGAAAGAGAG 180  
288 CACTGCTCAAGCCCGCTACATATGTTACCTGAGGAGCAGACAACTCCAGAAAGAGAG 347  
181 GGCTGTGACAGACCCGGACAGCAGCTAGTCTTCCCGACCCCGGCTTCAACACAGC 240  
348 GGCTGTGACAGACCCGGACAGCAGCTAGTCTTCCCGACCCCGGCTTCAACACAGC 407  
241 CTCGCCCAAGAAAGACCGGCAATGATGATGCTGTTGAGAGATGCTGCGCAGCTCC 300  
408 CTCGCCCAAGAAAGACCGGCAATGATGATGCTGTTGAGAGATGCTGCGCAGCTCC 467  
301 ATCACTGGGCTGTGGACCCCTCACTCTCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCT 360  
468 ATCACTGGGCTGTGGACCCCTCACTCTCTCTCTCACTGCTGCTGCTGCTGCTGCTGCT 527  
361 TGCTCTATTTCCGGCTGGGGGACAGCTGACAGCCCGGCTGCTGCTGCTGCTGCTGCTG 420  
528 TGCTCTATTTCCGGCTGGGGGACAGCTGACAGCCCGGCTGCTGCTGCTGCTGCTGCTG 587  
421 CGATGGCCCAATCACTACATTTGAGCAGCAGAAAGTGTAGAAAGCTTACCCGCAAC 472  
588 CGATGGCCCAATCACTACATTTGAGCAGCAGAAAGTGTAGAAAGCTTACCCGCAAC 639

RESULT 12  
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LOCUS BE867930  
DEFINITION 601443517F1 NIH\_MGC\_65 Homo sapiens cDNA clone IMAGE:3847565 5',  
BE867930  
ACCESSION BE867930  
VERSION BE867930.1 GI:10316706  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 973)  
NIH-MGC http://mgi.nci.nih.gov/



TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@nsf.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LAM9562 row: a column: 06  
High quality sequence stop: 714.  
Location/Qualifiers  
1. .973  
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/mol\_type="mRNA"  
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/clone="IMAGE:3847565"  
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/lab\_host="DH10B (phage-resistant)"  
/clone\_id="N1H.MGC\_65"  
/note="Organ: colon; Vector: PCMV-SPORT6; Site: 1; NotI; Site: 2; SalI: Cloned unidirectionally. Primer: dfr. Average insert size 1.8 kb. Library constructed by Life Technologies."  
BASE COUNT 241 a 302 c 288 g 142 t  
ORIGIN  
Query Match 62.9%; Score 431.8; DB 10; Length 973;  
Best Local Similarity 89.5%; Pred. No. 1.5e-89;  
Matches 511; Conservative 0; Mismatches 52; Indels 8; Gaps 4;  
Db 7 AAGGGTTGAGTCAAGCTCACTCCAGCCCTGGCAGAGCCCTGTTGAGAGAGC 66  
267 AAGGGTTGAGTCAAGCTCACTCCAGCCCTGGCAGAGCCCTGTTGAGAGAGC 326  
QY 67 CGGCTACTCTGTGGGGCGAGCTCATGCCGCCAGATGGCTCTGACAGCAGCCACTGC 126  
Db 327 CGGCTACTCTGTGGGGCGAGCTCATGCCGCCAGATGGCTCTGACAGCAGCCACTGC 386  
QY 127 CTCAAGC---CCGTCATACATCTCACTGGGGCAGCAGCACTCCAGAGAGAGG 182  
Db 387 CTCAAGC---CCGTCATACATCTCACTGGGGCAGCAGCACTCCAGAGAGAGG 446  
QY 183 CTGTGACAGACCCGAGCAGCACTGAGTCTCCGCCAGCCGCTTCAACAAGAGCT 242  
Db 447 CTGTGACAGACCCGAGCAGCACTGAGTCTCCGCCAGCCGCTTCAACAAGAGCT 506  
QY 243 CCCCACAAAGACACCGCAATGACATGCTGGTGAAGATGGCATGCCAGTCTCAT 302  
Db 507 CCCCACAAAGACACCGCAATGACATGCTGGTGAAGATGGCATGCCAGTCTCAT 566  
QY 303 CACCTGGGCTGTGGAGACCCGTCCTCCTCAGCTGCTGTCATCTGGCAGCAGCTG 362  
Db 567 CACCTGGGCTGTGGAGACCCGTCCTCCTCAGCTGCTGTCATCTGGCAGCAGCTG 625  
QY 363 CTTCAATTTCCGGCTGGGG--CAGCAGCTCCAGCCCGAGTTAGCTGCTCAACCTTG 420  
Db 626 CTTCAATTTCCGGCTGGGG--CAGCAGCTCCAGCCCGAGTTAGCTGCTCAACCTTG 685  
QY 421 CGATGGCCCAATCATTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
Db 686 CGATGGCCCAATCATTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 745  
QY 481 ATCAAGACACATGCTG--TGCCAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 539  
Db 746 TAAACGACACATGCTG--TGCCAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 805  
QY 540 TGAATCCGGGGGCTGCTGTGTACAG 570  
Db 806 TGAATCCGGGGGCTGCTGTGTACAG 836

RESULT 13  
BM982377/c  
LOCUS  
DEFINITION BM982377 761 bp mRNA linear EST 21-FEB-2003  
UT-CF-EN1-acs-o-17-0-UT-UT-CF-EN1 Homo sapiens cDNA clone  
BM982377  
ACCESSION BM982377  
VERSION 1 GI:19605813  
KEYWORDS  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 761)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 9704447  
PUBMED 8889548  
COMMENT Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
The following repetitive elements were found in this cDNA  
sequence: 17-100, >LINE2 (matched complement)  
Seq primer: M13 FORWARD  
POLYA=yes.

FEATURES  
source  
Location/Qualifiers  
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/clone\_id="UI-CF-EN1"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site: 1; EcoR I; Site: 2; Not I;  
UI-CF-EN1 is a normalized cDNA library containing the  
following tissue(s): Primary Lung Cystic Fibrosis  
Epithelial cells. The library was constructed according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was ligated to an EcoR I adaptor, digested with Not  
I, and cloned directionally into pT73-Pac vector. The  
oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (drr)18 tail. The  
sequence tag for this library is CTGCTCAGGT.  
TAG-IRB-UI-CF-EN1  
TAG-TISSUE-Human Lung Epithelial Cell lines untreated LPS  
6hr to LPS 24h  
TAG-Seq-CTGCTCAGGT"

BASE COUNT 172 a 170 c 222 g 195 t 2 others  
ORIGIN  
Query Match 62.4%; Score 428.4; DB 12; Length 761;  
Best Local Similarity 99.3%; Pred. No. 8.2e-89;  
Matches 429; Conservative 0; Mismatches 3; Indels 0; Gaps 0;





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, Thu Oct 16 09:48:39 2003

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 15, 2003, 19:44:50 ; Search time 47.1708 Seconds

(without alignments)  
7516.609 Million cell updates/sec

Title: US-09-856-320A-1\_COPY\_272\_958

Perfect score: 1275

Sequence: 1 atcctcaagggttcgagtg.....aggagacgaggaagaacaat 687

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
	Ygapop 10.0	Ygapext 0.5
	Fgapop 6.0	Fgapext 7.0
	Delop 6.0	Delext 7.0

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1661050

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+np\_model -DEV=x1p  
-O=/cgn2\_1/USPTO.spool\_P/US09856320/runat\_15102003\_105639\_8524/app\_query.fasta\_1.2318  
-DB=SPTRMBL\_23 -OFMT=FASTA -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09856320\_ECGN\_1\_159\_efunal\_15102003\_105639\_8524 -NCPV=6 -ICPV=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTRMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_podent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirs:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1235.5	96.9	275	4 Q8IXD7	Q8IXD7 homo sapien

2	1062	83.3	249	11 Q9QVNA	Q9QVNA mus musculu
3	1062	83.3	276	11 Q9QVNA	Q9QVNA mus musculu
4	683	53.6	260	4 Q8IW69	Q8IW69 homo sapien
5	679	53.3	255	4 Q96R00	Q96R00 mus musculu
6	678	53.2	254	11 Q8CGR4	Q8CGR4 mus musculu
7	671.5	52.7	276	11 Q8CGR6	Q8CGR6 mus musculu
8	630	49.4	251	11 Q9DB08	Q9DB08 mus musculu
9	623.5	48.9	293	11 Q9D140	Q9D140 mus musculu
10	603	47.3	250	11 Q8CGR5	Q8CGR5 mus musculu
11	597.5	46.9	234	11 Q9CV76	Q9CV76 mus musculu
12	590	46.3	246	11 Q921R9	Q921R9 mus musculu
13	588	46.1	245	11 Q9QUR9	Q9QUR9 mus musculu
14	587.5	46.1	235	11 Q63274	Q63274 ratu
15	587	46.0	236	11 Q9R0T7	Q9R0T7 mus musculu
16	583.5	45.8	239	11 Q63275	Q63275 ratu
17	581.5	45.6	261	11 Q9JW70	Q9JW70 mus musculu
18	574.5	45.1	261	6 Q9N101	Q9N101 sagulus oe
19	574.5	45.1	261	6 Q29474	Q29474 canis famli
20	564.5	44.3	269	4 Q8IU55	Q8IU55 homo sapien
21	564	44.2	251	11 Q54854	Q54854 ratu
22	562.5	44.1	247	11 Q9CPN7	Q9CPN7 mus musculu
23	560.5	44.0	237	13 Q91515	Q91515 fugu rubrip
24	560.5	44.0	244	13 Q80GW3	Q80GW3 angulla ja
25	560	43.9	249	11 Q91VE3	Q91VE3 mus musculu
26	558.5	43.8	245	13 Q42160	Q42160 petromycon
27	558.5	43.6	261	11 Q8C232	Q8C232 mus musculu
28	556.5	43.6	263	11 Q9JW71	Q9JW71 mus musculu
29	556	43.6	240	13 Q98TH0	Q98TH0 engraulis j
30	556	43.6	246	11 Q88301	Q88301 mus musculu
31	556	43.6	253	11 Q91Y82	Q91Y82 mus musculu
32	555.5	43.6	222	13 Q8AV11	Q8AV11 oncorhynch
33	554.5	43.5	263	11 Q9JW69	Q9JW69 mus musculu
34	552.5	43.3	254	6 Q42159	Q42159 petromycon
35	552.5	43.3	254	6 Q9XSN6	Q9XSN6 sus scrofa
36	551	43.2	247	11 Q9CPN9	Q9CPN9 mus musculu
37	549.5	43.1	247	13 Q42158	Q42158 petromycon
38	549	43.1	238	13 Q9W706	Q9W706 paralicthy
39	548.5	43.0	247	13 Q42608	Q42608 petromycon
40	547	42.9	247	11 Q9D7Y7	Q9D7Y7 mus musculu
41	544.5	42.7	242	13 Q92099	Q92099 paratote
42	543.5	42.6	261	11 Q88309	Q88309 mus musculu
43	541.5	42.5	242	13 Q9W707	Q9W707 paralicthy
44	541	42.4	247	4 Q8NH44	Q8NH44 homo sapien
45	539.5	42.3	242	13 Q93266	Q93266 pseudopleur

## ALIGNMENTS

RESULT 1

ID	Q8IXD7	PRELIMINARY;	PRT;	275 AA.
AC	Q8IXD7;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, last annotation update)			
DE	Variant form hippostasin/KIK11.			
GN	KIK11.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Nakamura T., Mitsui S., Miki T., Yamaguchi N.;			
RT	"Molecular cloning and expression of a variant form of			
RT	hippostasin/KIK11 in prostate."			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB078780; BAC54105.1; -			
SQ	SEQUENCE 275 AA; 30165 MW; 257AA2B28F40E2C4 CRC64;			

Alignment Scores:

3.2e-98

Length:

275

Score: 1235.50 Matches: 229  
 Percent Similarity: 90.16% Conservative: 0  
 Best Local Similarity: 90.16% Mismatches: 0  
 Query Match: 96.90% Indels: 25  
 DB: 4 Gaps: 1

US-09-856-320a-1\_copy\_272\_958 (1-687) x Q81XD7 (1-275)

```

OY 1 ATCATCAAGGGGTTTCAGTGCAGCAAGCTCCACCTCCAGCCCTGGCAGGAGCCCTGTTCAG 60
    |||||
DB 22 IteiletygllyheglucylsyrProhlsSerGlnProtrpInlaIaIaIaIaIaIaIaIaIa 41
OY 61 AAGAGCGGCTACTCTGTGGGGGAGCGCTCATGCCCCAGATGGCTCTGACAGAGCC 120
    |||||
DB 42 LysThrArgLeuLeuLeuGlyAlaThrLeuIleAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 61
OY 121 CACTGCTCAAGGCC----- 135
    |||||
DB 62 HisCysLeuLysProtrpIValSerLeuThrSerProThrHisValSerProAspLeuSer 81
    |||||
OY 136 -----CGCTACATAGTTCACCTGGGGCAGCAGCAGC 165
    |||||
DB 82 SerSerAsnTyrCysLeuSerHisLeuSerArgTyrIleValHisLeuGlyGlnHisAsn 101
    |||||
OY 166 CTCCAGAGAGGAGGAGGCTGTGAGCAGACCCGAGAGCCACTAGTCTTCCCCAGCCC 225
    |||||
DB 102 LeuGlnLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 121
OY 226 GCGTTCACACACACCGCTCCCAACAAGACACACCGAATGATCATGCTGGTGAAGATG 285
    |||||
DB 122 GlyPheAsnHisSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMet 141
OY 286 GCATGCGCCAGTTCATCATCTGGGCTGTGAGCCCTGACCCCTGCTCATCGCTGTGTC 345
    |||||
DB 142 AlaSerProValSerIleThrIleThrAlaValArgProLeuThrLeuSerSerArgCysVal 161
OY 346 ACTGCTGGCAGCAGTGCCTCATTTCCGGCTGGGGAGCAGCCGCGAGCCCGGTTAAGC 405
    |||||
DB 162 ThrAlaGlyThrSerCysLeuIleSerGlyTyrPheLysSerThrSerProGlnLeuArg 181
OY 406 CTGCTGCACACCTTGGGATGCGGCAACATCACCATCATGATGAGCAGCAGAGTGTGAGAC 465
    |||||
DB 182 LeuProHisThrLeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysGlnLys 201
OY 466 GCTTACCCCGGCAACATCAGACACACCATGTGTGTGCCAGCTGACGAGAGGGGCAAG 525
    |||||
DB 202 AlaTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLys 221
OY 526 GACTCTGCGCAGGCTGACTCCGGGGGCGCTGCTGTGTAACAGTCTCTCAAGGCAT 585
    |||||
DB 222 AspSerCysGlnIleLysPheArgLysGlyProLeuValCysAsnGlnSerLeuGlnGlyIle 241
OY 586 ANTCCTGGGCGCAGGATCGTGTGCGATCACCAGCAAGCCGTGTGTACAGAGAGT 645
    |||||
DB 242 IleSerTrpGlyLysProCysAlaIleThrArgLysProGlyValIleTyrThrLysVal 261
OY 646 TGCAGATATGTGGATGATGATCAGAGAGCAGATGAAGAACAAT 687
    |||||
DB 262 CysLysTyrValAspTrpIleGlnGlnIleThrMetLysAsnAsn 275
  
```

## RESULT 2

Q9QYN4 PRELIMINARY; PRT; 249 AA.  
 AC 09QYN4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE HIPOSTASIN (2310015108RIK protein).  
 GN PRS520 OR 2310015108RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Yamaguchi N., Mitsui S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mitsui S., Yamaguchi N.;
RT "cDNA cloning of a novel brain serine protease, Hipostasin.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai T., Shingawa A., Shibata K., Yoshino H., Itoh M., Ishii Y.,
RA Akawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamaguchi T.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Saramoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shinata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
RA Wushaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AB016226; BAA88825.1; -
DR EMBL: AK009720; BAB26461.1; -
DR EMBL: AK009360; BAB26241.1; -
DR HSSP: P00763; IDPO.
DR MEROPS: S01.257; -.
DR MGD: MGI:192977; Prs520.
DR InterPro: IPR001254; Ser.protease_Try.
DR Pfam: PF00089; trypsin.1.
DR SMART: SM00020; Tryp_Spc.1.
DR PROSITE: PS00240; TRYPSIN_DOM.1.
DR PROSITE: PS00134; TRYPSIN_HIS.1.
DR PROSITE: PS00135; TRYPSIN_SER.1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 249 AA; 27604 MW; F9F99CB457D727D5 CRC64;
  
```

## Alignment Scores:

Pred. No.: 2,94e-83 Length: 249  
 Score: 1062.00 Matches: 186  
 Percent Similarity: 91.27% Conservative: 23  
 Best Local Similarity: 81.22% Mismatches: 20  
 Query Match: 83.29% Indels: 0  
 DB: 11 Gaps: 0

US-09-856-320a-1\_copy\_272\_958 (1-687) x Q9QYN4 (1-249)

```

OY 1 ATCATCAAGGGGTTTCAGTGCAGCAAGCTCCACCTCCAGCCCTGGCAGGAGCCCTGTTCAG 60
    |||||
DB 21 IteiletygllytlytucylsyrProhlsSerGlnProtrpInlaIaIaIaIaIaIaIaIaIa 40
OY 61 AAGAGCGGCTACTCTGTGGGGGAGCGCTCATGCCCCAGATGGCTCTGACAGAGCC 120
    |||||
DB 41 LysThrArgLeuLeuGlyAlaThrLeuIleAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 60
OY 121 CACTGCTCAAGGCCCGCTACATAGTTCACCTGGGGCAGCAGCAGCAGTGTGAGAGAG 180
    |||||
DB 61 HisCysArgLysProHisTyrValIleLeuLeuGlyGlnHisAsnLeuGlyLysThrAsp 80
OY 181 GCGTGTGAGCAGACCGGAGCAGCAGCAGTGTGCTTCCCGACCCGGGCTTCAACAACAGC 240
  
```



OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 DR Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: BC040887; AHA0887.1; -  
 KW Hypothetical protein.  
 SW SEQUENCE 260 AA; 28090 MW; EF5934EB96295660 CRC64;

## Alignment Scores:

Score:	148e-50	Length:	260
Percent Similarity:	683.00	Matches:	116
Best Local Similarity:	70.54%	Conservative:	42
Query Match:	51.79%	Mismatches:	64
	53.57%	Indels:	2
	4	Gaps:	2

US-09-856-320a-1\_COPY\_272\_958 (1-687) x Q81W69 (1-260)

```

OY 1 ATCATCAAGGGGTTTCGATGCAAGCTCACTCCAGCCCTGGCAGCAGCCCTGTTTCGAG 60
    ::::: ||| |||||:::|||||||:::|||||||:::|||||||:::|||||||:::
Db 33 ValLeuGlYglYHisGlucysGlnProHisSerGlnProTrpGlnAlaIleuPheGln 52
OY 61 AAGACCGGCTACTGTGTGGGGGAGCGCTCATCGCCCGCAGATGCTCTGACAGCAGCC 120
    ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 53 GlYGlInGlnLeuGlnCysGlnValIleuValGlyGlyAsnTrpValIleuThrAlaIa 72
OY 121 CACTGCTCAAGCCCGCTACATAGTTCACTCGGGGAGACCAACCTCCAGAGGAGGAG 180
    ||||| |||||:::||||| || ||||| ||:::||||| :::::
Db 73 HisCysLysAlaProLysIleThrValArgLeuGlyAspHisSerLeuGlnAsnLysAsp 92
OY 181 GGGTGTGAGCAGACCCGAGACGACCTGATCCCTCCCGCCCGCGCTTCAACACAGC 240
    ||| ||||| ::||| |||||:::||||| ::|||:::|||||
Db 93 GlyProGlnGlnIleuIleProValIleGlnSerIleProHisProCysTyrAsnSer 112
OY 241 CTCGCCCAACAACACCGCAATGACATATGCTGTGTAAGTGGCATGCCACAGTCTCC 300
    ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 113 ---AspValGlnAspHisAsnHisAspLeuMetLeuGlnIleuArgAspGlnAlaSer 131
OY 301 ATCACTGGGCTGTGGACCCCTCACCTCTCTCAAGCTGTGTCACCTGTGTGCACACG 360
    ::| ::|||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 132 LeuGlYSerLysValLysProIleSerLeuAlaAspHisCysThrGlnProGlyGlnLys 151
OY 361 TGGCTCATTTCCGCTGTGGGGGAGCAGCTGACGCCCGCCAGTTACGCTGCTCACACCTG 420
    ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 152 CysThrValSerGlyTrpGlyThrValThrSerProArgLysAsnProAspThrLeu 171
OY 421 CGATGGCCCAACATCACTATGAGCAGACCAAGATGTGAGAACGCTTACCCCGCAC 480
    ||||| ::||| ::|||:::|||||:::|||||:::|||||:::|||||
Db 172 AsnCysAlaGlnValLysIlePheProGlnLysLysCysGlnAspAlaTyrProGlyGln 191
OY 481 ATCAACAGACACCATGTGTGTGTGCAGCTGACAGAGAGGGGAGCAAGACTCTCCAGAGT 540
    ||||| |||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 192 IleThrAspValMetValCysAlaGlySerSerLysGlyAla---AspThrCysGlnGly 210
OY 541 GACTCGGGGGCCCTGTGTGTGTGTACCAAGTCTTTCAGAGCATTTATCTCGGGGCGCAG 600
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 211 AspSerGlyGlyProLeuValCysAspGlyAlaLeuGlnGlyIleThrSerTrpGlySer 230
OY 601 GATCCCTGTGCATCAACCCGAAAGCTGTGTACACCAAGTCTGCAATATGTGGAC 660
    ||||| ::||| |||||:::|||||:::|||||:::|||||:::|||||
Db 231 AspProCysGlyArgSerAsnLysProGlyValTyrThrAsnIleCysArgTyrIleuAsp 250
OY 661 TGGATCCAGAG 672
    |||||:::|||||
Db 251 TrpIleLysLys 254

```

RESULT 5  
 O96R00 PRELIMINARY: PRT: 255 AA.  
 AC O96R00:  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)  
 DE 01-MAR-2003 (TREMBlrel. 23, last annotation update)  
 DR Protiogen.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catartini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21226193; PubMed=11327827;  
 RA Takayama T.K., Carter C.A., Deng T.;  
 RT "Activation of prostate-specific antigen precursor (pro-PSA) by  
 RT prostin, a novel human prostatic serine protease identified by  
 RT degenerate PCR."  
 RL Biochemistry 40:1679-1687(2001).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 DR EMBL: AF303046; AAK62813.1; -  
 DR HSSP: P00761; 1ANI.  
 DR MEROPS: S01.081; -  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR Pfam: PF00089; trypsin\_1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 KW Hydrolase; Protease; serine protease.  
 SW SEQUENCE 255 AA; 27986 MW; 00D5B79E1B49468F CRC64;

## Alignment Scores:

Pred. No.:	3.27e-50	Length:	255
Score:	679.00	Matches:	124
Percent Similarity:	66.53%	Conservative:	35
Best Local Similarity:	51.88%	Mismatches:	66
Query Match:	53.25%	Indels:	14
	4	Gaps:	3

US-09-856-320a-1\_COPY\_272\_958 (1-687) x Q96R00 (1-255)

```

OY 1 ATCATCAAGGGGTTTCGATGCAAGCTCACTCCAGCCCTGGCAGCAGCCCTGTTTCGAG 60
    ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 21 LeuLeuGlnLysAlaProLysValProHisSerGlnProTrpGlnAlaIleuLysGln 40
OY 61 AAGACCGGCTACTGTGTGGGGGAGCGCTCATCGCCCGCAGATGCTCTGACAGCAGCC 120
    ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 41 ArgGlyArgPheAsnGlyAlaSerLeuIleSerProHisTrpValIleuSerAlaIa 60
OY 121 CACTGCTCAAGCCCGCTACATAGTTCACTGTGGGGGAGCAGACCACTCCAGAGAGGAG 180
    ||||| ::||| ::|||:::|||||:::|||||:::|||||:::|||||
Db 61 HisCysGlnSerArgPheMetArgValArgLeuGlyGlnHisAsnLeuArgLysArgAsp 80
OY 181 GGGTGTGAGCAGACCCGAGACGCTGAGTCTTCCCGCCCGCGCTTCAACACAGC 240
    ||| ||||| |||||:::|||||:::|||||:::|||||:::|||||
Db 81 GlyProGlnGlnIleuArgThrThrSerArgValIleProHisProArgTyrGln----- 98
OY 241 CTCGCCCAACAACACCGCAATGACATATGCTGTGTAAGTGGCATGCCAGTCTCC 300
    ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 99 -----AlaArgSerHisArgAsnAspIleMetLeuLeuValGlnProAlaArg 116
OY 301 ATCACTGGGCTGTGGACCCCTCACCTCTCTCAAGCTGTGTACCTGTGTCAGTGGCAGCAG 360
    ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 117 LeuAsnProGlnValArgProAlaValLeuProThrArgCysArgProHisProGlyGlnAla 136
OY 361 TGGCTCATTTCCGCTGTGGGGGAGCAGCTC-----AGCCGC 396
    |||||:::|||||
Db 137 CysValValSerGlyTrpLysLeuValSerHisAsnGlnProGlyThrAlaLysSerPro 156
OY 397 -----CAGTTAGCCTGTGCTCAACCTTGCAGTGGGCCCAATCACTCAATTGAGCAG 450
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 157 ArgSerGlnValSerLeuProAspThrLeuHisCysAlaAsnIleGlyIleIleSerArg 176
OY 451 CAGAGTGTGAGAGACGCTTACCCGGGCAACATCAACAGACCACTGCTGTGTCAGGCTG 510
    |||||:::|||||

```



```

Db 177 ThSerCysAspLysSerTyrProGluYargLeuThrAsnThrMetValCysAlaGlyAla 196
QY 511 CAGGAAGGGGCGAAGACTCTGCCAGGAGTACTCCGGGGCCCTGTGGTGTAAACGAG 570
Db 197 GluGlyArgGlyAlaGlnSerCysGlnGlyAspSerGlyGlyProLeuValCysGlyGly 216
QY 571 TCTCTCAAGGCAATATATCTCTGGGGCCAGGATCCGTGGGATCACCCGAAGGCTGTG 630
Db 217 TleuGlnGlyIleValSerTyrPheLysPylProCysAspAsnThrThrLysProGly 236
QY 631 GTCTACAGAAAGTCTGCAATATGTGACTGTGATCCAGAGACATGAAGAAACAT 687
Db 237 ValTyrThrLysValCysHisTyrLeuGlnIleThrPheArgGluThrMetLysArgAsn 255

```

## RESULT 6

```

08CGR4 PRELIMINARY: PRT: 254 AA.
ID 08CGR4
AC 08CGR4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Prostlin.
GN KLR15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22325484; PubMed=12437987;
RA Olson A.Y., Lundwall A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus
RT musculus."
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M., Mural R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY152434; AAN78422.1; -.
SQ SEQUENCE 254 AA; 28042 MW; AA9E38BEBDD01861 CRC64;

```

## Alignment Scores:

```

Pred. No.: 3,98e-50 Length: 254
Score: 678.00 Matches: 124
Percent Similarity: 66.67% Conservative: 34
Best Local Similarity: 52.32% Mismatches: 65
Query Match: 53.18% Indels: 14
DB: 11 Gaps: 3

```

US-09-856-320A-1\_COPY\_272\_958 (1-687) x 08CGR4 (1-254)

```

QY 1 ATCATCAAGGGGTTGAGTGCAGACCTCACTCCAGCCCTGGAGAGCCCTGTTCGAG 60
Db 20 ValLeuGlnGlyGlnGlyValProHisSerGlnProThrGlnValAlaLeuPheGlu 39
QY 61 AAGACGGGCTACTCTGTGGGGCGAGCTCATGCCGCCAGATGGCTTCAGACAGCC 120
Db 40 ArgGlyArgPheAsnGlyAlaPheLeuIleSerProArgTyrValLeuThrAlaAla 59
QY 121 CAGTCCGTCAAGCCCGCTCATAGTTCACCTGGGGAGAGCAACCTCCGAAGAGAGAG 180
Db 60 HisCysGlnThrArgPheMetArgValArgLeuGlyGlnHisAsnLeuArgLysPheAsp 79
QY 181 GGGTTGAGAGAGAGCCGAGACGACATGATCTCCGCCAGCCCGGCTTCACAAAGAGC 240
Db 80 GlyProGlnGlnLeuArgSerValSerArgIleLeuProHisProGlyTyrGlu----- 97
QY 241 CTCGCCCAAGAGAGCCGAGATGACATCATGTGGTGAAGATGGATGGCCAGTGTCC 300
Db 98 -----AlaArgTyrThrHisArgHisAspIleMetLeuLeuArgLeuPheLysProAlaArg 115
QY 301 ATCACTGGGGTGGAGCCGCTGCTCTGACGCTGTGTGTCACATGGTGGGACAGAGC 360
Db 301 ATCACTGGGGTGGAGCCGCTGCTCTGACGCTGTGTGTCACATGGTGGGACAGAGC 360

```

```

Db 116 LeuThrAlaTyrValArgProValAlaLeuProArgArgCysProLeuIleGlyGlnAsp 135
QY 361 TGCCTCATTTTCGGGCTGGGGC-----AGCAGCTCCAGCCCC----- 396
Db 136 CysValValSerGlyTyrPheLeuSerSerPheAsnAsnProGlyAlaThrGlySerGln 155
QY 397 -----CAGTTACGGCTCTCACACCTTGGGAGAGCCGCAACATCATTGAGAGC 450
Db 156 LysSerHisValArgLeuProAspThrLeuHisCysAlaAsnIleSerIleLeuSerGlu 175
QY 451 CAGAAGTGTGAGAGAGCCCTACCCGGGCAACATCAGACAGACACATGGTGTGGCAGCTG 510
Db 176 AlaSerCysAsnLysAspTyrProGlyArgValLeuProThrMetValCysAlaGlyAla 195
QY 511 CAGGAAGGGGCGAAGACTCTGCCAGGAGTACTCCGGGGCCCTGTGGTGTAAACGAG 570
Db 196 GluGlyGlyGlyThrAspSerCysGlnGlyAspSerGlyGlyProLeuValCysGlyGly 215
QY 571 TCTCTCAAGGCAATATATCTCTGGGGCCAGGATCCGTGGGATCACCCGAAGGCTGTG 630
Db 216 AlaLeuGlnGlyIleValSerTyrPheLysPylProCysAspAsnThrThrLysProGly 235
QY 631 GTCTACAGAAAGTCTGCAATATGTGACTGTGATCCAGAGACATGAAG 681
Db 236 ValTyrThrLysValCysSerTyrLeuGlnIleThrPheArgGluAsnValArg 252

```

## RESULT 7

```

08CGR6 PRELIMINARY: PRT: 276 AA.
ID 08CGR6
AC 08CGR6;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Glandular kallikrein KLR13.
GN KLR13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22325484; PubMed=12437987;
RA Olson A.Y., Lundwall A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus
RT musculus."
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M., Mural R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY152432; AAN78420.1; -.
SQ SEQUENCE 276 AA; 30360 MW; 33E189C67492FDC4 CRC64;

```

## Alignment Scores:

```

Pred. No.: 1.46e-49 Length: 276
Score: 671.50 Matches: 119
Percent Similarity: 69.03% Conservative: 37
Best Local Similarity: 52.65% Mismatches: 69
Query Match: 52.67% Indels: 1
DB: 11 Gaps: 1

```

US-09-856-320A-1\_COPY\_272\_958 (1-687) x 08CGR6 (1-276)

```

QY 10 GGGTTGAGAGAGCCCTCACTCCAGCCCGGAGGAGCCCTGTTCGAGAAGAGCGG 69
Db 40 GlyTyrThrCysLeuProHisSerGlnProThrGlnAlaLeuLeuIleArgGlyArg 59
QY 70 CTACTGTGTGGGGGAGGAGCTCATGCGCCAGATGAGTGTCTGACAGAGCCAGTGGCTC 129
Db 60 LeuLeuGlyGlyGlyValLeuValHisProLysTyrValLeuThrAlaLeuHisCysArg 79
QY 130 AAGCCCGGTAACATAGTTCACCTGGGGGAGAGACACTCCAGAAAGAGAGGCTGTGAG 189
Db 130 AAGCCCGGTAACATAGTTCACCTGGGGGAGAGACACTCCAGAAAGAGAGGCTGTGAG 189

```





```

Query Match: 47,298 Indels: 6
DB: 11 Gaps: 2
US-09-856-320a-1_copy_272_958 (1-687) x O9CVR5 (1-250)

QY 1 ATCATCAAGGGGTTTCAGAGTCCAGTCCAGCCCTGGCAGAGCCCTGTTGAG 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 24 Iletlgluylgylrgrgysvalargasnserglprotrpnlvalalaaleuinala 43
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 AAGAGC-----CGGCTACTGTGTGGGAGCGAGCTGATCCGCCAGATGGCTGTGACA 114
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 44 GYrProglYhlsArghleucysglYglYvalleuenserprglntprvalIlethr 63
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 115 GCAGCCCATGCTCCAGAGCCCGGCTACATGTTCCAGTGGGAGCAGCAATCCAGAG 174
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 AlalaHlsCysAlaIrgPrroIleuHlsValAlaleuIlyshlsAsnIleArgArg 83
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 GAGAGGGGCTGTGAGCAGAGCCGAGCAGCCATGAGTCCCTCCAGCCCGGCTTAC 234
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 84 TrpGlualaIthrIngIlnValAlargValAlaIargGlValIProhIsProglntYrGl 103
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 235 AACAGCCTCCCAACAAAGACACCCGCAATGATCATGCTGTGGTGAAGATGGCATGCCA 294
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 104 -----ProglAlaHlsAspAsnAspIleuMetleuIyshlsleuIlnIyS 119
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 295 GTCTCATGACATGCTGGCTGTGAGCCCTGACCCCTGCTCATGCTGTGCTGCTGCTG 354
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 120 ValArgleuIylarglAlaValIyShrIleSerValAlaIaserSerCysAlaSerProglY 139
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 355 AACAGCTGCTCATTTCCGGCTGGGAGCAGACGTCCAGCCCATGATGCTGCTGCTGAC 414
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 140 ThrProCysArvalSerIyglYrIleAlaSerIleAlaAlaIyYrProthr 159
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 415 ACCTTGCGATGCGCCCAATCATGATGATGACACAGCAAGTGTGAGAACGCTTACCC 474
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 160 AlaIeugIlnCysValasnValasnlIleMetSerGlInAlaIyShlsArglAlaIyYrPro 179
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 475 GGCACATCAGACAGACACCATGTGTGTGCCAGGCTGACAGAGGGGAGCAAGACTGCTGC 534
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 180 GlyIleIleThrSerIyglYValIyAlaIyProIlnIyglYIySAspSerCys 199
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 535 CAGGCTGACATGCGGGGCGCTGCTGTGTGAACAGCTGTCAAGGATCATGCTGCTG 594
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 200 GlngIyAspSerIyglYrProIeuValIySglYglYlnIeuIlnIyValIySerTTP 219
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 595 GGCAGGATCCGTGTGCGATGACCCGAAAGCTGTGTGTACAGAAAGTGTGCATAAT 654
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 220 GlyMetGlInArgCysAlaMetProglYrIyProglYvalIyAlaIasnIeuCysAsnYr 239
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 655 GTGGACTGATCCAGAGAGCATGAAGAACAT 687
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 240 HlsSerTrpIleGlInArgThrMetGlInSerAsn 250
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
O9CVR5 PRELIMINARY: PRT: 234 AA.
AC O9CVR5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 2310008B01Rik protein (Fragment).
GN 2310008B01Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shindagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

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RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderrelli R., Barsh G.,
RA Blake J., Boiffelli D., Bojunga N., Carrinzi P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monhaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitlaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001)
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: AK009217; BAB26143.1; -.
DR HSSP: P00763; IDPO.
DR MEROPS: S01.020; -.
DR MGD: MGI:1916761; 2310008B01Rik.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: Pf00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYSPC; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
FT NON_TER
SQ
SEQUENCE 234 AA; 2588 MW; 6D81E609EDD39110 CRC64;

Alignment Scores:
Pred. No.: 3,47e-43 Length: 234
Score: 597.50 Matches: 108
Percent Similarity: 63.91% Conservative: 39
Best Local Similarity: 46.96% Mismatches: 78
Query Match: 46.86% Indels: 5
DB: 11 Gaps: 4

US-09-856-320a-1_copy_272_958 (1-687) x O9CVR5 (1-234)

QY 1 ATCATCAAGGGGTTTCAGAGTCCAGTCCAGCCCTGGCAGAGCCCTGTTGAG 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9 IletYrAsnIyglValIyCysValIySAsnSerGlProtrpnlvalIyglYeuPrhIs 28
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 AAGAGCGGCTACTGTGTGGGCGAGCGCTCATGCGCCCAAGATGCTCTGACAGCACC 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 29 GlyIySylrIleuArgIyCysglYglYValIleuValAspArgIyStrpValIleuThrAlaIa 48
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CACTGCTCAAGCCCGGCTCATGATGATGACCTTGGGCGAGCAGCAACCTCCAGAGAGAG 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 49 HlsCys---ArgAspIyStrpValIyAlargIleuGlYglIlnIleSerIeuThrIySAsp 67
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 GCGTGTGAGAGAGAGCCGAGCAGCATGAGTCTTCCGCCAGCCCGGCTTCAACAGAC 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 68 TrpThrIglInIleuArgIlnIshTrIhrPheserIleThrHlsProSerIyglInIyAla 87
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 CTCGCCAACAAGACAGCAGCAATGATCATGCTGTGTAAGATGGCATGCCAGTCTCC 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 88 TyrGlInAsn-----HlsIlnHlsAspIleuArgIleuArgIleuAsnIrgProIleHls 105
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 ATGACTGTGGCTGTGGAGCCCTGACACCTCTCTCTACAGCTGTGTACTGTGCTGACAGC 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 106 LeuThrArgAlaIyAlargProValAlaIeIeuProSerSerCysValIyThrIrgIyAlaMet 125
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 TGCCCTATTTCGCTGTGGGAGCAGCTGACAGCCCGGCTGAGTTCAGCTGCTGACAGCTTG 420
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 CysHlsValSerIyTrpIyTrpIyTrpIyTrpIyTrpIyTrpIyTrpIyTrpIyTrpIy 145
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 421 CGATGCGCCAAACATCATGATGAGCAGCAGAAAGTGTGAGAACGCTTACCCCGGCAAC 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 146 GlnGlyLeuAsnLeuSerThrValSerAsnGluThrCysArgAlaValAlaPheProGlyArg 165
QY 481 ATCAAGACACACCATGTTGTGTCAGAGCTGCAGAGAGGAGGAGAGGAGTCTGCGCAGGT 540
Db 166 ValThrGluAsnMetLeuCysAlaGly---GlyGluAlaGlyLysAspAlaCysGlnGly 184
QY 541 GACTCCGGGGGCGCTGTGCTGTGTACACAGTCTTCAAGGCATTATTCCTGGGGCCAG 600
Db 185 AsperGlyGlyProLeuValCysGlyLysValLeuGlnGlyLeuValSerTyrPheSer 204
QY 601 ---GATCCGTGTGGATCACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 657
Db 205 ValGlyProCysGlyGlnGlyLysGlyLysProGlyValTyrThrLysValCysLysTyrThr 224
QY 658 GACTGATCCAGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 687
Db 225 AsprThrLeuArgIleValIleArgAsnAsn 234

```

## RESULT 12

092LR9 PRELIMINARY; PRT; 246 AA.

```

AC 092LR9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Trypsinogen 16.
GN TRYGN16 OR TRYPSINOGEN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Balb/c;
RA Rowen L., Hood L.;
RT "Comparison between strains Balb/c and 129 in a region of the mouse T
RT cell receptor beta locus.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Balb/c;
RA MEDLINE-21103195; PubMed-11160223;
RA Chen F., Rowen L., Hood L., Rothenberg E.V.;
RT "Differential transcriptional regulation of individual TCR Vbeta
RT segments before gene rearrangement.";
RL J. Immunol. 166:1771-1780(2001).
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF107342; AAC79093.1; -
DR HSSP; P00763; IDPO.
DR MEROPS; S01.063; -
DR MGD; MGI:2148749; Trypnl6.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; Trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ HYDROLYASE 246 AA; 26134 MW; 34E173B18CA2F463 CRC64;

```

## Alignment Scores:

```

Pred. No.: 1 55e-42 Length: 246
Score: 590.00 Matches: 114
Percent Similarity: 63.76% Conservative: 32
Best Local Similarity: 49.78% Mismatches: 77
Query Match: 46.27% Indels: 6
DB: 11 Gaps: 3

```

US-09-856-320A-1\_COPY\_272\_958 (1-687) x 092LR9 (1-246)

```

QY 1 ATCAAGAGGGGTTGCAAGTCCAGGCTCCTCCAGCCCTGGCAGGAGCCCTGTTCCAG 60
Db 24 IleValGlyGlyTyrThrCysArgGluAsnSerValProTyrGlnValSerLeu---Asn 42
QY 61 AAGACGGCGGTACTGTGTGGGGCCAGGCTCATGCGCCCGAGATGGCTCTGCACAGACC 120
Db 43 SerGlyTyrHisPheCysGlyGlySerLeuIleAsnAspGlnTyrValValSerAlaIa 62
QY 121 CAGTCCCTCAGGCCCCGTACATAGTCACTGGGGGAGGAGCAACCTCCAGAGAGAG 180
Db 63 HisCysTyrLysTyrThrArgIleGlnValArgLeuGlyGluHisAsnIleAsnValLeuGlu 82
QY 181 GCGTGTGAGCAGACCCGAGCAGCAGTGTGCTTCCCGCCAGCCCGGCTTCAACAAAGC 240
Db 83 GlysAsnGluGlnPheIleAspAlaIaLysIleIleLysHisProAsnPheAsnArgLys 102
QY 241 CTCCCAACAAAGACCCAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
Db 103 ThrLeuAsn-----AsnAspIleMetLeuIleLysLeuSerSerProValThr 118
QY 301 ATCAAGCTGGGCTGTGCGACCCCTCAGCCTCTCCAGCTGTGATGCTGTGGCAGCAGC 360
Db 119 LeuAsnAlaArgValAlaThrValAlaLeuProSerSerCysAlaProAlaGlyThrGln 138
QY 361 TGCCATCATTCCTGGCTGGGGGAGCAGCTCAGACCCCGAGTACGCTGCTCAGACCTTG 420
Db 139 CysLeuIleSerGlyTyrGlyLysAsnThrLeuSerPheGlyValSerGluProAsnLeu 158
QY 421 CGATGCGCCCAACATCAGCATATGAGCAGCAGAGAGTGTGAGAAAGCCTACCCCGGCAAC 480
Db 159 GlnCysLeuAspAlaProLeuLeuProGlnAlaAspCysGlnAlaSerTyrProGlyLys 178
QY 481 ATCAAGACACACCATGTTGTGTCAGAGCTGCAGAGAGGAGGAGGAGGAGGAGGAGGAGT 540
Db 179 IleThrGlyAsnMetValCysAlaGlyPheLeuGlnGlyLysAspSerCysGlnGly 198
QY 541 GACTCCGGGGGCGCTGTGCTGTGTACACAGTCTTCAAGGCATTATTCCTGGGGCCAG 600
Db 199 AsperGlyGlyProValCysAsnGlyLeuGlnGlyIleValSerTyrPheLys 218
QY 601 GATCCGTGTGGATCACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db 219 Gly---CysAlaLeuProAspAsnProGlyValTyrThrLysValCysAsnTyrValAsp 237
QY 661 TGGAATCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687
Db 238 TrpIleGlnAspThrIleAlaIaAsn 246

```

## RESULT 13

090UK9 PRELIMINARY; PRT; 246 AA.

```

AC 090UK9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE TESP4 (0910001B19RIK protein) (Trypsinogen 9).
GN TC OR 0910001B19RIK OR TRYPSINOGEN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RA MEDLINE-99436155; PubMed-10506205;
RA Ohmura K., Kohno N., Kobayashi Y., Yamagata K., Sato S.,
RA Kashiwabara S., Baba T.;
RT "A homologue of pancreatic trypsin is localized in the acrosome of
RT mammalian sperm and is released during acrosome reaction.";
RL J. Biol. Chem. 274:29426-29432(1999).
RN [2]
RP SEQUENCE FROM N.A.

```



Best Local Similarity:	45.34%	Mismatches:
Query Match:	46.08%	Indels:
DB:	11	Gaps:



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Db      63  HiscysTyrIlysSerArgIleGlnValArgLeuGlyIuhHisnIleAsnValLeuGlu 82
QY      181  GGCTGTGAGACAGCCGGACAGCCACTGAGCTCCTCCGCCACCCCGGCTTCAACACAGC 240
Db      83  GlyAsnGlnGlnPheValAsnSerAlaLysIleIleLysHisProAsnPheAsnSerArg 102
QY      241  CTCCCAACAAAGAACACCGCAATGACATCATCTGTGTGAAGATGGCATGCCATGCTCC 300
Db      103  ThrLeuAsn-----AsnAspIleMetLeuIleLysLeuAlaSerProValThr 118
QY      301  ATCACCTGGCGCTGTGGACCCCTCACCCCTCCTCACGCTGTGTCACTGCTGGACACAGC 360
Db      119  LeuAsnAlaArgValAlaThrValAlaLeuProSerSerCysAlaProAlaGlyThrGln 138
QY      361  TGCCTCATTTCCGGCTGGGGGACAGCAGTCCAGCCCGCCAGTTACGCTGCTCACACCTTG 420
Db      139  CysLeuIleSerGlyTrpGlyAsnThrLeuSerPheGlyValAsnAsnProAspLeuLeu 158
QY      421  CGATGGCCCAACATCACCATCATTTGAGCACACAGAGTGTGAGAACGCTTACCCGGCAC 480
Db      159  GlnCysLeuAspAlaProLeuLeuProGlnAlaAspCysGlnAlaSerTyrProGlyLys 178
QY      481  ATCACAGACACCATGGGTGTGTGCCAGCGTGCAGAAAGGGGCAAGACATCCTGCCAGGT 540
Db      179  IleThrAsnAsnMetIleCysValGlyPheLeuGlnGlyIleLysAspSerCysGlnGly 198
QY      541  GACTCGGGGGCCCTCTGTGTGTAAACAGTCTTCAAGCATTAATCTCTGGGGCCAG 600
Db      199  AspSerGlyGlyProValValCysAsnGlyGlnLeuGlnGlyIleValSerTrpGlyTyr 218
QY      601  GATCCGTGTGGCATCACCCGAAAGCCTGTGTCTACACGAAAGTGTCAAAATATGTGGAC 660
Db      219  Gly---CysAlaLeuLysAspAsnProGlyValTyrThrLysValCysAsnTyrValAsp 237
QY      661  TGGATCCAGAGACGATGAAGAACAAT 687
Db      238  TrpIleGlnAsnThrIleAlaAlaAsn 246
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Search completed: October 15, 2003, 20:25:43  
Job time : 51.1708 secs



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 15, 2003, 17:34:35 ; Search time 11.0583 Seconds  
(without alignments)  
5843.068 Million cell updates/sec

Title: US-09-856-320A-1\_COPY\_272\_958  
Perfect score: 1275  
Sequence: 1 atcacaaggggttcagtg.....aggagacagtaagaacaat 687

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 255726

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+n2p.model -DEV=xlp  
-O=/cgn2.1/USPTO\_spool\_P/US09856320/runat\_15102003.105639.8511/app\_query.fasta.1.2318  
-DB=SwissProt.41 -OEMT=faetan -SUFFIX=esp -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human4.0.cdi -LIST=45  
-NOALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFILE=plc -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09856320.ecgn.1.1.32.etrnat.15102003.105639.8511 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPHLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7  
Database : SwissProt.41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	1258	98.7	250	1	KLKB_HUMAN	Q9ubx7 homo sapien
2	736	57.7	250	1	KLK9_HUMAN	Q9ukg9 homo sapien
3	687	53.9	260	1	NRPN_RAT	O88780 rattus norv
4	684	53.6	260	1	NRPN_MOUSE	O91955 mus musculu
5	682	53.5	256	1	KLKE_HUMAN	O91255 homo sapien
6	681	53.4	260	1	KLK8_HUMAN	O60259 homo sapien
7	677.5	53.1	277	1	KLKD_HUMAN	O9u4t3 homo sapien
8	644.5	50.5	293	1	KLK5_HUMAN	O9y337 homo sapien
9	621	48.7	251	1	KLKE_HUMAN	O9p0g3 homo sapien
10	606	47.5	248	1	KLKC_HUMAN	O9ukr0 homo sapien
11	605.5	47.5	261	1	KLK7_RAT	P00758 rattus norv
12	600.5	47.1	261	1	KLK7_MOUSE	P36373 rattus norv
13	595.5	46.7	261	1	KLK3_MOUSE	P00756 mus musculu
14	594	46.6	248	1	TRX3_CHICK	O90629 gallus gall
15	591.5	46.4	263	1	KLKR_PRANA	P32824 priamus nat
16	591	46.4	246	1	TRX2_RAT	P00763 rattus norv
17	588	46.1	238	1	TRY3_SALSA	P35033 salmo salar
18	587	46.0	246	1	TRY1_RAT	P00762 rattus norv

19	585.5	45.9	261	1	KLK8_RAT	P36374 rattus norv
20	581.5	45.6	261	1	KLK2_RAT	P26376 rattus norv
21	577.5	45.3	259	1	KLK2_HUMAN	P20151 homo sapien
22	577.5	45.3	261	1	KLK9_MOUSE	P15949 mus musculu
23	577	45.3	231	1	TRYP_PIG	P00761 sus scrofa
24	577	45.3	244	1	KLK6_HUMAN	O92876 homo sapien
25	571	44.8	246	1	TRX2_MOUSE	P07146 mus musculu
26	570.5	44.7	246	1	KLK_PIG	P00752 sus scrofa
27	568	44.5	247	1	TRX2_CANFA	P06877 canis faml
28	567.5	44.5	259	1	TRX2_RAT	P00759 rattus norv
29	566.5	44.4	261	1	KLK1_MOUSE	P15947 mus musculu
30	564.5	44.3	244	1	KLK6_RAT	P36375 rattus norv
31	564.5	44.3	261	1	KLK6_MOUSE	P00755 mus musculu
32	564	44.2	243	1	TRX1_BOVIN	P00760 bos taurus
33	562	44.1	262	1	KLK1_HUMAN	O90627 gallus gall
34	561	44.0	248	1	TRX1_CHICK	O07272 macaca fasc
35	557	43.7	244	1	TRX2_XENLA	P19799 xenopus lae
36	557	43.7	248	1	TRX2_CHICK	O90628 gallus gall
37	556.5	43.6	257	1	KLK1_MACFA	P15946 mus musculu
38	556.5	43.6	261	1	KLKB_MOUSE	P19799 xenopus lae
39	556	43.6	243	1	TRX1_XENLA	O29463 bos taurus
40	556	43.6	247	1	TRX2_BOVIN	P08426 rattus norv
41	553	43.4	247	1	TRX3_RAT	P35032 salmo salar
42	552.5	43.3	231	1	TRY2_SALSA	P12788 rattus norv
43	552.5	43.3	247	1	TRY4_RAT	P00757 mus musculu
44	552	43.3	256	1	KLK4_MOUSE	P12323 cavia porce
45	551.5	43.3	239	1	KLK2_CAVPO	

## ALIGNMENTS

RESULT 1  
ID KLKB\_HUMAN STANDARD; PRT; 250 AA.  
AC Q9UBX7; O75837; O9N565;  
DT 16-OCT-2001 (rel. 40; Created)  
DT 16-OCT-2001 (rel. 40; Last sequence update)  
DE 15-SEP-2003 (rel. 42; Last annotation update)  
DE Kallikrein 11 precursor (EC 3.4.21.-) (Hippostasin) ("trypsin-like  
protease").  
GN KLK11 OR PRSS20 OR TLSP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
ON NCBI\_TaxID=9606;  
RX [1]  
RP TISSUE=Hippocampus; (ISOFORM 1).  
RX MEDLINE=98438738; PubMed=9765601;  
RA Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;  
RT "CDNA cloning and expression of a novel serine protease, TLSP.\*";  
RL Biochim. Biophys. Acta 1399:225-228(1998).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Hippocampus, and Prostate;  
RX MEDLINE=20130117; PubMed=10662248;  
RA Mitsui S., Yamada T., Okui A., Komitani K., Uemura H., Yamaguchi N.;  
RT "A novel isoform of a kallikrein-like protease, TLSP/Hippostasin,  
RT (PRSS20), is expressed in the human brain and prostate.\*";  
RL Biochem. Biophys. Res. Commun. 272:205-211(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=20130117; PubMed=10662248;  
RA Yousef G.M., Scorilas A., Diamandis E.P.;  
RT "Genomic organization, mapping, tissue expression, and hormonal  
RT regulation of trypsin-like serine protease (TLSP PRSS20), a new  
RT member of the human kallikrein gene family.\*";  
RL Genomics 63:86-96(2000).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=20510030; PubMed=11054574;  
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,  
RA Moss P., Paepel B., Wang K.;

\*Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.\*  
 RT Gene 257:119-130(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Iamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,  
 RA Burkhardt-Schulz K., Gordon L., Dias J., Ramirez M., Stiliwgen S.,  
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Barnes J.,  
 RA Dangnan L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S.,  
 RA Andreise T., Trankheim M., Altix C., Amico-Keller G., Coefield J.,  
 RA Dares S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
 RA Olsen A.S., Carrano A.V.,  
 RT \*Sequence analysis of chromosome 19q13.4.\*  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 RP [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE-Testis;  
 RX MEDLINE-22388257; PubMed-12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedlin T.B., Toshlyuk S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L., Hulys S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,  
 RA Schnerker A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT \*Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.\*  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: POSSIBLE MULTIFUNCTIONAL PROTEASE. EFFICIENTLY CLEAVES  
 CC B2-PHE-ARG-4-METHYLCOUMARYL-7-AMIDE, A KALLIKREIN SUBSTRATE, AND  
 CC WEAKLY CLEAVES OTHER SUBSTRATES FOR KALLIKREIN AND TRYPSIN.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named Isoforms-2;  
 CC Name-1;  
 CC IsoId=Q9UBX7-1; Sequence-Displayed;  
 CC Name-2;  
 CC IsoId=Q9UBX7-2; Sequence-VSP\_005402;  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKIN AND PROSTATE. ISOFORM  
 CC 1 IS EXPRESSED PREFERENTIALLY IN BRAIN; ISOFORM 2 IN PROSTATE.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AB012917; BAA33404.1; ALT\_INIT.  
 DR EMBL: AB013730; BAA8713.1; -  
 DR EMBL: AB041036; BAA96797.1; -  
 DR EMBL: AF164623; AAD47815.1; -  
 DR EMBL: AF243527; AAG33364.1; -  
 DR EMBL: AC011473; AAG23257.1; -  
 DR EMBL: BC022068; AAH22068.1; -  
 DR HSSP: P00763; IDPO.  
 DR MEROPS: S01.257; -  
 DR Genew: HGNC:6359; KLIK1.  
 DR MIM: 604434; -  
 DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR001254; Ser\_protease TRY.  
 DR Pfam: PF00089; trypsin.1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRY\_PPC.1.  
 DR PROSITE: PSS0240; TRYPSIN\_DOM.1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS.1.  
 DR PROSITE: PS00135; TRYPSIN\_SER.1.  
 KW Hydrolyase; Serine protease; Glycoprotein; Signal; Zymogen;  
 KW Alternative splicing.  
 FT SIGNAL 1  
 FT PROPEP 19 21  
 FT CHAIN 22 250  
 FT ACT\_SITE 62 62  
 FT ACT\_SITE 110 110  
 FT ACT\_SITE 203 203  
 FT DISULFID 28 163  
 FT DISULFID 47 63  
 FT DISULFID 135 237  
 FT DISULFID 142 209  
 FT DISULFID 174 188  
 FT DISULFID 199 224  
 FT CARBOHYD 99 99  
 FT CARBOHYD 165 165  
 FT CARBOHYD 181 181  
 FT CARBOHYD 210 210  
 FT VARSPLIC 1  
 SQ SEQUENCE 250 AA; 27466 MW; 192D910DBCC7A56 CRC64;  
 FT  
 FT  
 Alignment Scores:  
 Pred. No.: 1e-80 Length: 250  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.67% Indels: 0  
 DB: 1 Gaps: 0  
 US-09-856-320a-1\_copy\_272\_958 (1-687) x KLRB\_HUMAN (1-250)  
 QY 1 ATCATCAAGAGGAGTTCAGATGCAAGCCCTCACTCCAGCCCTGGAGAGCCCTGTTGAG 60  
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 Db 22 ILELEISGLYHEGLUCYSYSPROHISSEGLINPROTRPGLNLALEUPLHEGLU 41  
 |||||  
 QY 61 AAGAGCGGCTACTGTGTGGGGGAGCGCTAGCCGCCAGATGCTCTGACAGCACC 120  
 |||||  
 Db 42 LYSTHRAIGLEULEUCYSGLYALATHREULELALAPROAIGTRPLEUPLHIALA 61  
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 QY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGAGACACAACTCCGAAGAGAG 180  
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 Db 62 HISCYSLEUYSPROAIGTRYILEVALHISLEUGLYGLNHISANLEUGINTLYSGLU 81  
 |||||  
 QY 181 GGCTGTAGAGAGACCGGAGAGCAGTCTCCGCCAGCCCGGCTTCACACAGC 240  
 |||||  
 Db 82 GLYCSEGLUINTHRAIGTRHIALATHGLISERPHEROHISPROGLYPIHESANHSER 101  
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 QY 241 CTCGCCCAAGAACAGCAGCCGAATGACATCATCTGCTGAAGATGACATGCTCC 300  
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 Db 102 LEUPROASNLYSPHISAPHSAGHANAAPRIEMETLEUVALYSMETLASSERPROVALSER 121  
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 QY 301 ATGACCTGGGCTGTGCACCCCTACCCCTCTCTCAACGCTGTGTCACCTGTGGACACAG 360  
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 Db 122 ILETHTRPALVALAARGPROLEUPLHLEUSERSERARGYSVALTHRALAGLYTHSER 141  
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 QY 361 TGGCTATTTCCGGCGGGGAGACAGTCCAGGCCCAAGTACGCTGCTCCACACTTG 420  
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 Db 142 CYSLEULESERGLYTRPGLYSERTHNSETPRGIMLEUARGLEUPROHISITRLEU 161  
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 QY 421 CGATGGCCCAATCATCATCATGAGACACAAAGTGTGAGAAAGCCCTACCCGGGCAAC 480  
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 Db 162 ARGCYALASNLNLEHRIELLEGLHISGLINLYSCYSGLUSNLALEYTRPCOGLYAN 181  
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 QY 481 ATGACAGACACCATGGTGTGTGCCAGCGGTGCAGAAAGGGGACAGACTCTCCAGCGT 540





ID NRPN\_MOUSE STANDARD: PRT: 260 AA.  
AC 061955;  
DR 15-JUL-1999 (Rel. 38, Created)  
DR 15-JUL-1999 (Rel. 38, Last sequence update)  
DR 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuropeptide precursor (EC 3.4.21.-) (NP) (Kallikrein 8).  
GN KIK8 OR PRS19 OR NRPN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BALB/c; TISSUE-Hippocampus;  
RX MEDLINE=95348817; PubMed=7623137;  
RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,  
RA Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;  
RT "Expression and activity-dependent changes of a novel limbic-serine  
RT protease gene in the hippocampus.";  
RL J. Neurosci. 15:5088-5097(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;  
RT "Cloning and assignment of mouse neuropeptide gene, prs19 to chromosome  
RT 7B4.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.  
RC STRAIN-BALB/c; TISSUE-Brain;  
RX MEDLINE=98225202; PubMed=9556608;  
RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,  
RA Shiosaka S., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;  
RT "Characterization of recombinant and brain neuropeptide, a  
RT plasticity-related serine protease.";  
RL J. Biol. Chem. 273:11189-11196(1998).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.  
RC TISSUE-Hippocampus;  
RX MEDLINE=99134351; PubMed=9933620;  
RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,  
RA Shiosaka S., Hakoshima T.;  
RT "Crystal structure of neuropeptide, a hippocampal protease involved in  
RT kindling epileptogenesis.";  
RL J. Biol. Chem. 274:4220-4224(1999).  
CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND  
CC HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST  
CC FIBRONECTIN.  
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-,  
CC -1- ENZYME REGULATION: STRONGLY INHIBITED BY DIISOPROPYL  
CC FLUOROPHOSPHATE, LEUPEPTIN AND (4-AMIDINOPHENYL)METHANESULFONYL 1-  
CC FLUORIDE.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE LIMBIC SYSTEM OF  
CC MOUSE BRAIN AND IS LOCALIZED AT HIGHEST CONCENTRATION IN PYRAMIDAL  
CC NEURONS OF THE HIPPOCAMPAL CA1-3 SUBFIELDS.  
CC -1- MASS SPECTROMETRY: MW-26613; METHOD-MALDI; RANGE-29-260.  
CC -1- MASS SPECTROMETRY: MW-26229; METHOD-MALDI; RANGE-33-260.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL: D30785; BA06451.1; -  
DR EMBL: AB032202; BAA92435.1; -  
DR PIR: I56559; I56559.  
DR PDB: INPM; 23-MAR-99.  
DR MEROPS: S01.244; -  
DR MGD: MGI:892018; KIK8.

DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR001254; Ser-protease\_Try.  
DR Pfam: PF00089; trypsin\_1.  
DR PRINTS: PR00722; CHYMOTRYPSIN.  
DR SMART: SM00020; TRYP\_SPC; 1.  
DR PROSITE: PS00240; TRYPIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPIN\_HIS; 1.  
DR PROSITE: PS00135; TRYPIN\_SER; 1.  
KW Hydrolase; Serine protease; Glycoprotein; zymogen; signal;  
KW 3D-structure.  
FT SIGNAL. 1 28  
FT PROPEP 29 32  
FT CHAIN 33 260  
FT ACT\_SITE 73 73  
FT ACT\_SITE 120 120  
FT ACT\_SITE 212 212  
FT DISULFID 39 173  
FT DISULFID 58 74  
FT DISULFID 145 246  
FT DISULFID 152 218  
FT DISULFID 184 198  
FT DISULFID 208 233  
FT CARBOHYD 110 110  
FT STRAND 34 34  
FT STRAND 37 38  
FT TURN 41 42  
FT TURN 45 46  
FT STRAND 52 52  
FT TURN 53 54  
FT STRAND 55 64  
FT TURN 65 66  
FT STRAND 67 70  
FT STRAND 72 74  
FT HELIX 80 83  
FT STRAND 87 87  
FT TURN 88 89  
FT STRAND 96 98  
FT STRAND 100 105  
FT TURN 107 108  
FT TURN 114 115  
FT TURN 118 119  
FT STRAND 122 126  
FT STRAND 140 141  
FT TURN 148 149  
FT STRAND 151 156  
FT STRAND 170 170  
FT STRAND 172 178  
FT HELIX 181 187  
FT TURN 189 191  
FT TURN 194 195  
FT STRAND 196 200  
FT TURN 202 203  
FT STRAND 206 206  
FT TURN 209 210  
FT TURN 212 213  
FT STRAND 215 218  
FT TURN 219 220  
FT STRAND 221 228  
FT STRAND 235 235  
FT TURN 236 237  
FT STRAND 238 238  
FT STRAND 240 244  
FT HELIX 245 256  
SQ SEQUENCE 260 AA; 28523 MW; B55F6BEB37CD60E CRC64;  
Alignment Scores:  
Pred. No.: 1.21e-40  
Score: 684.00 Length: 260  
Percent Similarity: 68.42% Matches: 121  
Best Local Similarity: 53.07% Conservative: 35  
Query Match: 53.65% Mismatches: 70  
DB: 1 Indels: 2  
Gaps: 2

[illegible]

RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McNulty J.,
RA	Moss P., Paepker B., Wang K.;
RT	"Sequencing and expression analysis of the serine protease gene
RT	cluster located in chromosome 19q13 region.";
RL	Gene 257:119-130(2000).
RM	[3]
RP	PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RX	MEDLINE=94289486; PubMed=8018728;
RA	Dihanch M.E., Spiess M.;
RL	"A novel serine proteinase-like sequence from human brain.";
Biochim. Biophys. Acta 1218:225-228(1994).	
CC	-1- FUNCTION: Protease whose physiological substrate is not yet known.
CC	-1- SUBCELLULAR LOCATION: Secreted (Probable).
CC	-1- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named Isoforms=4;
CC	Name=1;
CC	IsoId=Q9H2R5-1; Sequence=Displayed;
CC	Name=2;
CC	IsoId=Q9H2R5-2; Sequence=VSP_005405;
CC	Name=3;
CC	IsoId=Q9H2R5-3; Sequence=VSP_005406, VSP_005407;
CC	Name=4;
CC	IsoId=Q9H2R5-4; Sequence=VSP_005404;
CC	-1- TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also
CC	expressed in the prostate, salivary, and adrenal glands and in the
CC	colon testis and kidney.
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC	-----
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; AF242195; AACG9469.1; -
DR	EMBL; AF242195; AAG09470.1; -
DR	EMBL; AF242195; AAG09471.1; -
DR	EMBL; AF242195; AAG09472.1; -
DR	EMBL; AF243527; AAG33354.1; -
DR	EMBL; X75363; CAA53145.1; ALT_SEQ.
DR	HSSP; P00763; IDPO.
DR	MEROPS; S01.081; -
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR	InterPro; IPR001314; Chymotrypsin.
DR	InterPro; IPR001254; Ser_protease_Try.
DR	Pfam; PF00089; trypsin; 1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	PROSITE; PS50240; TRYPSIN_DOM: 1.
DR	PROSITE; PS00134; TRYPSIN_HIS: 1.
DR	PROSITE; PS00135; TRYPSIN_SER_FALSE_NEG.
KW	Hydrolase; Serine protease; Glycoprotein; Signal; Zymogen;
KW	Alternative splicing.
KW	SIGNAL
FT	PROPEP 17 16
FT	ACTIVATION PEPTIDE (POTENTIAL).
FT	KALLIKREIN 15.
FT	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	Missing (in isoform 4).
FT	/FtId=VSP_005404.
FT	Missing (in isoform 2).
FT	/FtId=VSP_005405.
FT	V -> G (in isoform 3).
FT	/FtId=VSP_005406.
FT	Missing (in isoform 3).
FT	/FtId=VSP_005407.
FT	SHNPGVAGSPRSQ -> PLSSP (IN REF. 2).
FT	CONFLICT 147 160

SQ SEQUENCE 256 AA; 28087 MM; B5EBF8D6022786B5 CRC64;  
 Alignment Scores:  
 Pred. No.: 1.67e-40 Length: 256  
 Score: 682.00 Matches: 124  
 Percent Similarity: 66.95% Conservative: 36  
 Best Local Similarity: 51.88% Mismatches: 65  
 Query Match: 53.49% Indels: 14  
 DB: 1 Gaps: 3

US-09-856-320A-1\_COPY\_272\_958 (1-687) x KLF\_HUMAN (1-256)  
 OY 1 ATCATCAAGGGTTGATGAGAGCCCTACATCCCGCCCTGGACAGACCCCTGTTCAG 60  
 DB 22 LeuLeuGluGlyAspGlyCysAlaAlaProHisSerGlnProGlnValAlaLeuGlyGlu 41  
 OY 61 AAGAGCGGCTACTCTGTGGGCGAGCGCTACGCCCCAGATGGCTCTGACAGCAGCC 120  
 DB 42 ArgGlyArgPheAsnGlyAlaSerLeuIleSerProHisTrpValLeuSerAlaAla 61  
 OY 121 CACTGCTCAAGCCCCGCTACATAGTTCACCTGGGCGAGCAGACCTCCAGAGAGAG 180  
 DB 62 HisCysGlnSerArgPheMetArgValArgLeuGlyGlnHisAsnLeuArgLysArgSp 81  
 OY 181 GGGCTGAGCAGAGCCCGCAGCAGCTGATGCTCCCGCCCGCCGCTTCACAGCAGC 240  
 DB 82 GlyProGluGlnLeuArgThrThrSerArgValIleProHisProArgLysGlu----- 99  
 OY 241 CTCCCAACAAGACACCGCATGATGATGCTGGTGAAGATGATGATGATGATGATGAT 300  
 DB 100 -----AlaArgSerHisArgAsnHisPheMetLeuLeuArgLeuValGlnProAlaArg 117  
 OY 301 ATCACTGGCTGTGGCGAGCCCTACCTCTCTCCAGCTGTGTCATGCTGGCAGCAGC 360  
 DB 118 LeuAsnProGlnValArgProAlaValLeuProThrArgCysProHisProGlyGluAla 137  
 OY 361 TGCCCATTCGCGCTGGGCGAGCAGCAGC-----AGCCCC 396  
 DB 138 CysValValSerGlyTyrGlyLeuValSerHisAsnGlnProGlyThrAlaGlySerPro 157  
 OY 397 -----CAGTTAGCGCTGCTACACCTTGGAGATGCGGCAACATCACCATGATGAGCAG 450  
 DB 158 ArgSerGlnValSerLeuProAspPheThrLeuHisCysAlaAsnIleSerIleLeuSerSp 177  
 OY 451 CAGAAAGTGTGAAGAGCCCTACCCCGGAGCATCACAGACACCATGCTGTGCGAGCGTG 510  
 DB 178 ThrSerCysAspLysSerTyrProGlyArgLeuThrAsnThrMetValCysAlaGlyAla 197  
 OY 511 CAGGAGGGGGGAGAGCTGCTGCGAGGAGTCCCGGGGCGCCCTGCTGTGAACAG 570  
 DB 198 GluGlyArgGlyAlaGlySerCysGlnGlyAspSerGlyGlyProLeuValCysGlyGly 217  
 OY 571 TCTCTCAAGGATATATCTCTGGGAGGAGATCCGTGCGATCACCAGGAGAGCTGTG 630  
 DB 218 IleLeuGlnGlyIleValSerTyrGlyAspValProCysAspAsnThrThrLysProGly 237  
 OY 631 GTCTACACGAAAGTCTGCAATATAGTGAGCTGATTCAGAGAGCAGATGAGAGACAT 687  
 DB 238 ValTyrThrLysValCysHisTyrLeuGlnIleThrIleArgGluThrMetLysArgAsn 256

RESULT 6  
 KLF\_HUMAN STANDARD; PRT; 260 AA.  
 AC 060259; Q9HCB3; Q9UUL9; Q9UQ47;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neutropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Ovacin) (Serine  
 DE protease TADG-14) (tumor-associated differentially expressed gene-14  
 DE protein).  
 GN KLF8 OR PRSS19 OR TADG14 OR NRPN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE-Hippocampus;  
 RX MEDLINE=96372070; PubMed=9714609;  
 RA Yoshida S., Taniguchi K., Hirata A., Shiosaka S.;  
 RT "Sequence analysis and expression of human neutropsin cDNA and gene.";  
 RL Gene 213:9-16(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE-Brain;  
 RX MEDLINE=99203457; PubMed=10102990;  
 RA Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;  
 RT "A novel form of human neutropsin, a brain-related serine protease, is  
 RT generated by alternative splicing and is expressed preferentially in  
 RT human adult brain.";  
 RL Eur. J. Biochem. 260:627-634(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE-Ovary;  
 RX MEDLINE=99413504; PubMed=10485494;  
 RA Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,  
 RA O'Brien T.J.;  
 RT "Cloning of tumor-associated differentially expressed gene-14, a novel  
 RT serine protease overexpressed by ovarian carcinoma.";  
 RL Cancer Res. 59:4435-4439(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Gan L., Gellinas R., Gown A.M., Moss P., Smith R., Wang K.;  
 RT "Molecular cloning and characterization of a novel serine protease,  
 RT ovacin, a potential molecular marker for ovarian carcinomas.";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=20510030; PubMed=11054574;  
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,  
 RA Moss P., Paepfer B., Wang K.;  
 RT "Sequencing and expression analysis of the serine protease gene  
 RT cluster located in chromosome 19q13 region.";  
 RL Gene 257:119-130(2000).  
 RN [6]  
 RP SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).  
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,  
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Barnes J.,  
 RA Dangnan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,  
 RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Cosfield J.,  
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,  
 RA Ariellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
 RA Olsen A.S., Carraro A.V.;  
 RT "Sequence analysis of chromosome 19q13.4.";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND  
 CC HIPPOCAMPAL PLASTICITY.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=060259-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=060259-2; Sequence=VSP\_005401;  
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS PREDOMINANTLY EXPRESSED IN THE  
 CC PANCREAS WHILE ISOFORM 2 IS EXPRESSED IN ADULT BRAIN AND  
 CC HIPPOCAMPUS. BOTH FORMS ARE ALSO FOUND IN FETAL BRAIN AND  
 CC PLACENTA. NOT DETECTED IN KIDNEY, SPLEEN, LIVER AND LUNG.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.  
 CC -----  
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CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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CC -----
DR EMBL: AF135024; AAD26425.2; -.
DR EMBL: AC011473; AAG23259.1; -.
DR EMBL: AL050220; CAB43320.1; ALT_INIT.
DR HSSP: P00763; IDPO.
DR MEROPS: S01.306; -.
DR Genew: HGNC:6361; KIK13.
DR MIM: 605505; -.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro: IPR001254; Ser_protease_1ry.
DR SMART: PF00089; trypsin; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KM Hydrolyse: Serine protease; Glycoprotein; Signal.
FT SIGNAL 1 16
FT CHAIN 17 277
FT ACT_SITE 76 76 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 124 124 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 218 218 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 42 178
FT DISULFID 61 77 BY SIMILARITY.
FT DISULFID 157 224 BY SIMILARITY.
FT DISULFID 189 203 BY SIMILARITY.
FT DISULFID 214 239 BY SIMILARITY.
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 170 180 VNPPTLOCAN -> GMPHPRPEAP (IN REF. 3).
SQ SEQUENCE 277 AA; 30570 MW; BA8A9B8DCFB5D542 CRC64;

Alignment Scores:
Pred. No.: 3.45e-40 Length: 277
Score: 677.50 Matches: 120
Percent Similarity: 71.56% Conservative: 41
Best Local Similarity: 53.33% Mismatches: 63
Query Match: 53.14% Indels: 1
DB: 1 Gaps: 1

US-09-856-320a-1_COPY_272_958 (1-687) x KIKD_HUMAN (1-277)
OY 10 GGGTTCGAGTCAAGCCCTACCTCCAGCCCTGGCAGGCGCCCTTTCCGAGAGACGGCG 69
DB 39 GLYTYRHCYSRPHRPHISERGLNPRGRLNALALALEUVALGLNGLYARG 58
OY 70 CTACTCTGTGGGGGAGCCCTGATGCCCCAGATGGCTCCCTGACAGAGCCCATGCTGC 129
DB 59 LEUUCYSGLYGLYVALLEUVALHISPROLYSTRVALLEUTHALALAHISCYSLAU 78
OY 130 AAGCCCGCCTACATGATGTCACCTGGGAGGAGCAACATCCAGAAAGGAGAGGGCTGTAG 189
DB 79 LYSGLUGLYLEUVALTYRLEUVALYHISALALEUVALGLYVALGLNALAGLYGLU 98
OY 190 CAGACCCGCGACGACCTAGTCTCCGCCACCCCGGCTTCAACACAGCCCTCCCAAC 249
DB 99 GLNVALARGGLVALVALHISERLEPRHISPROGLYRGLARGYSEPRROTHRHS 118
OY 250 AAGACACCCGCAATGACATGCTGGTGAAGATGCGATCGACAGCTCATCATCAGCTGG 309
DB 119 LEUASNHSASRHSASRHSASRHSASRHSASRHSASRHSASRHSASRHSASRHSASRHS 138
OY 310 GCTGGGAGCCCTCACCCCTGCC--TCACGCTGTGTCATGCTGGGAGACACAGCCCTC 366
DB 310 GCTGGGAGCCCTCACCCCTGCC--TCACGCTGTGTCATGCTGGGAGACACAGCCCTC 366

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DB 139 TYRILEGLNTHLEUPROLEUSERHISASNAARGLEUTHPRGGLYTHRTHRCYSARG 158
OY 367 APTTCGGCTGGGAGCAGCATGTCACGCCCGCTACGCTGCTCACACCTTGGGATGC 426
DB 159 VALSERGLYTRPGLYTHRTHRTHRTHRTHRTHRTHRTHRTHRTHRTHRTHRTHRTH 178
OY 427 GCCAACATCACCATCATTTGATGAGCACGAGAGTGTGAAAGCCCTACCCCGGCAACATCA 486
DB 179 ALAASNILEGLNLEUARGSERASPGIUGLYCYSARGIUNVALTYRPROGLYSLIETHR 198
OY 487 GACACCATGCTGTGTGCCACGCTGACGAGAGGGGGCAGAGACTCTGCGCAGGTCATCC 546
DB 199 ASPASNMELEUCYALAGLYTHRISGLUGLYLYSASPSEPCYSGIUNGLYASPSER 218
OY 547 GGGGCGCTCTGTGTGTATACCATGCTGTCAAGGCAATATCTCTGGGGCCAGGATCCG 606
DB 219 GLYGLYPROLEUVALCYASNARGHTRHREUVALYGLIILEVALSERTRPGLYASPHRPO 238
OY 607 TGTGCGATCACCCGAAAGCTGTGTACACGAAAGTCTGCAATATGTCAGTCGATC 666
DB 239 CYSGLYINPROASPARGPROGLYVALTYRTHARVALSERARGTYRVALLEUTHRILE 258
OY 667 CAGGAGAGGANGAAG 681
DB 259 ARGGLUTHRILEARG 263

RESULT 8
KIK5_HUMAN
ID KIK5_HUMAN STANDARD; PRT; 293 AA.
AC Q9Y337; O9HBG8;
DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 15-SEP-2003 (rel. 42, Last annotation update)
DE Kallikrein 5 precursor (EC 3.4.21.-) (Stratum corneum tryptic enzyme)
GN (Kallikrein-like protein 2) (KIK-L2).
OS KIK5 OR SCLT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP TISSUE=Stratum corneum;
RC MEDLINE=99445563; PubMed=10514489;
RA Britsland M., Egelund T.;
RT "Purification, molecular cloning, and expression of a human stratum
RT corneum trypsin-like serine protease with possible function in
RT desquamation.";
RL J. Biol. Chem. 274:30033-30040(1999).
RN [2]
RP TISSUE=Stratum corneum;
RC MEDLINE=20118156; PubMed=10652563;
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome
RT 19q13.3-q13.4.";
RL Anticancer Res. 19:2843-2852(1999).
RN [3]
RP TISSUE=Stratum corneum;
RC MEDLINE=20510030; PubMed=11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McQuaig J.,
RA Moss P., Faerber B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [4]
RP TISSUE=Ovary;
RC MEDLINE=22388257; PubMed=12477932;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Mak S.I., Wang J., Hsieh F.,
RA Dlatchenko L., Marusina K., Farmer A.A., Rudin G.M., Hong L.,

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RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=20118156; PubMed=10652563;  
RA Tousef G.M., Luo L.-Y., Diamandis E.P.;  
RT "Identification of novel human kallikrein-like genes on chromosome  
19q13.3-q13.4.";  
RL Anticancer Res. 19:2843-2852(1999).  
RN  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RA Tousef G.M., Magkara A., Scorilas A., Diamandis E.P.;  
RT "Cloning of new alternatively spliced forms of the kallikrein-like  
gene 5 (KLK-15).";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN  
[3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=20510030; PubMed=11054574;  
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McNally J.,  
Moss P., Paepker B., Wang K.;  
RT "Sequencing and expression analysis of the serine protease gene  
cluster located in chromosome 19q13 region.";  
RL Gene 257:119-130(2000).  
RN  
[4]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RA Lamedin J.E., McCready P.M., Skowronski E., Viswanathan V.,  
Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
Pan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,  
Danganan L., Ertler A., Christensen M., Georgescu A., Ayala J., Liu S.,  
Andrzejewski T., Frankheim M., Attix C., Amico-Keller G., Coetfield J.,  
Darracq S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  
Astellano A., Sanders C., Ow D., Nolan M., Tiron S., Kobayashi A.,  
Olsen A.S., Carraro A.V.;  
RT "Sequence analysis of chromosome 19q13.4.";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
CC  
[1]- SUBCELLULAR LOCATION: Secreted (Probable).  
CC  
[1]- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=2;  
Name=1;  
Name=2;  
IsoId=Q9UKR0-1; Sequence=Displayed;  
Name=1;  
Name=2;  
IsoId=Q9UKR0-2; Sequence=VSP\_005403;  
[1]- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.  
CC  
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CC  
CC  
EMBL: AF135025; AAD26426.2; -;  
EMBL: AF135025; AAF06065.1; -;  
EMBL: AF243527; AAG33365.1; -;  
EMBL: AC011473; AAG23258.1; -;  
HSSP: P00763; IDPO.  
MEROPS: S01.020; -;  
Gene: HGNC:6360; KLK12.  
MIM: 605539; -;  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0006508; P:proteolysis and peptidolysis; NAS.  
DR InterPro: IPR001254; Ser\_protease\_try.  
DR Pfam: PF00089; trypsin; 1.  
DR SMART: SM00020; Tryp\_spc; 1.  
DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
KW Hydrolase; serine protease; glycoprotein; signal;  
KW Alternative splicing.  
FT SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 248 KALLIKREIN 12.  
FT ACT\_SITE 62 62 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT ACT\_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).  
FT DISULFID 26 161 BY SIMILARITY.

FT DISULFID 47 63 BY SIMILARITY.  
FT DISULFID 133 235 BY SIMILARITY.  
FT DISULFID 140 206 BY SIMILARITY.  
FT DISULFID 172 186 BY SIMILARITY.  
FT DISULFID 196 222 BY SIMILARITY.  
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 163 163 KYDWMIMRN -> NSTLVIGTSMNNSCOF (In  
FT VASPLIC 236 248 Isoform 2).  
FT  
FT  
SO SEQUENCE 248 AA; 26733 MW; B473E98F8BAF703 CRC64;  
/Frid=VSP\_005403.  
Alignment Scores:  
Pred. No.: 3.39e-35 Length: 248  
Score: 606.00 Matches: 114  
Percent Similarity: 63.91% Conservative: 33  
Best Local Similarity: 49.57% Mismatches: 79  
Query Match: 47.53% Indels: 4  
DB: 1 Gaps: 3  
US-09-856-320a-1\_copy\_272\_958 (1-687) x KLKc\_HUMAN (1-248)  
QY 1 ATGATCAAGGGGTTGAGTGCAGAGCCCTACCCAGCCGCGAGGAGCCCTGTTCGAG 60  
DB 22 IIEPHEANGLYTHRGUCYSGLYARGANSEGLNPROTPRLNVALGYLEUPHEGLU 41  
QY 61 AAGACGGCGTACTGTGTGGGCGAGCCGATGAGCCGAGATGCTGTGACAGAGCC 120  
DB 42 GLYTHSERLEUARGYSGLYGVALLEUILEASPHISARGTPRVALLLEUPTALALA 61  
QY 121 CAGTCGCTCAAGCCCGCTCATGATGACCTGGGCGAGACAACTCCAGAGAGAG 180  
DB 62 HISCYSERGLYSERATGYTPRVALLGLEGILNHSERLEUSERTGLNLEASP 81  
QY 181 GCGTGTGAGCAGACCCGAGCCAGCTGCTCCGAGCCGCTGCTCAACAGAGC 240  
DB 82 TPTPTGLNGLNLEARGHISERGLYPHSEVALTRHISPROGLYTRLEUGLYALA 101  
QY 241 CTGCCCCAAGAGCCAGCCAAATGACATGATGCTGTGTAAGTGGCATGCTGTC 300  
DB 102 -----SERHISERHISGLNHSISASPLEUARGLEUARGLEUPROVALARG 119  
QY 301 ATGACCTGGGCTGTGCGACCCCTGACCTGCTGACAGCTGTGCTGCTGACAGC 360  
DB 120 VALTHSERSERVALGPNPROLEUPROLEUPROASNPYSALATHTALAGLYTHGLY 139  
QY 361 TGCCTGATTTCCGCTGTGGGCGAGCAGCTGACAGCCGAGTACGCTGCTGACAGCTTG 420  
DB 140 CYHHSVALSERGLYTPRGLYIETHRNHISPROARGANPROHERPROASPLEU 159  
QY 421 CGATGCGCCCAATCAACCATGATGAGCAGCAGAGAGTGTGAGAGCCGTACCCGAGC 480  
DB 160 GLNCLYSLEUASINLEUSERTILEVALSERHISALATHTHCYSISGLYVALTYTPRGLYARG 179  
QY 481 ATCAAGACACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
DB 180 ILEHISERASMETVALCYSLAAGLY--GLYVALPROGLYNASPRALCYSGINGLY 198  
QY 541 GACTCGGCGGCGCTGT 600  
DB 199 ASPSERGLYGLYPROLEUVALCYSGLYGVALLEUGLNLGLEYUVALSERTPGLYSER 218  
QY 601 ---GATCCGTCGTCGATCAACCCGAGGAGCCGCTGTGTGTGTGTGTGTGTGTGTGT 657  
DB 219 VALGLYPROCYGLYGLNAPRGLYIETHRNHISPROARGANPROHERPROASPLEU 238  
QY 658 GACTGATCCAGGAGAGCATGAGAGCAAT 667  
DB 239 ASPTPRILEARGMETILEMETARGASNP 248  
RESULT 11  
KLK1\_RAT  
ID KLK1\_RAT STANDARD; PRT; 261 AA.





KLK3\_MOUSE STANDARD: PRT: 261 AA.  
 ID KLK3\_MOUSE  
 AC P00756;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glutathione S-transferase K3 precursor (EC 3.4.21.35) (Tissue kallikrein)  
 DE (mGK-3) (7S nerve growth factor gamma chain) (gamma-NGF).  
 GN KLK3 OR KLK-3 OR NGF.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclerogathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=85076169; PubMed=6548955;  
 RA Ullrich A., Gray A., Wood W.I., Hayflick J., Seeburg P.H.;  
 RT "Isolation of a cDNA clone coding for the gamma-subunit of mouse  
 RT nerve growth factor using a high-stringency selection procedure.";  
 RL DNA 3:387-392(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=85257431; PubMed=3848399;  
 RA Evans B.A., Richards R.I.;  
 RT "Genes for the alpha and gamma subunits of mouse nerve growth factor  
 RT are contiguous.";  
 RL EMBO J. 4:133-138(1985).  
 RN [3]  
 RP SEQUENCE OF 25-261.  
 RA MEDLINE=81264363; PubMed=7263706;  
 RA Thomas K.A., Baglan N.C., Bradshaw R.A.;  
 RT "The amino acid sequence of the gamma-subunit of mouse submaxillary  
 RT gland 7 S nerve growth factor.";  
 RL J. Biol. Chem. 256:9156-9166(1981).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.  
 RA STRAIN-Sykes Webster; TISSUE-Submaxillary gland;  
 RA MEDLINE=96035451; PubMed=9351801;  
 RA Bax B., Blundell T.L., Murray-Rust J., McDonald N.O.;  
 RT "Structure of mouse 7S NGF: a complex of nerve growth factor with  
 RT four binding proteins";  
 RL Structure 5:1275-1285(1997).  
 CC -1- FUNCTION: 7S NGF ALPHA CHAIN STABILIZES THE 7S COMPLEX. THE BETA  
 CC DIMER PROMOTES NEURITE GROWTH. THE GAMMA CHAIN IS AN ARGININE-  
 CC SPECIFIC PROTEASE; IT MAY ALSO HAVE PLASMINOGEN ACTIVATOR  
 CC ACTIVITY, AS WELL AS MITOGENIC ACTIVITY FOR CHICK EMBRYO  
 CC FIBROBLASTS.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in  
 CC small molecule substrates. Highly selective action to release  
 CC kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of  
 CC Met-|-Xaa or Leu-|-Xaa.  
 CC -1- SUBUNIT: 7S NERVE GROWTH FACTOR IS COMPOSED OF TWO ALPHA CHAINS,  
 CC A BETA DIMER COMPOSED OF IDENTICAL CHAINS, AND TWO GAMMA CHAINS.  
 CC -1- MISCELLANEOUS: THIS PRECURSOR IS CLEAVED INTO SEGMENTS TO PRODUCE  
 CC THE ACTIVE FORM OF THE GAMMA CHAIN, WHICH OCCURS NATURALLY AS  
 CC COMBINATIONS OF EITHER TWO OR THREE SEGMENTS HELD TOGETHER BY  
 CC DISULFIDE BONDS: B1 + A OR B1 + C + B2.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X01389; CAA25645.1; -;  
 CC EMBL; X01798; CAA25928.1; -;  
 CC EMBL; X01798; CAA25930.1; -;  
 CC PIR; A91005; NMSG.  
 CC PDB; 1SGF; 27-MAY-98.  
 CC MEROPS; S01.170; -;

DR MGD: MGI:97322; Ngfg.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR Pfam: PF00089; trypsin; 1.  
 DR SMART: SM00020; Tryp\_Spc; 1.  
 DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase; Serine protease; Glycoprotein; Multigene family; Zymogen;  
 KW Signal; Growth factor; 3D-structure.  
 FT SIGNAL 1  
 FT PROPEP 18  
 FT CHAIN 25  
 FT CHAIN 25  
 FT CHAIN 25  
 FT ACT\_SITE 112  
 FT ACT\_SITE 65  
 FT ACT\_SITE 120  
 FT ACT\_SITE 213  
 FT DISULFID 31  
 FT DISULFID 50  
 FT DISULFID 152  
 FT DISULFID 184  
 FT DISULFID 198  
 FT DISULFID 209  
 FT CARBOHYD 102  
 FT DOMAIN 25  
 FT DOMAIN 112  
 FT DOMAIN 112  
 FT DOMAIN 165  
 FT CONFLICT 108  
 FT STRAND 26  
 FT STRAND 29  
 FT STRAND 30  
 FT HELIX 33  
 FT TURN 37  
 FT STRAND 39  
 FT TURN 44  
 FT TURN 45  
 FT TURN 57  
 FT TURN 58  
 FT STRAND 59  
 FT STRAND 62  
 FT HELIX 72  
 FT STRAND 74  
 FT STRAND 75  
 FT STRAND 79  
 FT TURN 80  
 FT TURN 81  
 FT TURN 85  
 FT STRAND 86  
 FT TURN 97  
 FT STRAND 99  
 FT HELIX 103  
 FT TURN 105  
 FT TURN 118  
 FT STRAND 122  
 FT TURN 126  
 FT STRAND 148  
 FT STRAND 149  
 FT STRAND 151  
 FT STRAND 159  
 FT STRAND 167  
 FT STRAND 170  
 FT STRAND 172  
 FT HELIX 181  
 FT TURN 187  
 FT TURN 194  
 FT STRAND 196  
 FT STRAND 207  
 FT TURN 210  
 FT TURN 211  
 FT STRAND 213  
 FT TURN 216  
 FT TURN 219  
 FT TURN 220  
 FT STRAND 222  
 FT TURN 229  
 FT TURN 234  
 FT TURN 237  
 FT STRAND 241  
 FT HELIX 246  
 FT HELIX 250  
 FT TURN 259

SO SEQUENCE 261 AA; 28998 MW; 4870748E174AF7C8 CRC64;

Alignment Scores: 1.83e-34 Length: 261  
 Pred. No.: 595.50 Matches: 105  
 Score:



Percent Similarity: 63.988  
 Best Local Similarity: 44.498  
 Query Match: 46.718  
 DB: 1  
 Caps: 1

US-09-856-320a-1\_COPY\_272\_958 (1-687) x KLR3\_MOUSE (1-261)

QY 1 ATCATCAAGGGGTTTCAGTCCAGACCTCACTCCAGCCCTGGAGGAGGAGCCCTGTTGAG 60  
 DB 25 ILEVALGlyGlyPheLysCysGlyLysAsnSerGlnProThrPheValAlaValArg 44  
 QY 61 AAGACGGGCTACTCTGGGGGAGGAGCCCTGATGCCCCAGATGCGCTTCAGAGCACC 120  
 DB 45 TTTTGTGlnTyrLeuLysGlyGlyValLeuLeuAspProAsnTyrPheValLeuThrAlaAla 64  
 QY 121 CACTGCTCAAGCCCGCTACATAGTTCACTGCGGGGAGCACAACCTCCAGAGAGAG 180  
 DB 65 HiscysTyrAspAsnTyrLysValThrLeuGlyLysAsnLeuPheLysAspGlu 84  
 QY 181 GGCTGTGAGCAGACCCGAGCAGCCACTGACTCTCCCGCCAGCCCGGCTTCACACAGC 240  
 DB 85 ProSerAlaGlnHisArgPheValSerLysAlaIleProHisProGlyPheAsnMetSer 104  
 QY 241 CTCCCAACAA-----GACACCGCAATGACATCAGCTGCTG 279  
 DB 105 LeuMetArgLysHisIleArgPheLeuGlyTyrAspTyrSerAsnLeuMetLeu 124  
 QY 280 AAGATGGCATGCGCAGTCTTCATCACCCTGGGCTGGAGCCCTCCCTCCACGC 339  
 DB 125 ArgLeuSerLysProAlaAspIleThrAspThrValLysProIleThrLeuProThrGlu 144  
 QY 340 TGTGTCACTCTGGCAGCAGCCTGCTCATTCGCGCTGGGAGCAGCAGTCCAGCCCGCAG 399  
 DB 145 GlnProLysLeuLysSerLysThrCysLeuAlaSerGlyTyrPheLysIleThrProThrLys 164  
 QY 400 TTAGCGCTGCGTCACACTGCTGAGCGGCAATGCTGCTGAGCAGAGAGT 459  
 DB 165 PheGlnPheThrAspAspLeuTyrCysValAsnLeuLysLeuProAsnGluAspCys 184  
 QY 460 GAGACCGCTTACCCCGGCAACATCAGACACCATGCTGTGTCAGCAGCAGAGAGG 519  
 DB 185 AlAlaLysAlaHisIleGlyLysValThrAspAlaMetLeuLysAlaGlyLysMetLeuAspGly 204  
 QY 520 GCGAAGAGACTCCCGCAGGCTGACTCCGGGGCCCTCTGCTGTAACTCTCTTCA 579  
 DB 205 GlnLysAspThrLysGlyLysGlyAspSerGlyGlyProLeuIleCysAspGlyValLeuGln 224  
 QY 580 GGCATTATCTCTGGGGGAGGAGATCCGTCGTCATCACCAGGAGCCCTGCTGCTACAGC 639  
 DB 225 GlyIleThrSerThrPheLysThrProGlyGlyLysProAspMetProGlyValTyrThr 244  
 QY 640 AAGTCTGCAATATGTGACTGATCCAGCAGAGCAGTGAAGAACAT 687  
 DB 245 LysLeuAsnLysPheThrSerThrPheLysAspThrMetAlaLysAsn 260

RESULT 14  
 TRY3\_CHICK STANDARD; PRT; 248 AA.  
 AC 090629;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, last sequence update)  
 DT 28-FEB-2003 (Rel. 41, last annotation update)  
 DE trypsin IT-P29 precursor (EC 3.4.21.4).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=95251611; PubMed=7733885;  
 RA Wang K., Gan L., Lee I., Hood L.E.;

RT "Isolation and characterization of the chicken trypsinogen gene  
 RT family.";  
 RL Biochem. J. 307:471-479(1995).  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-I-Xaa, Lys-I-Xaa.  
 CC -1- SUBCELLULAR LOCATION: Extracellular.  
 CC -1- TISSUE SPECIFICITY: HIGH LEVELS ARE SEEN IN THE PANCREAS WHILE  
 CC LOWER LEVELS ARE FOUND IN THE LIVER, SPLEEN AND THYMUS.  
 CC -1- SIMILARITY: BELONGS TO TRYPSIN FAMILY S1.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb.sib.ch](mailto:license@isb.sib.ch)).  
 CC -----

DR EMBL: U15157; AAA79914.1; -.  
 DR PIR: S55066; S55066.  
 DR HSP: P00763; IDPO.  
 DR MEROPS: S01.151; -.  
 DR InterPro: IPR001254; Ser.protease\_Try.  
 DR Pfam: PF00089; trypsin\_1.  
 DR SMART: SM00020; trypsin\_1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM, 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS, 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER, 1.  
 KM Hydrolyase; Serine protease; Digestion; Pancreas; Zymogen; Signal;  
 KW Multigene family.  
 FT SIGNAL 1 16  
 FT PROPEP 17 25  
 FT CHAIN 26 248  
 FT ACT\_SITE 65 65  
 FT ACT\_SITE 109 109  
 FT ACT\_SITE 202 202  
 FT DISUPEID 32 162  
 FT DISUPEID 50 66  
 FT DISUPEID 134 235  
 FT DISUPEID 141 208  
 FT DISUPEID 173 187  
 FT DISUPEID 198 222  
 FT SITE 196 196 REQUIRED FOR SPECIFICITY (BY SIMILARITY).  
 SQ SEQUENCE 248 AA; 26622 MW; ESE16B0762B588E CRC64;

Alignment Scores:  
 Pred. No.: 2.33e-34 Length: 248  
 Score: 594.00 Matches: 112  
 Percent Similarity: 65.048 Conservative: 35  
 Best Local Similarity: 46.598 Mismatches: 73  
 Query Match: 46.598 Indels: 6  
 DB: 1 Gaps: 3

US-09-856-320a-1\_COPY\_272\_958 (1-687) x TRY3\_CHICK (1-248)

- QY 1 ATCATCAAGGGGTTTCAGTCCAGACCTCACTCCAGCCCTGGAGGAGGAGCCCTGTTGAG 60  
 DB 26 ILEVALGlyGlyTyrThrCysProGlnHisSerValProTyrGlnValSerLeu---Asn 44  
 QY 61 AAGACGGGCTACTCTGGGGGAGGAGCCCTGATGCCCCAGATGCGCTTCAGAGCACC 120  
 DB 45 serGlyTyrHisPheLysGlyGlySerLeuIleAsnSerGlnTyrPheValLeuSerAlaAla 64  
 QY 121 CACTGCTCAAGCCCGCTACATAGTTCACTGCGGGGAGCACAACCTCCAGAGAGAG 180  
 DB 65 HiscysTyrLysSerArgIleGlnValArgLeuGlyGlyTyrAsnIleAspValGlnGlu 84  
 QY 181 GGCTGTGAGCAGACCCGAGCAGCCACTGACTCTCCCGCCAGCCCGGCTTCACACAGC 240  
 DB 85 AspSerGlnValValArgSerSerValIleIleArgHisProLysTyrSerIle 104  
 QY 241 CTCCCAACAAACACACGCAATGACATCAGCTGTAAGATGCAATCCAGCTCCAGCTCC 300  
 DB 105 ThrLeuAsn-----AsnAspIleMetLeuIleLysLeuAlaSerAlaValGlu 120

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OY 301 ATCAGCTGGCTGTCGACCCCTCAGCCTCTCTCAGCCTGTGTCACGTGACGAC 360
DB 121 TyrSerAlaAspIleGlnProIleAlaLeuProSerSerCysAlaIleGlyThrGlu 140
OY 361 TGCCCATTTCCGGCTGGGGAGCGACGTCGACCCCGCATTAAGCCTGCTCAGACCTTG 420
DB 141 CysLeuIleSerGlyTyrPglYAsnThrLeuSerAsnGlyTyrAsnTyrProGluLeuLeu 160
OY 421 CGATCGCCACATCACCATTGATGACGACGAGATGTGAGAACCCCTACCCGCGAC 480
DB 161 GlnCysLeuAsnAlaProIleLeuSerAspGlnGlyCysGlnGlnAlaIleTyrProGlyAsp 180
OY 481 ATCAGACACACCATGCTGTGTCAGCAGCTGACGAGAGGGGGGACGAGCTCTGCGACGGT 540
DB 181 IleThrSerAsnMetIleCysValGlyPheLeuGlnGlyGlyAspSerCysGlnGly 200
OY 541 GACATCGGGGGCCCTGCTGTGTACAGAGTCTTCAAGCATATATCTCTGCGGGCCAG 600
DB 201 AspSerGlyGlyProValIleCysAsnGlyGluLeuGlnGlyIleValSerTyrPglYle 220
OY 601 GATCCGTGTCGATCAGCCGGAAGCCTGTGTCTACAGAAAGTCTGCAATATGTGAC 660
DB 221 Gly--CysAlaLeuIleGlyTyrProGlyValIleTyrThrIleValCysAsnTyrValAsp 239
OY 661 TGGATCCAGAGACGAGT 678
DB 240 TrpIleGlnGluThrIle 245

RESULT 15
KIKR_PRANA STANDARD; PRT; 263 AA.
AC P32824.
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glandular kallikrein, renal precursor (EC 3.4.21.35) (Tissue kallikrein).
OS Pteromys natalensis (African soft-furred rat) (Mastomys natalensis).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mastomys.
OX NCBI_TaxID=10112;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=94226702; PubMed=7909667;
RA Fahnestock M.;
RT "Characterization of kallikrein cDNAs from the African rodent Mastomys."
RL DNA Cell Biol. 13:293-300(1994).
CC -1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS IN KININOGEN TO RELEASE LYS-BRADYKININ.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-I-Xaa bonds in small molecule substrates. Highly selective action to release kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of Met-I-Xaa or Leu-I-Xaa.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC -----
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CC -----
DR EMBL, X17352; CA35232.1; -.
DR PIR, I83227; S15686.
DR HSSP, P00757; 1SGF.
DR MEROPS, S01.160; -.
DR InterPro, IPR001254; Ser_protease_Try.
DR Pfam, PF00089; trypsin; I.

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DR SMART, SM00020; Tryp_Spc; 1.
DR PROSITE, PS50240; TRYPsin_DOM; 1.
DR PROSITE, PS00134; TRYPsin_HIS; 1.
DR PROSITE, PS00135; TRYPsin_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Multigene family; Zymogen;
KW Signal.
FT SIGNAL 1 18 PROBABLE.
FT PROPEP 19 24 ACTIVATION PEPTIDE (PROBABLE).
FT CHAIN 25 263 GLANDULAR KALLIKREIN, RENAL.
FT ACT_SITE 65 65 CHARGE RELAY SYSTEM.
FT ACT_SITE 121 121 CHARGE RELAY SYSTEM.
FT ACT_SITE 215 215 CHARGE RELAY SYSTEM.
FT DISULFID 31 175 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 153 221 BY SIMILARITY.
FT DISULFID 186 200 BY SIMILARITY.
FT DISULFID 211 236 BY SIMILARITY.
FT CAROHD 102 102 N-LINKED (GLCNAC...) (PROBABLE).
SQ SEQUENCE 263 AA; 29130 MW; ABB8023BB00337D5 CRC64;

Alignment Scores:
Pred. No.: 3,49e-34 Length: 263
Score: 591.50 Matches: 106
Percent Similarity: 63.03% Conservative: 44
Best Local Similarity: 44.34% Mismatches: 79
Query Match: 46.39% Indels: 9
DB: 1 Gaps: 2

US-09-856-320a-1_copy_272_958 (1-687) x KIKR_PRANA (1-263)
OY 1 ATCATCAAGGGGCTTGCAGTGCAGAGCCTCCAGCCCTGGCAGGAGCCCTGTTCGAG 60
DB 25 IleIleGlyGlyPheAsnGlyGlnIleAsnSerGlnProThrPheIleAlaIleValIleGlyArg 44
OY 61 AAGAGCGGCGTACTGTGTGGGGGCGAGCTATCGCCCGCCAAATGGCTCTCAGACAGCC 120
DB 45 PheAlaIleGlyGlnCysGlyIleValIleLeuAsnPalaeAsnTyrValIleThrIleAlaIle 64
OY 121 CACTGCTCAAGCCCGCTGATCATGATTCACCTGGGCGAGCAACCTCCAGAGAGGAG 180
DB 65 HisCysTyrAsnAlaPheIleTyrGlnValIlePheLeuGlyAsnAlaIlePheGlnAspIle 84
OY 181 GCGTGTGAGCAGACCCGGAAGCAGCTGAGTCCCTCCCGCCAGCCCGGCTTCAACAGAGC 240
DB 85 ProSerAlaGlnIleGlnIleLeuIleSerIleAlaIleProIleHisProGlyPheAsnMetSer 104
OY 241 CTCGCCAACAAGAACAC-----CGCAATGACATCATGCTG 276
DB 105 LeuLeuAsnIleAspHisThrProIleHisProIleAspAspTyrSerAsnAspLeuMetLeu 124
OY 277 GTGAAGATGGCATGCGCCAGCTCCATCATCTGAGCTGGGCGAGCCCGCTACCCCTGCTCA 336
DB 125 ValArgLeuIleValProIleGlnIleThrAspValValIleAspIleProIleHisProThr 144
OY 337 CGTGTGTCACTGCTGGCAGCAGCTGCTCATTTCCGGCTGGGCGAGCAGCTCC--AGC 393
DB 145 GluIleProThrValGlySerArgCysLeuIleAspGlyTyrPglYSerThrThrProThr 164
OY 394 CCCAGTTAGCCCTGCGCTCAGACCTTGGAGATGGCGCAACATCAGCATATGTAGCAGCAG 453
DB 165 GluIlePheGlyIleThrSerHisAspIleGlnCysValIleTyrLeuGlnIleLeuIleSerAspIle 184
OY 454 AAGGTGTGAAGCGCTACCCCGGCAACATCAGACAGCATGATGTTGGCGAGGTGAG 513
DB 185 ValCysAlaIleAlaHisThrGlnIleValIleThrAspThrMetLeuCysAlaIleGlnMet 204
OY 514 GAAGGGGCAAGAGACTCTGTCAGAGGTACTCCGGGGGCGCTGTGTTGTAACCACTCT 573
DB 205 AspIleGlyIleAspThrIleCysValGlyAspSerGlyGlyProIleIleCysAspGlyVal 224
OY 574 CTTCAAGGCAATTATCTCTGGGGCGCAGAGATCCGCTGTGATCAGACCGAAGCCGTGCTC 633
DB 225 LeuGlnGlyIleThrSerTyrPglYProThrPheIleAlaLeuProAsnValProGlyIle 244

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QY 634 TACACGAAAGTCTGCAAAATATGTGACTGGATCCAGGAGACGATGGAACAAT 687  
|||||  
:::  
Db 245 TTTThrlYslleuIleGIuTYrArGserTrrPleIylsAspvAlMeAlaAsnAsn 262  
|||||  
:::  
|||||

Search completed: October 15, 2003, 20:20:58  
Job time : 15.0563 secs

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 15, 2003, 20:04:15 : Search time 18.8338 Seconds  
(without alignments)  
7015.902 Million cell updates/sec

Title: US-09-856-320A-1\_COPY-272\_958  
Perfect score: 1275  
Sequence: 1 atcacaaggaggttcagtg.....aggagacgatgaagacaat 687

Scoring table: BIOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 566616

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cgn2.1/USPTO.spool.p/US09856320/r/unat.15102003.105640.8549/app.query.fasta.1.2318  
-DB=PIR.76 -QFMT=fastan -SUFFIX=ppr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-NNITS=b1ts -START=1 -END=1 -MATRIX=bls0sum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR.SCOPE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09856320@cgn.1.1.74@runat.15102003.105640.8549 -NCPV=6 -ICPV=3  
-NO\_WMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR.76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	684	53.6	260 2	I56559 neuropsin - mouse
2	605.5	47.5	265 1	KORPT tissue kallikrein
3	600.5	47.1	261 2	B31136 tissue kallikrein
4	595.5	46.7	261 1	NGMSG 7S nerve growth fa
5	594	46.6	248 2	S55066 trypsin (EC 3.4.21
6	591.5	46.4	263 2	S15686 tissue kallikrein
7	591	46.4	246 1	TRRT2 trypsin (EC 3.4.21
8	588	46.1	238 2	S31779 trypsin (EC 3.4.21
9	587	46.0	246 1	TRRT1 trypsin (EC 3.4.21
10	585.5	45.9	261 2	A34079 tissue kallikrein
11	581.5	45.6	259 1	B31136 tissue kallikrein
12	578	45.3	232 1	KOPG tissue kallikrein
13	577.5	45.3	261 2	A29586 tissue kallikrein
14	577.5	45.3	261 2	A29745 tissue kallikrein

15	577	45.3	231 1	TRPCTR trypsin (EC 3.4.21
16	574.5	45.1	261 2	S45303 tissue kallikrein
17	571	44.8	246 2	B25528 trypsin (EC 3.4.21
18	568	44.5	247 1	TRDG trypsin (EC 3.4.21
19	567.5	44.5	259 1	KORPTN tonin (EC 3.4.21)
20	565.5	44.4	261 2	A25606 tissue kallikrein
21	564.5	44.3	244 2	A44284 tissue kallikrein
22	564.5	44.3	261 1	KOMS1 tissue kallikrein
23	564	44.1	229 1	TRBOTR trypsin (EC 3.4.21
24	562	44.1	262 1	KOHU tissue kallikrein
25	560	43.9	248 2	S55067 trypsin (EC 3.4.21
26	556.5	43.6	257 2	S33772 tissue kallikrein
27	556.5	43.6	261 2	S01971 tissue kallikrein
28	556	43.6	243 2	A35871 trypsin (EC 3.4.21
29	556	43.6	247 2	S13813 trypsin (EC 3.4.21
30	553	43.4	247 2	A27547 trypsin (EC 3.4.21
31	552.5	43.3	231 2	S31778 trypsin (EC 3.4.21
32	552.5	43.3	247 2	S05494 trypsin (EC 3.4.21
33	552	43.3	256 1	NGMSA 7S nerve growth fa
34	551.5	43.3	239 2	A27207 tissue kallikrein
35	551.5	43.3	261 1	A32297 semenogelase (EC 3
36	550	43.1	246 1	TRDGC trypsin (EC 3.4.21
37	548.5	43.0	259 2	A29746 tissue kallikrein
38	548.5	43.0	261 1	S35711 semenogelase (EC 3
39	548.5	43.0	261 2	A41020 tissue kallikrein
40	546	42.8	253 2	A53968 serine proteinase
41	544.5	42.7	242 2	S31775 trypsin (EC 3.4.21
42	544.5	42.7	242 2	S49489 trypsin (EC 3.4.21
43	544.5	42.7	242 2	S31776 trypsin (EC 3.4.21
44	543.5	42.6	261 2	JE0236 tissue kallikrein
45	542.5	42.5	261 1	TRMSMS tissue kallikrein

## ALIGNMENTS

RESULT 1  
156539  
neuropsin - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 21-Jul-2000  
C:Accession: I56559  
R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nis  
J. Neurosci. 15, 5088-5097, 1995  
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease  
A:Reference number: I56559; PMID:95348817; PMID:7623137  
A:Accession: I56559  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-260 <RES>  
A:Cross-references: GB:D30785; NID:91648847; PIDN:BAA06451.1; PID:91020091  
C:Superfamily: trypsin; trypsin homology  
F:33-252/Domain: trypsin homology <TRY>

## Alignment Scores:

Pred. No.: 4.5e-42  
Score: 684.00  
Percent Similarity: 68.42%  
Best Local Similarity: 53.07%  
Query Match: 53.65%  
DB: 2  
Length: 260  
Matches: 121  
Conservative: 35  
Mismatch: 70  
Indels: 2  
Gaps: 2

US-09-856-320A-1\_COPY\_272\_958 (1-687) x I56559 (1-260)

OY	1	ATCATCAAGGGGTTGACGACGCTACCTCCAGCCCTGGAGGAGCCCTGTCGAG	60
		:	
DB	33	ITLEAUGLUGIYARGGLUCYSLIEPROHISSEKGINPOTIRPGLNLAIALEUPHEGIN	52
		:	
OY	61	AAGACGGGCTACTCTGTGGGCGACGCTCATGGCCCGAGATGGCTCTGCACAGCACC	120
		:	
DB	53	GLYGLIATRGLEUILLECYGLIYVALLLEUVALIGIYAPATGTRPVALLLEUTHALALA	72
		:	
OY	121	CACATGCCCTCAAGCCCGCTACATAGTTCAACCTGGGGGACGACACACCTCCAGAGGAGGAG	180
		:	

Db HisCysLysIysGlnIlystYrSerValnIgrLeuGIAspHisSerLeuInserArtya92

73

181 GGTGTGAGCAAGACCCGGAGCAAGCCATGATCTTCCACCACCCGGCTTCAACAACAGC 240  
|||||  
|||||

Db GlnProGluInIleGlnValnIaGlnSerIleGlnHisProCysArtyaHisnSer 112

93

241 CTCCCAACAAAGACACCCGCAATACATCATGCTGGTGAACATGGCATGCCAGTCTCC 300  
|||  
|||

Db AsnPro---GluAspHisSerHisAspIleMetLeuIleArgLeuGlnAsnSerAlaAsn 131

113

301 ATCACTGGGTGGTGGAGACCCCTCAACCTCTCTCAAGCTGTGTCACTCTGTGCACACAGC 360  
|||  
|||

Db LeuGIAspIlystValIlystProValGlnLeuAlaAsnLeuCysProIlystValGIlyGlnIly 151

132

361 TGCCATATTCCTCGGCTGGGAGCAGCATCCACGCCACCCAGTTAGGCTCGCTCACACCTTG 420  
|||  
|||

Db CysIleIleSerGIYTrpGIYThrValIThrSerProGlnGlnIAsnPhreProAsnThrLeu 171

152

421 CGATGCGCGCAACATACCATCATCTTTGAGCACCGAAGGTGTGAAGACGCTTACCCCGGCAGC 480  
|||||  
|||

Db AsnCysAlaGlnValIlystIleYrSerGlnAsnIlystCysGlnArgAlaIytrProGIlyst 191

172

481 ATCAAGACAGACCATGCTGTGTGCCAGCGTGCAGGAAGGGGCGCAAGAGATCTTCGCCAGGCT 540  
|||||  
|||

Db IleThrTrpGlnGIYMetValIlystAlaGIY--SerSerAsnGlyAlaAspPhrCysGlnGIY 210

192

541 GACTTCGGGGGGCCCTGTCTGTATACCAAGTCTTTCACAGGATATATCTCGGGGGCCAG 600  
|||  
|||

Db AspSerGIYGIYProLeuValIlystAspGIYMetLeuGlnGIYIleThrSerTrpGIYSer 230

211

601 GATCCGGTGGCGATACACCCGAAGACCTGGTGTCTACACAGAAAGCTGTCAAAATATGTGAGC 660  
|||||  
|||

Db AspProCysGIYIlystProGlnIlystProGIYValIYTrpIlystIleCysArgGIYTrpThr 250

231

661 TGGATCCAGAGACGATGAGAGAC 684

QY

251 TrpIleIlystIlystHisMetAspAsn 258

## RESULT 2

tissue kallikrein (EC 3.4.21.35) precursor - rat  
N:Alternate names: glandular kallikrein; kininogenin; true tissue kallikrein  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 05-Apr-1993 #sequence\_revision 05-Apr-1983 #text\_change 16-Jun-2000  
C:Accession: A00944; A41429; A25137; JX0073; A23863; A33359  
R:Swift, G.H.; Daqorn, J.C.; Ashley, P.L.; Cummings, S.W.; MacDonald, R.J.  
Proc. Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982  
A:Title: Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence of  
A:Reference number: A00944; MUID:83117659; PMID:6961406  
A:Accession: A00944  
A:Molecule type: mRNA  
A:Residues: 1-265 <SWID>  
A:Experimental source: pancreatic  
R:Kato, H.; Nakanishi, E.; Enjyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.  
J. Biochem. 102, 1389-1404, 1987  
A:Title: Characterization of serine proteinases isolated from rat submaxillary gland: w  
A:Reference number: A41429; MUID:88198057; PMID:3462210  
A:Accession: A41429  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 29-53, 'X', 55-87 <KAT>  
R:Gerald, W.L.; Chao, J.; Chao, L.  
Biochim. Biophys. Acta 866, 1-14, 1986  
A:Title: Immunological identification of rat tissue kallikrein cDNA and characterization  
A:Reference number: A25137; MUID:86131678; PMID:3004582  
A:Accession: A25137  
A:Molecule type: mRNA  
A:Residues: 115-265 <GER>  
R:Inoue, H.; Fukui, K.; Miyake, Y.  
J. Biochem. 105, 834-840, 1989  
A:Title: Identification and structure of the rat true tissue kallikrein gene expressed i  
A:Reference number: JX0073; MUID:89327211; PMID:2753879  
A:Accession: JX0073

A:Molecule type: DNA  
A:Residues: 1-265 <INQ>  
A:Cross-references: GB:D00448; NID:g220792; PIDN:BA00346.1; PID:g220794  
A:Experimental source: Kidney  
R:Ashley, P.L.; MacDonald, R.J.  
Biochemistry 24, 4512-4520, 1985  
A:Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences  
A:Reference number: A23663; MUID:66051477; PMID:2998455  
A:Accession: A23663  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-265 <ASH>  
A:Cross-references: GB:M1563; NID:g205029; PIDN:AAA4464.1; PID:g205030  
A:Experimental source: submaxillary gland  
R:Wines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; MacDonald, R.J.  
J. Biol. Chem. 264, 7653-7662, 1989  
A:Title: Organization and expression of the rat kallikrein gene family.  
A:Reference number: A33359; MUID:89214217; PMID:2708383  
A:Accession: A33359  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 5-265 <MIN>  
A:Cross-references: GB:M23874; GB:J04701; GB:M23875; GB:M23876; NID:g205007; PIDN:AAA  
C:Comment: The kallikreins liberate lysyl-bradykinin, a vasoactive decapeptide, from  
C:Comment: The protein presumably assumes the two-chain form by cleavage between resi  
C:Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to releas  
C:Genetics:  
A:Introns: 20/1; 73/2; 169/1; 214/3  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; pancreas; serine proteinase; zymogen  
F:1-17/Domain: signal sequence #status predicted <IG>  
F:18-28/Domain: activation peptide #status predicted <AP>  
F:29-265/Product: tissue kallikrein, pancreatic #status predicted <MP>  
E:29-25/Domain: trypsin homology <TRY>  
E:35-177, 54-70, 156-223, 188-202, 213-238/Disulfide bonds: #status predicted  
E:69,124,217/Active site: His, Asp, Ser #status predicted

**Alignment Scores:**

Pred. No.:	2, 23e-36	Length:	265
Score:	605.50	Matches:	107
Percent Similarity:	63.56%	Conservative:	43
Best Local Similarity:	45.34%	Mismatches:	79
Query Match:	47.49%	Indels:	7
DB:	1	Gaps:	1

  

US-09-856-320A-1_COPY_272_958 (1-687) x KQRRP (1-265)	
QY 1 AATCATGAAGGGTTCGATGAGCAAGCCTCCACCCCTGGAGCAGCCCTGTCGAG	60
DB 29 ValValGlgYgLYrrnscysgluwtctnsrGlnProTrpGlnValAlaValTyrTyr	48
QY 61 AAGACGCGGCTACTCTGTGGGGCGAGCGCTATCGCCCGACATGGCTCTCCACAGCAGCC	120
DB 49 PheGlgYgluTyrLeucysglYgYValleuIleAspProserTrpValIleThrAlaAla	68
QY 121 CACTGCTCAAGCCCGGCTACATAGTTCACCTGGGGCAGCACAACTCCACAGAGAGAG	180
DB 69 HisCysAlaThrAspAsnTyrGlnValTyrLeuGlyArgAsnAsnIleuTyrGluAspGlu	88
QY 181 GCGTGGAGCAGACCCGCGACAGCAGCTAGTGCCTCCGCCACCCCGCGTCAACACAGC	240
DB 89 ProPheAlaGlnHisArgLeuValIserGlnSerPheProHisProGlyPheAsnGlnAsp	108
QY 241 CTC-----CCCAACAAGACACGCGAATGATCATCTGATG	277
DB 109 LeuIleTrpAsnHisThrArgGlnProGlyAspAspTyrSerAsnAspLeuMetLeuLeu	128
QY 280 AATATGGCATCGCCATCTCCATACACCTGGGGCTGGCAGACCCCTACACCTTCTCTACCC	338
DB 129 HisLeuSerGlnProAlaAspIleThrAspGlyValIleAspLeuProIleGlu	148
QY 340 TGATGTACGTGGTCCAGCTGCCTCAATTCGCGCTGGGCGACAGCTCCAGCCCCAG	399

Db	149	GIUPrPolysValGlySerThrCysLeuAlaSerGlyTTrpGlySerIleThrProAspGly	168
OY	400	TTAGCCGTCGCCACACCTTGGGATGCCGCACATCCATCATATTAGACACCGAAGTGT	459
Db	169	LeuGIuLeuSerAspAspLeuIleIleGlyValAlaIleAspLeuSerAsnGlyIuPAspCys	188
OY	460	GAGAACGCCCTACCCCGGCACACATCAGACACCATGGTGTGTGCCAGCCTGCAGAAAGG	519
Db	189	ValGIuAlaAlaIleValGlyIuValValThrAspLeuMetLeuCysIaGlyIuMetAspGly	208
OY	520	GGCAAGAGACTCCTGCGCAGGTCGACTCCGGGGGCCCTCGTGTGTATACCAAGTCCTTCA	579
Db	209	GlyIuAspTrpIleCysIuLeuSerPheGlyGlyIuProIleIleCysAsnIuValLeuGln	228
OY	580	GGCATTATCTCCTGGGGCCAGAGCTCGTGTGCATCACCCGAAGGCCGTGTCTACAG	639
Db	229	GlyIleThrIleSerTrpGlyIuPheAsnProCysGlyIuProIuGlyAspProGlyIleIuTrp	248
OY	640	AAAGCTCAATATATGGATCGATCGATCCGAGAGAGATGAACAACAT	687
Db	249	LysLeuIleIuPheThrProTrpIleIuGlyGluValMetLeuGlyGluAsn	264

### RESULT 3

Alignment Scores:  
 tissue kallikrein (EC 3.4.21.35) 7 precursor, submandibular - rat  
 A:Alternate names: glandular prokallikrein 7, submandibular; proteinase A  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 31-Mar-1990 #sequence  
 C:Accession: A31136; S10698; S10699; D41429; B41429; S09315  
 R:Chen, Y.P.; Chao, J.; Chao, L.  
 A:Title: Molecular cloning and characterization of two rat renal kallikrein genes.  
 A:Reference number: A31136; MUID:85088074; PMID:2843988  
 A:Accession: A31136  
 A:Molecule type: DNA  
 A:Residues: 1-261 <CHD>  
 A:Cross-references: GB:M19647; GB:J02837; NID:g204999; PIDN:AAA41461.1; PID:g205000  
 R:Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, F.  
 FEBS Lett. 265:137-140, 1990  
 A:Title: Substrate specificity of two kallikrein family gene products isolated from the  
 A:Reference number: S10698; MUID:90306305; PMID:2194829  
 A:Accession: S10698  
 A:Molecule type: protein  
 A:Residues: 25-36 <ELM>  
 A:Accession: S10699  
 A:Molecule type: protein  
 A:Residues: 112-139 <EL2>  
 R:Kato, H.; Nakamishi, E.; Enjyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.  
 J. Biochem. 102:1389-1404, 1987  
 A:Title: Characterization of serine proteinases isolated from rat submaxillary gland: with  
 A:Reference number: A41429; MUID:88198057; PMID:3482210  
 A:Accession: D41429  
 A:Molecule type: protein  
 A:Residues: 112-133 <KAT>  
 A:Accession: B41429  
 A:Molecule type: protein  
 A:Residues: 25-34,'D',36-45,'S',47-67,'X',69-75 <KA2>  
 R:Brady, J.M.; MacDonald, R.J.  
 Arch. Biochem. Biophys. 278:342-349, 1990  
 A:Title: The expression of two kallikrein gene family members in the rat kidney.  
 A:Reference number: S09315; MUID:90225801; PMID:2183721  
 A:Accession: S09315  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 43-45,'S',47-114,'A',116-261 <BR>  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: hydrolase; serine proteinase  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-261/Product: tissue prokallikrein 7, submandibular #status predicted <MAT>  
 F:25-253/Domain: trypsin homology <TRY>  
 F:65,120,213/Active site: His, Asp, Ser #status predicted

Pred. No.:	5,15e-36	length:	261
Score:	600.50	Matches:	109
Percent Similarity:	62.71%	Conservative:	39
Best Local Similarity:	46.19%	Mismatches:	81
Query Match:	47.10%	Indels:	7
DB:	2	Gaps:	1

US-09-856-320A-1\_COPY\_272\_958 (1-687) x A31136 (1-261,

QY	ATATCAAGAGGGGTTTCAGAGTCAGACCTCCACAGCTCCAGAGCCCTGGACAGGACGGCTTGTCAG	60
Db	25 ValIleGlyIylYrIyLysCysGluYsaAsnSerGlnProTrpGlnValAlaLeuYrSer	44
QY	61 AAGACGGGTACTCTGTGGGGGAGCGACGTCATACGCCGCCAATGGCTCTGTACAGACACC	120
Db	45 PheThrLysrIleuYrSclYglYalIleuIleAspProSerTerTrpValIleThrAlaIle	64
QY	121 CACTGGCTCAAGCCCCGCTACATAGTTCACCTGGGGGAGACACACCTCCAGAAGAGAG	180
Db	65 HisCysSerSerAsnAsnTrpGlnValTrpLeuGlyAlaGlnAsnIleuLeuGlnAspIu	84
QY	181 GCGTGTGAGCAACCCGGACAGCCACTAGTCTCTCCCAAGCCCGGCTTCACACACAGC	240
Db	85 ProPheAlaGlnHisArgLeuValSerGlnSerIlePheProHisIleProAspTrpLysProPhe	104
QY	241 CTC-----CCCAACAAGACCCCGCAATGACATGATCTGTGGT	275
Db	105 LeuMetLysGlnHisThrArgLysProGlyAspAspHisSerAsnAspLeuMetLeu	124
QY	280 AAGATGGCATCGCCAGCTTCATCAACCTGGGCTGTGGACCCCTACCCCTCTCTCAACG	335
Db	125 HisIleuSerGlnProIleAspIleThrAspGlyValIleValIleAspLeuProThrGln	144
QY	340 TGTGTACATGTGGGACAGCTGGCTCATTTCCGGCTGGGGAGAGCTCCAGCCCCAG	395
Db	145 GluProLysValGlySerThrCysLeuAlaSerGlyTrpGlySerThrLysProLeuIle	164
QY	400 TTAAGCGCTCTCACACCTTGGAGCGGCACACATACACATATGAGACACAGAAGGT	455
Db	165 TrpGluPheProAspArgLeuGlnCysValAsnIleHisIleuLeuSerAsnGlnLysCys	184
QY	460 GAGAACGCTTACCCCGGCAACATCACACAGACCAATGGTGTGTGGCAGCGTCCAGAAAGG	515
Db	185 IleLysAlaTrpLysGlnLysValIleThrAspLeuMetLeuCysAlaGlnGlyIleuLeuGlnGly	204
QY	520 GGCAGAAGATCTCTGCCAGGGGTACTCCGGGGGCCCTGTGCTGTATACACAGTCTTCA	575
Db	205 GlyLysAspThrCysThrGlyAspSerGlyIleProLeuLeuCysAspGlyValLeuGln	224
QY	580 GGCATTATCTCTGGGGGCCAGGATCCGTGTGGATACCCCAAAACCTGGTGTCTACAG	635
Db	225 GlyIleThrSerTrpGlySerValProCysAlaTrpIleAsnMetProAlaIleTyrThr	244
QY	640 AAGGTGCAAATATGTGATGATGATTCACAGGACAGAGAAAGAACAAAT	687
Db	245 LysIleuIleLysPheThrSerTrpIleLysGlnValMetLysGlnAsn	260

## RESULT 4

7S nerve growth factor gamma chain (EC 3.4.21.-) precursor - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 18-Dec-1981 #sequence revision 17-May-1985 #text change 18-Jun-1999  
C/Accession: A91005; A90949; A93510; A92541; A00942; A21053; A22705  
R/Evans, B.A.; Richards, R.I.  
EMBO J. 4, 133-138, 1985  
A>Title: Genes for the alpha and gamma subunits of mouse nerve growth factor are contig  
A/Reference number: A91005; MUID:5257431; PMID:3848399  
A/Accession: A91005  
A/Molecule type: DNA  
A/Residues: 1-261 <EYAS>  
R/Dillich, A.; Gray, A.; Wood, W.I.; Hayflick, J.; Seeburg, P.H.  
DNA 3, 387-392, 1984  
A/Title: Isolation of a cDNA clone coding for the gamma-subunit of mouse nerve growth





```

Db      65 HISCSTYRYSSEATRIIEGLINVALARGLEUGLYUTYRASNIIIESPVALINGLU 84
        |||||  ||  |||  |||||  :::::  |||||  ::|||
OY      181 GGCTTGAGCAGACCCGGAGACCCAGTCCCTCCCGCGGCTTCAACAAGC 240
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      85 ASPSERGLIVALARGSERSESERVALLIETLARGHISPROLYSTYRSESERILE 104
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY      241 CTCGCCAACAAAGACCCAGCATATCATCTGCTGGAGATGGCATGCCACTGCC 300
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      105 THRLEUASN-----ASNAPRIEMETLEUILEYSLIENALASERLALVALGLU 120
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY      301 ATACCTGGGGCTGGGAGCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 360
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      121 TYRSERLAASPIIEGLINPROLEALALEUPROSERSEYSAIALYSLAGLYTHRLU 140
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY      361 TGGCTCATTTCCGGCTGGGAGAGACATCTCCAGCCCGCTTACGCTCCACACCTTG 420
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      141 CYSLIETLIESERGLYTRPGLYASRTHRIEUSERASNGLYTYRASNTRYPROGLIUEU 160
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY      421 CGATGCCCAACATCCATCATTTGAGACACAGAAAGTGTGAGAACCGCTACCCGGCAG 480
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      161 GLNCYSLEUASNALAPROIIIEUSERASPIINGLYSGINGLUALATYRPROGLYASP 180
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY      481 ATCAGACAGACCATGGTGTGCCAGCGTGCAGAGAGGGGAGAGACTCCGCCAGGCT 540
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      181 ILEHRSERASNMEETILECYVALGLYPHELEUGLYGLYLYSASPSECTYSGINGLY 200
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY      541 GACTCCGGGGGCGCTCTGCTGTAAACCATCTCTTCAAGCATATATCTCGGGGCGCAG 600
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      201 ASPSERGLYLYSPROVALVALCYASNGLYGLIUEUGINGLYILEVALSERTRPGLYLE 220
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY      601 GATCCGCTGGCATACCCCGAAAGCCTGTCTCTACAGAAAGTGTGCAATATAGTGAGC 660
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      221 GLY---CYSLALALEUYSGLYTYRPROGLYVALTYRTHRIEUSVALCYASNTYRVALASP 239
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY      661 TGGATCCGAGACGATG 678
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      240 TRPILIEGLINGLUTHRILE 245
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

```

## RESULT 6

```

S15686
tissue kallikrein (EC 3.4.21.35) precursor, renal - multimammate rat (Mastomys natalensis)
C:Species: Mastomys natalensis
C>Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: 183227; S15686
R:Fannestock, M.
DNA Cell Biol. 13, 293-300, 1994
A:Title: Characterization of kallikrein cDNAs from the African rodent Mastomys.
A:Reference number: 160208; MUID:94226702; PMID:7909667
A:Accession: 183227
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-263 <RES>
A:Cross-references: EMBL:X17352; NID:955526; PIDN:CAA35232.1; PID:955527
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:23-255/Domain: trypsin homology <TRY>
F:65,121,215/Active site: His, Asp, Ser #status predicted

```

## Alignment Scores:

```

Pred. No.:      2 31e-35      Length:      263
Score:          591.50      Matches:      106
Percent Similarity: 63.03%      Conservative: 44
Best Local Similarity: 44.54%      Mismatches: 79
Query Match:    46.39%      Indels:    9
DB:             2          Gaps:      2

```

US-09-856-320a-1\_COPY\_272\_958 (1-687) x S15686 (1-263)

```

OY      1 ATCATCAAGGGGTTCGAGTGCAGCTTCATCCAGCGCTTGAGAGCCCTGTGCGAG 60
        |||||  |||||  |||  ::|||  |||||  |||  |||  |||  |||  |||
Db      25 ILEIIEGLYGLYPHEASNCYSGULYASNSERGLNPROTRPHISVALALVALTYRARG 44
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

```

OY      61 AAGACCGGCTACTGTGTGGGGGAGCCGCTACGCCCCAGATGGCTCTGACAGACGC 120
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      45 PHEALATGYTGLCYSGLYGLYVALLEUENASPRALASNTRPVALLEUTHRALA 64
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY      121 CACTGCTTCAGACCCCGGCTACATAGTTCACCTGGGGGAGACAACTCCAGAAAGAG 180
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      65 HISCSTYRYSASNPBYSRSTYGLINVALTRPLEUGLYLYSASASNPARGHEIUSPGLU 84
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY      181 GGCTTGAGCAGACCCGGAGACCCAGTACAGTACGCTCCCGCGGCTTCAACAAGC 240
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      85 PROSERLALGHNISGLINLEUILESERLYSALALPERONHISPROGLYPHEASNMETSER 104
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY      241 CTCGCCAACAAAGACAC-----CGCAATGACATCATGCTG 276
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      105 LEUENASNPYASPRHISTHTRPROHISPROGLIUSAPRYSERASNPRIEUSMETLEU 124
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY      277 GTGAAGATGGCATGGSCAGTCCATCCATCCATCCGCTGGGAGAGACGTC---AGC 336
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      125 VALARGLEUYSLYSPROALAGLUILETHRSAPVALVALYSPROIIIEASPRLEUPROTHR 144
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY      337 CGCTGTGTCACGTGTCAGACAGCTGCTCATATTCGGCTGGGAGAGACGTC---AGC 393
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      145 GLUGLUPROTHIVALGLYSERLARGYSLIENALASERGLYTRPGLYSETRHTRPROTHR 164
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY      394 CCCAGTTACGCTGCTCCACACCTTGCAGATGCCGCAACATCCATCATTTGAGACGAC 453
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      165 GLUGLUPHEGLUTYRSETHIASPRLEUNGLYVALTYRGLIUEUENASNPANGLU 184
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY      454 AAGCTGAGAACGCTTACCCGCGCAACATCCACAGACCATAGTGTTGCCAGCGTGAG 513
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      185 VALCYSAIALYSLALHISTHGLIUSVALITHRASPRHIMETLEUCYSLAGLYLUMET 204
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
OY      514 GAAGGGGCAAGACTCCCTCCAGGGTACTCCGGGGGCGCTGCTGTAAACAGTCT 573
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      205 ASPGLYGLYLSAPRTHRCYVALGLYASPERGLYGLYPROLEUIELCYASAPGLYAL 224
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY      574 CTTCAGCATATTCCTCTGGGCCAGGATCCGCTGTCGATACCCGAAAGCCTGTGTC 633
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      225 LEUNGINGLYIETHRSERTRPGLYPROTHRPROCYSAIALALEUPROASNPVALPROGLYLE 244
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY      634 TACAGAAAGTCTGCAATATGTGAGCTGATCCGAGAGAGATGAGAACAAAT 687
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      245 TYRTHRLYSLEUIIEGLIUTYRARGSERTRPILLEYASNPVALMETALASNPASN 262
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

## RESULT 7

```

TRRT2
trypsin (EC 3.4.21.4) II precursor - rat
N:Alternate names: trypsinogen II
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-Apr-1983 #sequence_revision 30-Sep-1987 #text_change 18-Jul-1997
C:Accession: A22657; A00949
R:Craik, C.S.; Choo, O.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984
A:Title: Structure of two related rat pancreatic trypsin genes.
A:Reference number: A22657; MUID:85054880; PMID:6094547
A:Accession: A22657
A:Molecule type: DNA
A:Residues: 1-246 <CRA>
R:MacDonald, R.J.; Stary, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982
A:Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences
A:Reference number: A00948; MUID:82265624; PMID:6896710
A:Accession: A00949
A:Molecule type: mRNA
A:Residues: 9-246 <MAC>
C:Comment: The trypsin II mRNA is present in much lower quantities than the trypsin I
C:Genetics:
A:Introns: 14/1; 67/2
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <AP>
F:24-246/Product: trypsin II #status predicted <ENZ>

```



trypsin (EC 3.4.21.4) I precursor - rat  
 M.Alternate names: trypsinogen I  
 C.Species: Rattus norvegicus (Norway rat)  
 C.Date: 17-Dec-1982 #sequence\_revision 17-Dec-1982 #text\_change 24-Sep-1999  
 C.Accession: B22657; A00948  
 R.Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.  
 J.Biol. Chem. 259, 14255-14264, 1984  
 A.Title: Structure of two related rat pancreatic trypsin genes.  
 A.Reference number: A22657; MUID:85054880; PMID:6094547  
 A.Accession: B22657  
 A.Molecule type: DNA  
 A.Residues: 1-246 <CRA>  
 A.Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508  
 A.Note: The authors translated the codon ATC for residue 6 as Leu and GAC for residue 17  
 R.MacDonald, R.J.; Stary, S.J.; Swift, G.H.  
 J. Biol. Chem. 257, 9724-9732, 1982  
 A.Title: Two similar but nonallelic rat pancreatic trypsin genes. Nucleotide sequences of  
 A.Reference number: A00948; MUID:82265624; PMID:6896710  
 A.Accession: A00948  
 A.Molecule type: mRNA  
 A.Residues: 1-246 <MAC>  
 A.Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508  
 C.Genetics:  
 A.Introns: 14/1; 67/2; 152/1; 197/3  
 C.Superfamily: trypsin; trypsin homology  
 C.Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-23/Domain: activation peptide #status predicted <APTP>  
 F:24-246/Product: trypsin I #status predicted <ENZY>  
 F:24-239/Domain: trypsin I #status predicted <TRY>  
 F:30-160-48-64-132-233,139-206,171-185/Disulfide bonds: #status predicted  
 F:63,107,200/Active site: His, Asp, Ser #status predicted  
 F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:  
 Pred. No.: 4,94e-35 Length: 246  
 Score: 587.00 Matches: 111  
 Percent Similarity: 63.32% Conservative: 34  
 Best Local Similarity: 48.47% Mismatches: 78  
 Query Match: 46.04% Indels: 6  
 DB: 1 Gaps: 3

US-09-856-320a-1\_COPY\_272\_958 (1-687) x TRRT1 (1-246)

```

OY      1 ATCATCAAGGGGTTGAGTGCAGAGCCCTGCACCTCCAGCCCTGGAGAGAGCCCTGTTCGAG 60
         |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      24 ILeValGlyGlyTyrThrCysProGlnHisSerValProTyrGlnValSerIeu---Asn 42

OY      61 AAGACGGGGCTACTCTGTGGGGGAGAGGCTCATCGCCCGGAGATGGCTCCTGACAGCAGCC 120
         |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      43 SerGlyTyrHisPheCysGlyGlySerIeuIleAsnAspGlnTrrPValValSerAlaIa 62

OY      121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGAGCAACCTCCAGAGAGAG 180
         |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      63 HisCysTyrLysSerArgIleGlnValArgLeuGlyGlnHisAsnIleAsnValLeuGln 82

OY      181 GGCTGTGAGCAGACCCGAGAGCCAGTCAAGTCCGCCAGCCCGGCTTCAACAACAGC 240
         |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      83 GlyAspGlnGlnPheIleAsnAlaIleValSerIleLeuLysHisProAsnTyrSerSerTrp 102

OY      241 CTCGCCAACAAGACACCGAGCATGATCATCGCTGGTGGAGATGGATGGCATGGCATGCC 300
         |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      103 ThrIeuAsn-----AsnAspIleMetIeuIleLysIeuSerSerProValIys 118

OY      301 ATCACTGGGGCTGGAGCCCTGCACCCCTCCCTCAACCTGTGCTGCTGGAGAGC 360
         |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      119 LeuAsnAlaArgValAlaProValAlaLeuProSerAlaCysAlaProAlaGlyThrGln 138

OY      361 TGCCATATTCGGGCTGGGGGAGAGCAGTTCAGCCGCCAGTTACGCGCTTCACACCTTG 420
         |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      139 CysIeuIleSerGlyTrrPglYAsnThrIeuSerAsnGlyValAsnAsnProAspIeuIeu 158

OY      421 CGATCGGCAACATCATCATTTAGACACCAAGAAAGTGTGAGACGCTTACCCGGCAAC 480

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DB      159 GInCysValAspAlaProValIeuSerGlnAlaAspCysGlnAlaIaIaTyrProGlyGln 178
         ::|||  ::|  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
OY      481 ATCAAGACACCATGTGTGTGCACGCTGCAGAGAGGGGAGAGAGCCTCCGAGGCT 540
         |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      179 IleThrSerMetIleCysValGlyPheLeuGlnGlyGlyAspSerCysGlnGly 198

OY      541 GACTCGGGGGCCCTGTGCTGTACACAGTCTCTCAAGGAGATATCTCTGGGGCCAG 600
         |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      199 AspSerGlyGlyProValValCysAsnGlyGlnLeuGlnGlyIleValSerTrpGlyTyr 218

OY      601 GATCGCTGCATATCAACCCGAAAGCCTGTGCTTCACGAAAGTCTGCAATATGTGAC 660
         |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      219 Gly---CysAlaLeuProAsnProGlyValTyrThrValCysAsnIleValGly 237

OY      661 TGCATCCAGAGAGAGATGAGAAACAAT 687
         |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      238 TrpIleGlnAspTrpIleAlaIaAsn 246

RESULT 10
A34079
tissue kallikrein (EC 3.4.21.35) P1 precursor - rat
M.Alternate names: kallikrein-related proteinase k8
C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 22-Jun-1999
C.Accession: A34079; S10700
R.Brady, J.M.; Wines, D.R.; MacDonald, R.J.
Biochemistry 28, 5203-5210, 1989
A.Title: Expression of two kallikrein gene family members in the rat prostate.
A.Reference number: A34079; MUID:89352606; PMID:2765531
A.Accession: A34079
A.Molecule type: DNA; mRNA
A.Residues: 1-261 <BRA>
A.Cross-references: GB:M27215; GB:M27216; GB:M27217; NID:g206638; PIDN:AAA42036.1; PI
A.Experimental source: prostate
R.Elmojaded, A.; Gutman, N.; Brillard, M.; Gauthier, F.
FEBS Lett. 265, 137-140, 1990
A.Title: Substrate specificity of two kallikrein family gene products isolated from t
A.Reference number: S10698; MUID:90306305; PMID:2194829
A.Accession: S10700
A.Molecule type: protein
A.Residues: 25-43;112-138 <ELM>
A.Experimental source: submaxillary gland
A.Note: 125-Lys was also found
C.Superfamily: trypsin; trypsin homology
C.Keywords: hydrolase; serine proteinase
F:25-253/Domain: trypsin homology <TRY>
F:25-111/Product: tissue kallikrein P1 light chain #status experimental <MAT1>
F:112-261/Product: tissue kallikrein P1 heavy chain #status experimental <MAT2>
F:65,120,213/Active site: His, Asp, Ser #status predicted


Alignment Scores:  

  Pred. No.: 6,31e-35 Length: 261  

  Score: 585.50 Matches: 105  

  Percent Similarity: 61.86% Conservative: 41  

  Best Local Similarity: 44.49% Mismatches: 83  

  Query Match: 45.92% Indels: 7  

  DB: 2 Gaps: 1



US-09-856-320a-1_COPY_272_958 (1-687) x A34079 (1-261)



```

OY      1 ATCATCAAGGGGTTGAGTGCAGAGCCCTGCACCTCCAGCCCTGGAGAGAGCCCTGTTCGAG 60
         |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      25 IleIleGlyGlyPheAsnCysGlyGlyValLeuIleHisProSerTrpValIleIleAlaIa 44

OY      61 AAGACGGGGCTACTCTGTGGGGGAGAGGCTCATCGCCCGGAGATGGCTCCTGACAGCAGC 120
         |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      45 PheAsnGlnProGlnCysGlyGlyValLeuIleHisProSerTrpValIleIleAlaIa 64

OY      121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGAGCAACCTCCAGAGAGAG 180
         |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      65 HisCysTyrSerValAsnTyrGlnValTrpLeuGlyArgAsnAsnIleuGlnAspGln 84

```


```

OY	181	-GGCTGTGAGCAGACCCGCGACAGCCACCTAGTCTCTCCCGACCCCGGCTCTCAACAAACG	240
		:::::	
Db	85	ProphetaIaGlnHIsArgLeuValSerGlnSerPheProHIsProGlyPheAsnLeuAsp	104
OY	241	CTC-----CCCAACAAGACCAACCCGATGACATCATCTGCTGTG	279
		:::	
Db	105	IleIleIysAsnHIsThrArgLysProIylAsnAspTyrSerAsnAspLeuMetLeuLeu	124
OY	280	AAGATGGCATGGCCAGTCTCCATCATCCCTGGGCTGGGCACCCCTCAACCTCTCCACAGC	339
		:::                 :::::     :::     :::	
Db	125	HIsLeuIysThrProIaAspIleThrAspGlyValIlyValIllaAspLeuProthrGlu	144
OY	340	TGTGTCACTGCTGGCACCACGCTGCTCATTTCCGGCTGGGCGACGACGCTCCAGCCCCAG	399
		:::                                  :::	
Db	145	GluProIylValGlySerThrCysLeuThrSerGlyTyrGlySerIleThrProLeuIys	164
OY	400	TTACGCCCTGCACACCTTGGAGTGGCCCAACATCACCATATTCAGTACACCAAGAAGT	459
		:::::             :::::	
Db	165	TrpGluPheProAspAspLeuGlnCysValAsnIleHIsLeuLeuSerAsnGluIylScys	184
OY	460	GAGAACGCTACCCCGGCACATCAACAGACCAACCATGTGTGTGTGCAGCGTGCAGAAAGG	519
		::                          ::	
Db	185	IleIylAsnTyrAsnAspGluValTyrAspAlaMetLeuCysAlaGlyIyluMetAspGly	204
OY	520	GGCAAGGACTCTCTGCACGGGTGACATCGGGGGCCCTCGTGCCTGTAACACCAAGCTTTTCA	579
		::	
Db	205	GlyIysAspIleCysLysGlyAspSerIylGlyProLeuIleCysAspGlyValLeuGln	224
OY	580	GGCATTTATCTCTGGGGCCAGAGATCCCTGTGCAGTACACCCGAACACCTGTGTCTTACAG	639
Db	225	GlyIleThrSerTyrGlySerMetProCysGlyIuProAsnIylProSerValTyrThr	244
OY	640	AAAGCTCAAAATATGTGACTGATCCAGAGACGATGAAAGAAAT	687
		::        :::::	
Db	245	LysLeuIleIysPheThrSerTyrIleLysValMetIylGluAsn	260

```

RESULT 11
B31136
tissue kallikrein (EC 3.4.21.35) 3 precursor, submandibular - rat
N/Alternate names: glandular prokallikrein 3, submandibular
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 22-Jun-1999
C/Accession: B31136
R/Chen, Y. P.; Chao, J.; Chao, L.
Biochemistry 27, 7198-7196, 1998
A/Title: Molecular cloning and characterization of two rat renal kallikrein genes.
A/Reference number: A31136; MUID:89088074; PMID:2849988
A/Accession: B31136
A/Molecule type: DNA
A/Residues: 1-259 <CHE>
A/Cross-references: GB:M19648; GB:J02837; NTD:g205002; PIDD:AAA51640.1; PID:g205004
A/Note: The authors translated the codon GTC for residue 230 as Cys
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; serine proteinase
F:1-18/Domain: signal sequence #status predicted <Sig>
F:25-25/Domain: tissue prokallikrein 3, submandibular #status predicted <Mat>
F:63,118,211/Active site: His, Asp, Ser #status predicted

Alignment Scores:
Pred. No.:      1,23e-34      Length:      259
Score:          581.50        Matches:     105
Percent Similarity: 61.02%    Conservative: 39
Best Local Similarity: 44.49%  Mismatches: 83
Query Match:    45.61%      Indels:      9
DB:             2           Gaps:        2

```

```

oy      1 ATCATCAAGGGGTTTCGAGTGCAGCCCTACTCCAGCCCTGGCAGGACGCCCTGTTCGAG 600
        ::::: |||:::||||::: ::||| ||||| ||||| |||:::
Db      25 ValValGlyGlyTyrLysCysGluLysAsnSerClnProTrpGlnValAlaValAlIle-- 433

```

0Y AAGAGCGGGCTACTGTGGGGGCGAGCGTCATACGGCCCAAGATGGCTCTTACAGACGCC 120  
 61 AAGAGCGGGCTACTGTGGGGGCGAGCGTCATACGGCCCAAGATGGCTCTTACAGACGCC 120  
 44 ---AsnAtgTyrLeuCySGlyGlyValLeuIleAspProSerThrValIleThrAlaIa 62  
 121 CACTGGCTCAAGACCCCGCTACATAGTTCACCTGGGGGAGCAGCAACCTTCAGACGAGAG 180  
 63 HtCysTyrSerHisAsnTyrHisValLeuLeuGlyArgAsnAsnLeuPheTyrAspIu 82  
 0Y 181 GGCTGTAGCAGACCCCGGACAGCCCATAGTCCTCCCCACCCCGGCTTAC----- 234  
 83 ProPheAlaGlnTyrArgValValAsnMetInsSerPheProHisProAspTyrAsnProPhe 102  
 0Y 235 -----AACAGCCTCCCGCCCAACAAAGACACACCCCAATGACATATCTGTG 279  
 103 PheMetLysAsnHisThrLeuPheProLysAspAsnHisSerAsnAspLeuMetLeu 122  
 0Y 280 AAGATGCGATCGCCAGTCCATCATCACTGGGCGTGTGGACCCCTACCCCTCTCTCAGC 339  
 123 HisLeuSerGluProIleAspIleThrAspGlyValIleAspLeuProThrGlu 142  
 0Y 340 TGTGTCATGCTGGGACCGAGCTGCTATTCCGGCTGGGGGACAGCTCAGGCCCGCAG 399  
 143 GluProLysValGlySerThrCysLeuAlaSerGlyTyrPserSerThrLysProLeuGlu 162  
 0Y 400 TTACGCCCTCCCTACACCTTCGCGATGCGCCAAATCACCATCATTTGACAGCAGAGTGT 459  
 163 TrpGluPheProAspAspLeuGlnCysValAsnIleAsnIleLeuSerAsnGluLysCys 182  
 0Y 460 GAGAACGCTTACCCCGGACACATCAGACACCACTGGTGTGCCAGCGTCAGGAAGG 519  
 183 IleLysAlaHisThrGlnMetValThrAspValMetLeuCysAlaGlyLeuGlnGlnGly 202  
 0Y 520 GCGAAGCACTCTGTCAGAGGTGACTCGGGGGCCCTCGTGGCTGTAACTGACTCTTCAA 579  
 203 GlyLysAspThrCysAsnGlyLysPserGlyLysProLeuLeuCysAspGlyValLeuGln 222  
 0Y 580 GGCATTATCTCTGGGGGCGCAGATCCGTGCGATCACCAGGAAGCTGGTGTCTACAGC 639  
 223 GlyIleThrSerTyrPserSerValProCysGlyGluThrAsnAlaProIleIleTyrThr 242  
 0Y 640 AAGCGTCGAATATGTGACTGGATCCAGGACAGACAGAGAACAT 687  
 243 LysLeuIleLysPheMetHisSerThrIleLysGluValMetLysGluAsn 258

RESULT 12

KOPG

tissue kallikrein (EC 3.4.21.35), pancreatic - pig (tentative sequence)

N:Alternate names: glandular kallikrein; kininogenin

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 24-Apr-1984 #sequence\_rev10n 31-Dec-1993 #text\_change 31-Mar-2000

C:Accession: A00938; A92895

R:Tschesche, H.; Mair, G.; Godec, G.; Fiedler, F.; Ehret, W.; Hirschauer, C.; Lemon, Adv. Exp. Med. Biol. 120, 245-260, 1979

A:Title: The primary structure of porcine glandular kallikreins.

A:Reference number: A90015

A:Accession: A00938

A:Molecule type: protein

A:Residues: 1-89, /GWL, /53-134, /D, /136-156, /H, /158, /B, /160-224, /B, /226-332 <TSC>

A:Note: the residue identified as 225-Asx is bound to carbohydrate; therefore, we have

R:Boyd, W.; Chen, Z.; Bartels, K.; Kutzbach, C.; Schmidt-Kastner, G.; Bartunk, H. J. Mol. Biol. 164, 237-282, 1983

A:Title: Refined 2 angstrom X-ray crystal structure of porcine pancreatic kallikrein

L: structure and its comparison with bovine trypsin.

A:Reference number: A92895; PMID:83189107; PMID:6551452

A:Contents: X-ray crystallography, 2 angstroms

A:Accession: A92895

A:Molecule type: protein

A:Residues: 1-224, /B, /226-232 <BOD>

C:Comment: The protein consists of two chains, A and B, held together by disulfide bonds

C:Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release

C:Superfamily: trypsin; trypsin homolog

C:Keywords: glycoprotein; hydrolase; pancreas; serine proteinase



Db 245 LysValValHisTyrArgLysTrpIleLeuSAsphRrIleAlaIaaSn 260

RESULT 14  
A:29745  
tissue kallikrein (EC 3.4.21.35) mGK-9 precursor, submandibular - mouse  
M:Alternate names: glandular kallikrein mGK-9; major epidermal growth factor-binding protein  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text\_change 22-Jun-1999  
C:Accession: C29746; A29745; A27120; I70015  
R:Drinkwater, C.C.; Evans, B.A.; Richards, R.I.  
Biochemistry 26, 6750-6756, 1987  
A:Title: Mouse glandular kallikrein genes: identification and characterization of the gene  
A:Reference number: A90522; MUID:88107594; PMID:3322387  
A:Accession: C29746  
A:Molecule type: DNA  
A:Residues: 1-261 <DB>  
A:Cross-references: GB:M17985; NID:g193476; PIDN:AAA37681.1; PID:g387166  
A:Experimental source: strain BALB/C, salivary gland  
R:Blaber, M.; Isaacson, P.J.; Bradshaw, R.A.  
Biochemistry 26, 6742-6749, 1987  
A:Title: A complete cDNA sequence for the major epidermal growth factor binding protein  
A:Reference number: A29745; MUID:88107593; PMID:3322386  
A:Accession: A29745  
A:Molecule type: mRNA  
A:Residues: 1-261 <BL>  
A:Cross-references: NM17962; NID:g192997; PIDN:AAA37541.1; PID:g309212  
R:Isackson, P.J.; Silverman, R.E.; Blaber, M.; Server, A.C.; Nichols, R.A.; Shooter, E.M.  
Biochemistry 26, 2082-2085, 1987  
A:Title: Epidermal growth factor binding protein: identification of a different protein  
A:Reference number: A27120; MUID:87299636; PMID:3304419  
A:Accession: A27120  
A:Molecule type: Protein  
A:Residues: 25-54;112-124,'X',126-130;165-184,'X',186-187,'X',189-192 <LSA>  
R:Evans, B.A.; Drinkwater, C.C.; Richards, R.I.  
J. Biol. Chem. 262, 8027-8034, 1987  
A:Title: Mouse glandular kallikrein genes: Structure and partial sequence analysis of the  
A:Reference number: I55260; MUID:87250386; PMID:3036794  
A:Accession: I70015  
A>Status: preliminary; translated from GB/EMBL/DDbJ  
A:Molecule type: DNA  
A:Residues: 70-122 <RBS>  
A:Cross-references: GB:M18608; NID:g198500; PIDN:AAA39351.1; PID:g198506  
C:Comment: This sequence is one of approximately twenty-five members of a gene family on  
C:Genetics:  
A:Gene: KAL.  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine proteinase; zymogen  
F:1-18/Domain: signal sequence #status predicted <IG>  
F:19-24/Domain: propeptide #status predicted <PRO>  
F:25-261/Product: tissue kallikrein mGK-9, submandibular #status experimental <MAT>  
F:25-253/Domain: trypsin homology <TRY>  
F:65,120,213/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Prid. NO.:	Length:	Matches:
2.4e-34	261	102
Score:	577.50	Conservative: 48
Best Local Similarity:	63.56%	Mismatches: 79
Query Match:	43.22%	Gaps: 7
	45.29%	
	Indels: 1	
	Gaps: 2	

US-09-856-320A-1\_COPY\_272\_958 (1-687) x A29745 (1-261)

OY 1 ATCATCAAGGGGTTCGATGCACAGCCCTCACGCCCTTGCGAG 60  
||||| |||||:::||||| ::||| ||||| |||||  
Db 25 lIeValGlgyPhelYscyglulYalnserscInProrPrlsValAlaValTyrArg 44  
61 AAAGAGGGGCTACTCTGTGGGGGAGCGCTATCGCCCCCAGATGGCTCTGACAGACC 120  
:::||||| |||::: |||||  
OY 45 TyrasnslutrytllecysgllglyvallleuleuaspAlaasntPrValleuthAlaAla 64  
||||| |||||  
OY 121 CATGCGCTCAAGGCCCGCGTACATAGTTCACTGGGGGAGGACACCTCCAGAGGAGAG 180  
||||| ||| |||||:::||||| ::||| |||||

Db 65 *IscsytyrTyrGluGluAlaAnLysValSerLeuGlyLysAsnAsnLeuTyrGluGlu* 84

QY 181 *GGCTGTGACGACGCCGACGACCCAGTCACTGCTCTCCACCCCGGCTTAAACACAGC* 240

Db 85 *ProSerAlaGlnHisIleArgLeuValSerIleSerPheLeuHisProGlyTyrAsnArgSer* 104

QY 241 *CTC-----CCCAACAAAGACCGGCAATGACATGACATGCGTGTG* 279

Db 105 *LeuHisArgAsnHisIleArgHisProGluTyrIleSerPheIleAsnAspLeuLeu* 124

QY 280 *AAGATGGCATGCGCCAGTCTCCATCCATCCCTGGGCTGTGGAGACCCCTCACTGACGC* 339

Db 125 *ArgLeuSerLysProAlaAspIleThrAspValValLysProIleAlaLeuProIleGlu* 144

QY 340 *TGTGTCACTGCTGGCACACAGTCTGCTATTTCCGGCTGGGCGACAGCTCCAGCCCCAG* 399

Db 145 *GluProLysLeuGlySerThrCysLeuAlaSerIleTyrPheIleSerThrProPheLys* 164

QY 400 *TTAGCGCTGCCTCACACCTTGCGATGGCGCCACATCACTCACTTGAACAGAAAGTGT* 459

Db 165 *PheIleAsnAlaLysAspLeuGlnCysValAsnLeuLysLeuLeuProAsnGluAspCys* 184

QY 460 *GAGAACGCTTACCCCGGACATCATCAGACACATGCTGTGTGCGACAGGAGAGG* 519

Db 185 *GlyLysAlaHisIleGlyLysValThrAspValMetLeuCysAlaGlyIleThrAspGly* 204

QY 520 *GGCAGAGACTCTCTCCACAGGGGACTCCGGGGGCGCTTGTGTGTAAACAGTCTTTCAA* 579

Db 205 *GlyLysAspThrCysLysGlyAspSerGlyGlyProLeuIleCysAspGlyValLeuGln* 224

QY 580 *GGCATTTATCTCTGGGCGCAGAGATCGCTGTGCGCATCCGCAAAAGCTGTGTCTACAG* 639

Db 225 *GlyIleThrSerTyrPheGlyPheThrProCysGlyGluProLysLysProGlyValTyrThr* 244

QY 640 *AAAGTGTGCAATATGTGATCGATCCAGACAGACATGATGAAGAAT 687*

Db 245 *LysLeuIleLysPheThrSerTyrPheLysAspThrMetAlaLysAsn 260*

RESULT 15

TRPGTR

trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)

N:Contains: trypsinogen

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 31-Mar-2000

C:Accession: A90568; A90568; A00947

R:Charles, M.; Roverey, M.; Guidoni, A.; Desnuelle, P.

Biochim. Biophys. Acta 69, 115-129, 1963

A:Title: Su le trypsinogene et la trypsine de porc.

A:Reference number: A90641

A:Accession: A90641

A:Molecule type: protein

A:Residues: 1-10 <CHAS>

R:Hermodson, M.A.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.

Biochemistry 12, 3146-3153, 1973

A:Title: Determination of the amino acid sequence of porcine trypsin by sequenator an

A:Reference number: A90368; MUID:73258692; PMID:4738933

A:Accession: A90368

A:Molecule type: protein

A:Residues: 9-231 <HER>

A>Note: at position 20, Ile and Val occur alternatively

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; pancreas; polymorphism; protein digestion; serine proteinase;

F:1-231/Product: trypsinogen #status experimental <ZYM>

F:1-8/Domain: activation peptide #status experimental <APV>

F:9-231/Product: trypsin #status experimental <MAT>

F:9-224/Domain: trypsin homology <TRY>

F:15-145,33-49,117-218,124-191,156-170,181-205/Disulfide bonds: #status predicted

F:48,92,186/Active site: His, Asp, Ser #status predicted

F:60,62,65,70/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:

Pred. No.: 2,64e-34 Length: 231

Score: 577.00 Matches: 110

Percent Similarity:	63.04%	Conservative:	35
Best Local Similarity:	47.83%	Mismatches:	77
Query Match:	45.25%	Indels:	8
DB:	1	Gaps:	4

US-09-856-320A-1\_COPY\_272\_958 (1-687) x TRPGTR (1-231)

QY	1	ATCATCAAGGGGTTCGAGCAAGGCTCACTCCGACCGCTCCAGAGCGACGCTTCGAG	60
Db	9	lIeValGlYglYtYrThrcysAlaAlaIAsnSerlIeProtyrGlInValSerLeuAsnSer	28
QY	61	AAGACCGGGCTACTGTGTGGGGCGACGCTCATGCCGCCCAAGATGGCTTCGACGACGCC	120
Db	29	gIySerHis--PheCyselYglYserLeuIleAsnSerGlnTrpValValSerAlaAla	47
QY	121	CAGTGGCTCAAGCCCGCTACATTAATTCACCTGGGGCGACCAACTCCAGAAAGAGAG	180
Db	48	HisCysTyrlYgSerArglIeGlnValArgLeuGlYcunHIsanHlIeAspValLeuGlu	67
QY	181	GGCTGTGACGACACCGGACCGGACCACTAGTCCCTCCCAACCCCGGCTTCAC--AAC	237
Db	68	GlYAsnGlYglNpheIleAsnAlaAlaIAsylIeIleThrHisProAsnPhaAsnGlYAsn	87
QY	238	AGCTTCGCCCAAAAGAACCCCGCAATACATCATGTCTGGTGAAGATGGCATGCCACATC	297
Db	88	ThrlLeuAsp-----AsnspIleMetLeuIleIlyslsLeuSerProAla	102
QY	298	TCCATCACCTGGGCTGTGGGACCCCTCACCCCTTCCTCCACGCTGTGCACGTGGCGAC	357
Db	103	ThrlLeuAsnSerArgValAlaIethrValSerLeuProArgSerCysAlaAlaIaglyThr	122
QY	358	AGCTGGCTCATTTCCGGCTGGGGGACGACGTCACAGCCCAAGTAAAGCGCTGCACACC	417
Db	123	GlucYsLeuIleSerGlyTyrPelYAsnThrIlySerSerIySerIyProSerLeu	142
QY	418	TTTCGATGGCCCAACATCACATCATCATTCATGAGCAGAGATGTGGAAGCGCTACCCGGC	477
Db	143	LeuGlncYsLeuIlyAlaProValIleuSerAspSerIyCysIySerSerIyProGly	162
QY	478	AACATCACAGAACCATGGTGTGTGCCAGGCTGCAGAAAGGGGCAAGACTCTGCAG	537
Db	163	GlInIleThrGlYAsnMetIleCysValGlYpHeLeuIleuGlncYglYlYsAspSerCysGln	182
QY	538	GGTGAATCCGGGGGCGCTGTGGTGTGAACCAAGTCTCTTCAAGGCATTAATCCGTGGGGC	597
Db	183	GlYAspSerGlyglYProValIValCysAsnGlYglInLeuGlncYglIleValSerTrpGly	202
QY	598	CAGGATCCGTGTGGCATCACCCGAAAGCGTGTGTCAACAGAAAGTCTGCATAATATGTG	657
Db	203	TyrGlY---CysAlaGlInIlyAsnIlysProGlyValYrThrlYsValCysAsnTyVal	221
QY	658	GACTGGATCCAGGAGCATGAAGACAT	687
Db	222	AsnTrpIleGlnIleGlnThrIleAlaIAsn	231

Search completed: October 15, 2003, 20:27:40  
Job time : 21.8338 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic acid - nucleic search, using sw model

Run on: October 15, 2003, 16:00:49 ; Search time 250.886 Seconds  
(without alignments)  
7105.351 Million cell updates/sec

Title: US-09-856-320a-1\_COPY\_272\_958

Perfect score: 687  
Sequence: 1 atccatcaagggttcgagtg.....aggagacatgaagaacaat 687

Scoring table: IDENTITY\_MTC  
Gapop 10.0 , Gapext 1.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
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7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
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13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	687	100.0	1186	US-10-205-823-211	Sequence 211, App
2	687	100.0	1204	US-09-946-374-169	Sequence 169, App
3	687	100.0	1204	US-10-015-387A-169	Sequence 169, App
4	687	100.0	1204	US-10-137-870-505	Sequence 505, App
5	687	100.0	1204	US-10-140-018-505	Sequence 505, App
6	687	100.0	1204	US-10-140-021-505	Sequence 505, App
7	687	100.0	1204	US-10-140-274-505	Sequence 505, App
8	687	100.0	1204	US-10-140-471-505	Sequence 505, App
9	687	100.0	1204	US-10-140-807-505	Sequence 505, App
10	687	100.0	1204	US-10-140-922-505	Sequence 505, App
11	687	100.0	1204	US-10-140-924-505	Sequence 505, App
12	687	100.0	1204	US-10-140-926-505	Sequence 505, App
13	687	100.0	1204	US-10-141-698-505	Sequence 505, App
14	687	100.0	1204	US-10-141-702-505	Sequence 505, App
15	687	100.0	1204	US-10-141-704-505	Sequence 505, App
16	687	100.0	1204	US-10-142-421-505	Sequence 505, App

17	687	100.0	1204	US-10-142-432-505	Sequence 505, App
18	687	100.0	1204	US-10-142-767-505	Sequence 505, App
19	687	100.0	1204	US-10-143-033-505	Sequence 505, App
20	687	100.0	1204	US-10-144-994-505	Sequence 505, App
21	687	100.0	1204	US-10-145-628-505	Sequence 505, App
22	687	100.0	1204	US-10-145-631-505	Sequence 505, App
23	687	100.0	1204	US-10-145-633-505	Sequence 505, App
24	687	100.0	1204	US-10-145-746-505	Sequence 505, App
25	687	100.0	1204	US-10-145-748-505	Sequence 505, App
26	687	100.0	1204	US-10-145-823-505	Sequence 505, App
27	687	100.0	1204	US-10-145-826-505	Sequence 505, App
28	687	100.0	1204	US-10-145-870-505	Sequence 505, App
29	687	100.0	1204	US-10-145-876-505	Sequence 505, App
30	687	100.0	1204	US-10-145-959-505	Sequence 505, App
31	687	100.0	1204	US-10-146-724-505	Sequence 505, App
32	687	100.0	1204	US-10-146-725-505	Sequence 505, App
33	687	100.0	1204	US-10-146-795-505	Sequence 505, App
34	687	100.0	1204	US-10-147-485-505	Sequence 505, App
35	687	100.0	1204	US-10-147-501-505	Sequence 505, App
36	687	100.0	1204	US-10-147-504-505	Sequence 505, App
37	687	100.0	1204	US-10-147-506-505	Sequence 505, App
38	687	100.0	1204	US-10-147-509-505	Sequence 505, App
39	687	100.0	1204	US-10-147-510-505	Sequence 505, App
40	687	100.0	1204	US-10-147-511-505	Sequence 505, App
41	687	100.0	1204	US-10-147-529-505	Sequence 505, App
42	687	100.0	1204	US-10-152-357-505	Sequence 505, App
43	687	100.0	1204	US-10-153-586-505	Sequence 505, App
44	687	100.0	1204	US-10-158-783-505	Sequence 505, App
45	687	100.0	1204	US-10-158-786-505	Sequence 505, App

## ALIGNMENTS

RESULT 1  
US-10-205-823-211  
Sequence 211, Application US/10205823  
GENERAL INFORMATION:  
US20030108963A1  
APPLICANT: Schlegel, Robert  
APPLICANT: Monahan, John E.  
APPLICANT: Endege, Wilson O.  
APPLICANT: Gannavarapu, Manjula  
APPLICANT: Gorbacheva, Bella  
APPLICANT: Hoersch, Sebastian  
APPLICANT: Kametkar, Shubhangi  
APPLICANT: Monsey, Angela M.  
APPLICANT: Glatz, Karen  
APPLICANT: Zhao, Xumei  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER  
FILE REFERENCE: MRI-044  
CURRENT APPLICATION NUMBER: US/10/205,823  
PRIOR FILING DATE: 2002-07-25  
PRIOR APPLICATION NUMBER: 60/307,982  
PRIOR FILING DATE: 2001-07-25  
PRIOR APPLICATION NUMBER: 60/314,356  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/325,020  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 60/341,746  
PRIOR FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: 60/362,158  
PRIOR FILING DATE: 2002-03-05  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: fastseq for Windows Version 4.0  
SEQ ID NO 211  
LENGTH: 1186  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-205-823-211

Query Match 100.0%; Score 687; DB 14; Length 1186;  
Best Local Similarity 100.0%; Pred. No. 1,9e-186;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATCTCAAGGGGCTGAGTGCAGACCTCTCCAGCCCTGGGAGGAGCCCTTTGAG 60
    |||
DB 185 ATCTCAAGGGGCTGAGTGCAGACCTCTCCAGCCCTGGGAGGAGCCCTTTGAG 244
    |||
QY 61 AAGAGCGGCTACTCTGTGGGGGAGCGCTCATCGCCCGAGATGGCTCTGACAGCAGCC 120
    |||
DB 245 AAGAGCGGCTACTCTGTGGGGGAGCGCTCATCGCCCGAGATGGCTCTGACAGCAGCC 304
    |||
QY 121 CACTGCTCAAGCCCGCTACATATGTTACCTGGGGGAGCACAACCTTCAGAGAGAG 180
    |||
DB 305 CACTGCTCAAGCCCGCTACATATGTTACCTGGGGGAGCACAACCTTCAGAGAGAG 364
    |||
QY 181 GGCTGTAGAGAGAGCGGAGAGCGCATGAGTCTTCCCGAGCCCGGCTTCAAGAACGC 240
    |||
DB 365 GGCTGTAGAGAGAGCGGAGAGCGCATGAGTCTTCCCGAGCCCGGCTTCAAGAACGC 424
    |||
QY 241 CTCCCAACAAAGACACCGCATGACATGCTGTGAAGATGGATGCCAGTCTCC 300
    |||
DB 425 CTCCCAACAAAGACACCGCATGACATGCTGTGAAGATGGATGCCAGTCTCC 484
    |||
QY 301 ATCACTGGGCTGTGCAGCCCTCACCCTCTCTACGCTGTCTACTGTGCGCAGCAGC 360
    |||
DB 485 ATCACTGGGCTGTGCAGCCCTCACCCTCTCTACGCTGTCTACTGTGCGCAGCAGC 544
    |||
QY 361 TGCTCTATTTCCGGCTGGGGAGAGAGCGTCCAGTACCGCCGCTTCAAGAACGC 420
    |||
DB 545 TGCTCTATTTCCGGCTGGGGAGAGAGCGTCCAGTACCGCCGCTTCAAGAACGC 604
    |||
QY 421 CGATGCGCCCAACATCACCATTGAGCAGCAGAGTGTGAAGACCGCTACCCGGGAGC 480
    |||
DB 605 CGATGCGCCCAACATCACCATTGAGCAGCAGAGTGTGAAGACCGCTACCCGGGAGC 664
    |||
QY 481 ATCAAGACACCATGCTGTGTGCGCAGGTGAGAGAGGGGAGAGAGCTCTGCGCAGGT 540
    |||
DB 665 ATCAAGACACCATGCTGTGTGCGCAGGTGAGAGAGGGGAGAGAGCTCTGCGCAGGT 724
    |||
QY 541 GACTCGGGGGGCGCTGTGTGTGTACACAGCTCTTCAAGGATTAATCTCTGGGGGAG 600
    |||
DB 725 GACTCGGGGGGCGCTGTGTGTGTGTACACAGCTCTTCAAGGATTAATCTCTGGGGGAG 784
    |||
QY 601 GATCGGTGTGCGATCACCCGAAAGCGTGTGTGTACAGAAAGTCTCAATATGTGTGAC 660
    |||
DB 785 GATCGGTGTGCGATCACCCGAAAGCGTGTGTGTGTACAGAAAGTCTCAATATGTGTGAC 844
    |||
QY 661 TGGATCCAGAGAGAGATGAAGAACAT 687
    |||
DB 845 TGGATCCAGAGAGAGATGAAGAACAT 871
    |||
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RESULT 2  
US-09-946-374-169

; Sequence 169, Application US/09946374  
; Publication No. US20030073129A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paonli, Nicholas F.

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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C1  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
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;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105694  
;; PRIOR FILING DATE: 1998-10-26  
;; PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 687; DB 11; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 1.9e-186;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTGGAGTGAAGCCTCACTCCAGCCCTGGCAGGACCCCTGTTGAG 60  
DB 169 ATCATCAAGGGGTTGGAGTGAAGCCTCACTCCAGCCCTGGCAGGACCCCTGTTGAG 228  
QY 61 AAGAGCGGGCTACTCTGTGGGGCAGAGCTATCGCCCAATGAGTGGCTCTGTGACAGAGCC 120  
DB 229 AAGAGCGGGCTACTCTGTGGGGCAGAGCTATCGCCCAATGAGTGGCTCTGTGACAGAGCC 288  
QY 121 CACTGCTCAAGCCCGGCTACATAGTTCACCTGGGGCAGACACCTCCAGAAAGAGAG 180  
DB 289 CACTGCTCAAGCCCGGCTACATAGTTCACCTGGGGCAGACACCTCCAGAAAGAGAG 348  
QY 181 GCGTGTGAGCAGACCCGGCAGAGCCACTGAGTCCCTCCAGCCCGGGCTTCAACAAGAGC 240  
DB 349 GCGTGTGAGCAGACCCGGCAGAGCCACTGAGTCCCTCCAGCCCGGGCTTCAACAAGAGC 408  
QY 241 CTTCCCAACAAGACACCCGCAATGACATCATGCTGTGTAAATGGCATCGGCAATCTTCC 300  
DB 409 CTTCCCAACAAGACACCCGCAATGACATCATGCTGTGTAAATGGCATCGGCAATCTTCC 468  
QY 301 ATCACTGGGCTGTGGAGACCCCTCAACCCCTCTCTCAAGCTGTGTACATGCTGGACAGGC 360  
DB 469 ATCACTGGGCTGTGGAGACCCCTCAACCCCTCTCTCAAGCTGTGTACATGCTGGACAGGC 528  
QY 361 TGCCTCATTTCCGGCTGGGGCAGACGTTCCAGCCCTTACGCTTGTGACCTTGGACACCTG 420  
DB 529 TGCCTCATTTCCGGCTGGGGCAGACGTTCCAGCCCTTACGCTTGTGACCTTGGACACCTG 588  
QY 421 CGATGCGGCACATATACCATCATTTATAGACACGAAAGTGTGAGAACGCTTACCCGGGCAAC 480  
DB 589 CGATGCGGCACATATACCATCATTTATAGACACGAAAGTGTGAGAACGCTTACCCGGGCAAC 648



OY	61	AAGAGCGGGCTACTGTGGGGGCGAGCGCTAATGGCCCCAGATGGGCTCTGACAGAGGC	120
Db	229	AAGACGGGGCTACTTGTGGGGGCGAGCGCTAATGGCCCCAGATGGGCTCTGACAGAGGC	288
OY	121	CAGTGCCTCAAGCCCCCGCTACATAGTTACCTGGGGGCGAGCACACCTCCAGAGAGAG	180
Db	289	CAGTGCCTCAAGCCCCCGCTACATAGTTACCTGGGGGCGAGCACACCTCCAGAGAGAG	348
OY	181	GGCTGTGAGCAGACCCGGGACAGCCACTAGTCTTCCCCACCCGGGCTTCAACAACAGC	240
Db	349	GGCTGTGAGCAGACCCGGGACAGCCACTAGTCTTCCCCACCCGGGCTTCAACAACAGC	408
OY	241	CTCCCCAACAAAGACACACGGCAATGACATCATGCGTGGTGAATGGCAATCGGCAAGCTCC	300
Db	409	CTCCCCAACAAAGACACACGGCAATGACATCATGCGTGGTGAATGGCAATCGGCAAGCTCC	468
OY	301	ATCACCTGGGGCTGTGCGACACCCCTCACCCCTCTCCACGCTGTGCACCTGTGGACACAGC	360
Db	469	ATCACCTGGGGCTGTGCGACACCCCTCACCCCTCTCCACGCTGTGCACCTGTGGACACAGC	528
OY	361	TGCCTCATTTCCGGCTGGGGGCGAGCAGTCCAGCCCCAGTTACGCTGCTGCACACCTTG	420
Db	529	TGCCTCATTTCCGGCTGGGGGCGAGCAGTCCAGCCCCAGTTACGCTGCTGCACACCTTG	588
OY	421	CGATGCGCGCAACATACCATCATTTAGACACAGAAAGTGTGAAGAGGCTTACCCCGGCAAC	480
Db	589	CGATGCGCGCAACATACCATCATTTAGACACAGAAAGTGTGAAGAGGCTTACCCCGGCAAC	648
OY	481	ATCACAGACACCATGTGTGTGCCAGCGGTGACGAAAGGGGGCGAAGAGACTCCAGCAGGT	540
Db	649	ATCACAGACACCATGTGTGTGCCAGCGGTGACGAAAGGGGGCGAAGAGACTCCAGCAGGT	708
OY	541	GACTCCGGGGGCCCTCTGTGTGTAAACAGTCTCTTCAAGGCAATTAATCTCTGGGGCGAG	600
Db	709	GACTCCGGGGGCCCTCTGTGTGTAAACAGTCTCTTCAAGGCAATTAATCTCTGGGGCGAG	768
OY	601	GATCCGCTGTGGCATACCCGAAAGCCTGTGTCTACAGAAAGTGTGCAAAATATGTGAC	660
Db	769	GATCCGCTGTGGCATACCCGAAAGCCTGTGTCTACAGAAAGTGTGCAAAATATGTGAC	828
OY	661	TGGATCCAGAGACGATGAAGAACAT	687
Db	829	TGGATCCAGAGAGATGAAGAACAT	855

NUMBER OF SEQ ID NOS: 550									
; SEQ ID NO 505									
; LENGTH: 1204									
; TYPE: DNA									
; ORGANISM: Homo Sapien									
US-10-140-018-505									
Query Match 100.0%; Score 687; DB 12; Length 1204;									
Best Local Similarity 100.0%; Prid. No. 1,9e-186;									
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	169	ATCATCAAGGGGCTCGAGTGCACCCCTACCTCCAGCCCTGGCGAGGCGCCCTGTTGGAG	228						
QY	61	AAGACGGGGCTACTCTGTGGGGCAGCCCTCATGCCCCAGATGGCTCTGACAGCAGCC	120						
DB	229	AAGACGGGGCTACTCTGTGGGGCAGCCCTCATGCCCCAGATGGCTCTGACAGCAGCC	288						
QY	121	CACGTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGACACAACCTCCAGAAAGAGAG	180						
DB	289	CACGTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGACACAACCTCCAGAAAGAGAG	348						
QY	181	GGCTGTAGCAGACCCGGCAGCCGACCTGATCTCTTCCCCACCCGGCTTCAACACAGC	240						
DB	349	GGCTGTAGCAGACCCGGCAGCCGACCTGATCTCTTCCCCACCCGGCTTCAACACAGC	408						
QY	241	CTCCCAACAAGACACCGCAANTGACATGCTGTGAAAGTGGATGGATGCCAGTCTCC	300						
DB	409	CTCCCAACAAGACACCGCAANTGACATGCTGTGAAAGTGGATGGATGCCAGTCTCC	468						
QY	301	ATCACCTGGGGCTGTGCGACCCCTCACCTCTCCGACAGCTGTGTCACTGCTGGCAGCAGC	360						
DB	469	ATCACCTGGGGCTGTGCGACCCCTCACCTCTCCGACAGCTGTGTCACTGCTGGCAGCAGC	528						
QY	361	TGCTCTATTTTCGGGCTGGGGAGCAGTCCAGCCCGCAAGTTACGCTGCTCAACCTTG	420						
DB	529	TGCTCTATTTTCGGGCTGGGGAGCAGTCCAGCCCGCAAGTTACGCTGCTCAACCTTG	588						
QY	421	CGATGGCCCAACATCATCATATTGAGCAGCAGAAAGTGTAGAAAGGCTTACCCCGGCAAC	480						
DB	589	CGATGGCCCAACATCATCATATTGAGCAGCAGAAAGTGTAGAAAGGCTTACCCCGGCAAC	648						
QY	481	ATCACAGACACCATGTGTGTGTGCCAGCGTCCAGAAAGGGGGCAAGAGACTCTCCAGAGT	540						
DB	649	ATCACAGACACCATGTGTGTGTGCCAGCGTCCAGAAAGGGGGCAAGAGACTCTCCAGAGT	708						
QY	541	GACTCCGGGGGCCCTCTGTGTCTGTAAACAATCTTCAAGGCAATTATCTCTGGGGCCAG	600						
DB	709	GACTCCGGGGGCCCTCTGTGTCTGTAAACAATCTTCAAGGCAATTATCTCTGGGGCCAG	768						
QY	601	GATCCGCTGTCGATACACCGAAAGCCGGGTCTTACACGAAACTCTGCAAAATATGTGGAC	660						
DB	769	GATCCGCTGTCGATACACCGAAAGCCGGGTCTTACACGAAACTCTGCAAAATATGTGGAC	828						
QY	661	TGGATCCAGAGACGATGAAGAACAAAT	687						
DB	829	TGGATCCAGAGACGATGAAGAACAAAT	855						
RESULT 6									
US-10-140-021-505									
; Sequence 505; Application US/10140021									
; Publication No. US20030138886A1									
GENERAL INFORMATION:									
; APPLICANT: Baker, Kevin P.									
; APPLICANT: Beresini, Maureen									
; APPLICANT: DeForge, Laura									
; APPLICANT: Desnoyers, Luc									
; APPLICANT: Filvaroff, Ellen									
; APPLICANT: Gao, Wei-Qiang									
; APPLICANT: Gerlitsen, Mary E.									
; APPLICANT: Goddard, Audrey									

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; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C167
; CURRENT APPLICATION NUMBER: US/10/140,021
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-021-505

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Query Match 100.0%; Score 687; DB 12; Length 1204;

Best Local Similarity 100.0%; Pred. No. 1,9e-186; Mismatches 0; Indels 0; Gaps 0;

Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATCATCAAGGGGTTGAGTGCAAGCCCTCACTCCAGCCCTGGCAGGAGCCCTGTTGAG 60
DB 169 ATCATCAAGGGGTTGAGTGCAAGCCCTCACTCCAGCCCTGGCAGGAGCCCTGTTGAG 228
QY 61 AAGCGGGGCTACTGCTGGGGGAGGCTGATGCGCCCGGAGATGGGCTCGAGAGCAGCC 120
DB 229 AAGCGGGGCTACTGCTGGGGGAGGCTGATGCGCCCGGAGATGGGCTCGAGAGCAGCC 288
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGCACAACCTCGAAGAGAGAG 180
DB 289 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGCACAACCTCGAAGAGAGAG 348
QY 181 GCGTGTAGAGACAGCCGAGACGACCTGCTCTCCCAACCCCGGCTCGAAGAGAG 240
DB 349 GCGTGTAGAGACAGCCGAGACGACCTGCTCTCCCAACCCCGGCTCGAAGAGAG 408
QY 241 CTCCCAACAAGACGACGCAATGATGCTGTGGAAGATGGGATGGGCTGCTCC 300
DB 409 CTCCCAACAAGACGACGCAATGATGCTGTGGAAGATGGGATGGGCTGCTCC 468
QY 301 ATCACTGGGCTGTGACCCCTCACCCCTCTCTCAAGCTGTGTCACTGTGAGCAGC 360
DB 469 ATCACTGGGCTGTGACCCCTCACCCCTCTCTCAAGCTGTGTCACTGTGAGCAGC 528
QY 361 TGCTCTATTTCCGGCTGGGGAGCAGCTCCAGCCCGGATTAAGGCTGCTCACCTTG 420
DB 529 TGCTCTATTTCCGGCTGGGGAGCAGCTCCAGCCCGGATTAAGGCTGCTCACCTTG 588
QY 421 CGATGGCCCAACATCATTGATGAGCAGCAGAGGTGAGAAGGCTGCTCCCGGAGC 480
DB 589 CGATGGCCCAACATCATTGATGAGCAGCAGAGGTGAGAAGGCTGCTCCCGGAGC 648
QY 481 ATCAAGACACATGATGTGTGCGAGGCTGAGAGAGGAGGAGGAGGAGGAGGAGG 540
DB 649 ATCAAGACACATGATGTGTGCGAGGCTGAGAGAGGAGGAGGAGGAGGAGGAGG 708
QY 541 GACTCGGGGGCCCTGCTGTGTGTAACCACTGCTTCAAGGATTAATCTCTGGGGCAG 600
DB 709 GACTCGGGGGCCCTGCTGTGTGTAACCACTGCTTCAAGGATTAATCTCTGGGGCAG 768
QY 601 GATCCGTTGCGATCAGCCGAAAGCCGTTGCTACAGAAAGCTGCAAAATATGTGAG 660
DB 769 GATCCGTTGCGATCAGCCGAAAGCCGTTGCTACAGAAAGCTGCAAAATATGTGAG 828
QY 661 TGGATCCAGGAGATGATGAAGCAAT 687
DB 829 TGGATCCAGGAGATGATGAAGCAAT 855

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# RESULT 7

US-10-140-274-505

Sequence 505, Application US/10140274

Publication No. US20030143674A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Beresini, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Maury E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P330R1C161

CURRENT APPLICATION NUMBER: US/10/140,274

CURRENT FILING DATE: 2002-05-06

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 505

LENGTH: 1204

TYPE: DNA

ORGANISM: Homo Sapien

US-10-140-274-505

Query Match 100.0%; Score 687; DB 12; Length 1204;

Best Local Similarity 100.0%; Pred. No. 1,9e-186; Mismatches 0; Indels 0; Gaps 0;

Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AAGCGGGGCTACTGCTGGGGGAGGCTGATGCGCCCGGAGATGGGCTCGAGAGCAGCC 120
DB 229 AAGCGGGGCTACTGCTGGGGGAGGCTGATGCGCCCGGAGATGGGCTCGAGAGCAGCC 288
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGCACAACCTCGAAGAGAGAG 180
DB 289 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGCACAACCTCGAAGAGAGAG 348
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QY 828 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGCACAACCTCGAAGAGAGAG 828
DB 828 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGCACAACCTCGAAGAGAGAG 855

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; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C177
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-924-505

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Query Match      100.0%; Score 687; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 1.9e-186;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATCATCAAGGGGTGGAGTGAAGCCCTCACTCCAGCCCTGGAGGAGCCCTGTTGAG 60
DB 169 ATCATCAAGGGGTGGAGTGAAGCCCTCACTCCAGCCCTGGAGGAGCCCTGTTGAG 228
QY 61 AAGAGCGGGCTACTGTGTGGGCGAGGCTCATGCCCCAGATGGCTCTGACAGAGCC 120
DB 229 AAGAGCGGGCTACTGTGTGGGCGAGGCTCATGCCCCAGATGGCTCTGACAGAGCC 288
QY 121 CACTGCTCAAGCCCCGCTACATAGTACCTGGGGGACACAACTCCAGAGAGAG 180
DB 289 CACTGCTCAAGCCCCGCTACATAGTACCTGGGGGACACAACTCCAGAGAGAG 348
QY 181 GCGCTGAGACAGACCCGAGCAGCAGTGAAGTCTCCCGCCGCTTCAACAACAGC 240
DB 349 GCGCTGAGACAGACCCGAGCAGCAGTGAAGTCTCCCGCCGCTTCAACAACAGC 408
QY 241 CTCGCCAACAAAGACACCGCAATGACATCATGTGTGTAGAGATGGCATCGCCAGTCC 300
DB 409 CTCGCCAACAAAGACACCGCAATGACATCATGTGTGTAGAGATGGCATCGCCAGTCC 468
QY 301 ATCAGCTGGGCTGTGTGAGACCCCTCACTCTCTCACTGTGTGTACCTGTGACAGC 360
DB 469 ATCAGCTGGGCTGTGTGAGACCCCTCACTCTCTCACTGTGTGTACCTGTGACAGC 528
QY 361 TGCCTCATATTCGGGCTGGGGGAGCAGTGCACGCCCCCAATGACGCTGTGCTACAGCTTG 420
DB 529 TGCCTCATATTCGGGCTGGGGGAGCAGTGCACGCCCCCAATGACGCTGTGCTACAGCTTG 588
QY 421 CGATGCGCCACATCATCACTATGAGCAGCAGAAAGTGTGAGAACGCTTACCCGCGCAAC 480
DB 589 CGATGCGCCACATCATCACTATGAGCAGCAGAAAGTGTGAGAACGCTTACCCGCGCAAC 648
QY 481 ATCAGAGACACCATGTGTGTGCGCAGCGTGCAGAGAAAGGGGAGAGAGCTCTGCCAGGT 540
DB 649 ATCAGAGACACCATGTGTGTGCGCAGCGTGCAGAGAAAGGGGAGAGAGCTCTGCCAGGT 708
QY 541 GACTCCGGGGGCTCTGTGTGTAAACAGTCTTCAAGGCAATATCTGCTGGGGCCAG 600
DB 709 GACTCCGGGGGCTCTGTGTGTAAACAGTCTTCAAGGCAATATCTGCTGGGGCCAG 768
QY 601 GATCCGTGTGATACCCGGAAGCCTGTGTGTACAGAGAAAGTGTGCAAAATATGTGAC 660
DB 769 GATCCGTGTGATACCCGGAAGCCTGTGTGTGTACAGAGAAAGTGTGCAAAATATGTGAC 828
QY 661 TGGATCCAGAGACATGAAGAACAT 687

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DB 829 TGGATCCAGAGACATGAAGAACAT 855

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## RESULT 12

US-10-140-926-505

Sequence 505, Application US/10140926

Publication No. US20030134356A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Deforge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerltzen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Collin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P330R1C187

CURRENT APPLICATION NUMBER: US/10/140,926

CURRENT FILING DATE: 2002-05-07

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 505

LENGTH: 1204

TYPE: DNA

ORGANISM: Homo Sapien

US-10-140-926-505

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Query Match      100.0%; Score 687; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 1.9e-186;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATCATCAAGGGGTGGAGTGAAGCCCTCACTCCAGCCCTGGAGGAGCCCTGTTGAG 60
DB 169 ATCATCAAGGGGTGGAGTGAAGCCCTCACTCCAGCCCTGGAGGAGCCCTGTTGAG 228
QY 61 AAGAGCGGGCTACTGTGTGGGCGAGGCTCATGCCCCAGATGGCTCTGACAGAGCC 120
DB 229 AAGAGCGGGCTACTGTGTGGGCGAGGCTCATGCCCCAGATGGCTCTGACAGAGCC 288
QY 121 CACTGCTCAAGCCCCGCTACATAGTACCTGTGGGAGCAGCAACCTCCAGAGAGAG 180
DB 289 CACTGCTCAAGCCCCGCTACATAGTACCTGTGGGAGCAGCAACCTCCAGAGAGAG 348
QY 289 CACTGCTCAAGCCCCGCTACATAGTACCTGTGGGAGCAGCAACCTCCAGAGAGAG 348
QY 241 CTCGCCAACAAAGACACCGCAATGACATCATGTGTGTAGAGATGGCATCGCCAGTCC 300
DB 409 CTCGCCAACAAAGACACCGCAATGACATCATGTGTGTAGAGATGGCATCGCCAGTCC 468
QY 409 CTCGCCAACAAAGACACCGCAATGACATCATGTGTGTAGAGATGGCATCGCCAGTCC 468
QY 241 CTCGCCAACAAAGACACCGCAATGACATCATGTGTGTAGAGATGGCATCGCCAGTCC 300
DB 409 CTCGCCAACAAAGACACCGCAATGACATCATGTGTGTAGAGATGGCATCGCCAGTCC 468
QY 301 ATCAGCTGGGCTGTGTGAGACCCCTCACTCTCTCACTGTGTGTACCTGTGACAGC 360
DB 649 ATCAGCTGGGCTGTGTGAGACCCCTCACTCTCTCACTGTGTGTACCTGTGACAGC 528
QY 469 ATCAGCTGGGCTGTGTGAGACCCCTCACTCTCTCACTGTGTGTACCTGTGACAGC 528
QY 361 TGCCTCATATTCGGGCTGGGGGAGCAGTGCACGCCCCCAATGACGCTGTGCTACAGCTTG 420
DB 529 TGCCTCATATTCGGGCTGGGGGAGCAGTGCACGCCCCCAATGACGCTGTGCTACAGCTTG 588
QY 421 CGATGCGCCACATCATCACTATGAGCAGCAGAAAGTGTGAGAACGCTTACCCGCGCAAC 480

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OY 1 ATCATCAAGGGGTTGAGTGCAGAGCTCACTCCAGCCCTGGCAGGACCCCTGTTCCAG 60
Db 169 ATCATCAAGGGGTTGAGTGCAGAGCTCACTCCAGCCCTGGCAGGACCCCTGTTCCAG 228
OY 61 AAGACGGGGCTACTCTGTGGGGGCGAGCGTCATCCGCCCAAGTGGCTCTGACAGCAGC 120
Db 229 AAGACGGGGCTACTCTGTGGGGGCGAGCGTCATCCGCCCAAGTGGCTCTGACAGCAGC 288
OY 121 CACTGCTCAAGCCCCGCTACATAGTTCACCTGGGGGCGAGCACAACCTCCAGAGAGAG 180
Db 289 CACTGCTCAAGCCCCGCTACATAGTTCACCTGGGGGCGAGCACAACCTCCAGAGAGAG 348
OY 181 GCGCTGAGCAGAGCCCGGAGCAGCCAGTGCCTTCCCGCCAGCCCGGCTTCAACAACAGC 240
Db 349 GCGCTGAGCAGAGCCCGGAGCAGCCAGTGCCTTCCCGCCAGCCCGGCTTCAACAACAGC 408
OY 241 CTCCCAACAAGAGACCCGCAATGACATGCTGGTGAAGATGGATCGGCACTGTC 300
Db 409 CTCCCAACAAGAGACCCGCAATGACATGCTGGTGAAGATGGATCGGCACTGTC 468
OY 301 ATCACTGGGCTGTGCGAGCCCTCACCCTCTCCACGCTGTGTCACCTGTCGACAGC 360
Db 469 ATCACTGGGCTGTGCGAGCCCTCACCCTCTCCACGCTGTGTCACCTGTCGACAGC 528
OY 361 TGCCCTCATTTCCGGCTGGGGGCGAGCAGCTCCAGCCCGGCTTCAACAACAGC 420
Db 529 TGCCCTCATTTCCGGCTGGGGGCGAGCAGCTCCAGCCCGGCTTCAACAACAGC 588
OY 421 CGATCGCCCAACATCATCATATTGAGCAGCAGAGTGAAGAGCGCTACCCCGGCAAC 480
Db 589 CGATCGCCCAACATCATCATATTGAGCAGCAGAGTGAAGAGCGCTACCCCGGCAAC 648
OY 481 ATCAAGACACCATGCTGTGTCAGCGTGCAGAGAGGGGGGCAAGAGCTCTGCCAGG 540
Db 649 ATCAAGACACCATGCTGTGTCAGCGTGCAGAGAGGGGGGCAAGAGCTCTGCCAGG 708
OY 541 GACATCGGGGGGCTCTGTGTCATCAAGGCTTCAAGGCTTATCTCTGGGGCCAG 600
Db 709 GACATCGGGGGGCTCTGTGTCATCAAGGCTTATCTCTGGGGCCAG 768
OY 601 GATCCGCTGTGCATCAGCCGGAAGGCTGTGTCATCAGAGAAAGTGTGCAAAATATGTGAGC 660
Db 769 GATCCGCTGTGCATCAGCCGGAAGGCTGTGTCATCAGAGAAAGTGTGCAAAATATGTGAGC 828
OY 661 TGGATCCAGAGAGCATGAAGAACAAT 687
Db 829 TGGATCCAGAGAGCATGAAGAACAAT 855
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## RESULT 15

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US-10-141-704-505
; Sequence 505, Application US/10141704
; Publication No. US20030134359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhen
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
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FILE REFERENCE: P3330R1C209
CURRENT APPLICATION NUMBER: US/10/141,704
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 505
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-141-704-505
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Query Match. 100.0%; Score 687; DB 12; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 1,9e-186;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 ATCATCAAGGGGTTGAGTGCAGAGCTCACTCCAGCCCTGGCAGGACCCCTGTTCCAG 60
Db 169 ATCATCAAGGGGTTGAGTGCAGAGCTCACTCCAGCCCTGGCAGGACCCCTGTTCCAG 228
OY 61 AAGACGGGGCTACTCTGTGGGGGCGAGCGTCATCCGCCCAAGTGGCTCTGACAGCAGC 120
Db 229 AAGACGGGGCTACTCTGTGGGGGCGAGCGTCATCCGCCCAAGTGGCTCTGACAGCAGC 288
OY 121 CACTGCTCAAGCCCCGCTACATAGTTCACCTGGGGGCGAGCACAACCTCCAGAGAGAG 180
Db 289 CACTGCTCAAGCCCCGCTACATAGTTCACCTGGGGGCGAGCACAACCTCCAGAGAGAG 348
OY 181 GCGCTGAGCAGAGCCCGGAGCAGCCAGTGCCTTCCCGCCAGCCCGGCTTCAACAACAGC 240
Db 349 GCGCTGAGCAGAGCCCGGAGCAGCCAGTGCCTTCCCGCCAGCCCGGCTTCAACAACAGC 408
OY 241 CTCCCAACAAGAGACCCGCAATGACATGCTGGTGAAGATGGATCGGCACTGTC 300
Db 409 CTCCCAACAAGAGACCCGCAATGACATGCTGGTGAAGATGGATCGGCACTGTC 468
OY 301 ATCACTGGGCTGTGCGAGCCCTCACCCTCTCCACGCTGTGTCACCTGTCGACAGC 360
Db 469 ATCACTGGGCTGTGCGAGCCCTCACCCTCTCCACGCTGTGTCACCTGTCGACAGC 528
OY 361 TGCCCTCATTTCCGGCTGGGGGCGAGCAGCTCCAGCCCGGCTTCAACAACAGC 420
Db 529 TGCCCTCATTTCCGGCTGGGGGCGAGCAGCTCCAGCCCGGCTTCAACAACAGC 588
OY 421 CGATCGCCCAACATCATCATATTGAGCAGCAGAGTGAAGAGCGCTACCCCGGCAAC 480
Db 589 CGATCGCCCAACATCATCATATTGAGCAGCAGAGTGAAGAGCGCTACCCCGGCAAC 648
OY 481 ATCAAGACACCATGCTGTGTCAGCGTGCAGAGAGGGGGGCAAGAGCTCTGCCAGG 540
Db 649 ATCAAGACACCATGCTGTGTCAGCGTGCAGAGAGGGGGGCAAGAGCTCTGCCAGG 708
OY 541 GACATCGGGGGGCTCTGTGTCATCAAGGCTTCAAGGCTTATCTCTGGGGCCAG 600
Db 709 GACATCGGGGGGCTCTGTGTCATCAAGGCTTATCTCTGGGGCCAG 768
OY 601 GATCCGCTGTGCATCAGCCGGAAGGCTGTGTCATCAGAGAAAGTGTGCAAAATATGTGAGC 660
Db 769 GATCCGCTGTGCATCAGCCGGAAGGCTGTGTCATCAGAGAAAGTGTGCAAAATATGTGAGC 828
OY 661 TGGATCCAGAGAGCATGAAGAACAAT 687
Db 829 TGGATCCAGAGAGCATGAAGAACAAT 855
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Search completed: October 15, 2003, 20:16:21  
Job time : 251.886 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 12:59:38 ; Search time 64.2767 Seconds  
(without alignments)  
4717.579 Million cell updates/sec

Title: US-09-856-320A-1\_COPY\_272\_958

Perfect score: 687  
Sequence: 1 atcatcaagggttcagtg.....aggagacgataagaacaat 687

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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2: /cgn2\_6/ptodata/2/lna/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/lna/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/lna/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/lna/PCrUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/lna/Backfiles1.seq:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	687	100.0	1192	3	US-08-944-483-8
2	687	100.0	1314	3	US-09-025-059-2
3	686.6	99.9	1292	4	US-09-205-258-189
4	685.8	99.8	1146	3	US-09-205-258-247
5	685.2	99.7	1166	3	US-08-944-483-7
6	660	96.1	1052	4	US-09-386-642-10
7	654.2	95.2	833	2	US-08-790-137-2
8	464.6	67.6	618	4	US-09-280-116-3
9	287	41.8	662	4	US-09-702-705-109
10	287	41.8	662	4	US-09-736-457-109
11	262.4	38.2	472	4	US-09-280-116-136
12	250	36.4	250	3	US-08-944-483-4
13	237.4	34.6	239	3	US-08-944-483-3
14	225	32.8	262	3	US-08-944-483-5
15	223.6	32.5	994	3	US-09-008-271A-19
16	220.4	32.1	1049	4	US-09-070-526-1
17	219.2	31.9	1049	4	US-09-386-642-9
18	191.8	27.9	1570	4	US-09-996-243-308
19	187.6	27.3	825	3	US-09-120-582-1
20	187.6	27.3	897	2	US-08-956-267A-1
21	182.4	26.6	1476	2	US-08-824-874-2
22	182.4	26.6	1476	4	US-09-210-084-2
23	182.4	26.6	1476	4	US-09-764-762-2
24	177.8	25.9	1341	4	US-08-983-075D-6
25	177.8	25.9	1358	4	US-08-983-075D-8
26	176.2	25.6	711	3	US-08-622-046B-2
27	176.2	25.6	711	3	US-08-622-046B-13

28	176.2	25.6	711	3	US-09-100-264-2	Sequence 2, Appl1
29	176.2	25.6	711	4	US-08-843-076D-2	Sequence 2, Appl1
30	176.2	25.6	760	3	US-08-768-859A-7	Sequence 7, Appl1
31	176.2	25.6	760	3	US-08-767-820A-7	Sequence 7, Appl1
32	176.2	25.6	766	3	US-08-768-859A-9	Sequence 9, Appl1
33	176.2	25.6	766	3	US-08-767-820A-9	Sequence 9, Appl1
34	176.2	25.6	766	3	US-08-622-046B-6	Sequence 6, Appl1
35	176.2	25.6	766	3	US-08-622-046B-17	Sequence 17, Appl1
36	176.2	25.6	766	4	US-09-100-264-6	Sequence 6, Appl1
37	176.2	25.6	822	3	US-08-843-076D-6	Sequence 6, Appl1
38	176.2	25.6	822	3	US-09-100-264-8	Sequence 8, Appl1
39	176.2	25.6	832	3	US-08-768-859A-5	Sequence 5, Appl1
40	176.2	25.6	832	3	US-08-768-859A-20	Sequence 20, Appl1
41	176.2	25.6	832	3	US-08-767-820A-5	Sequence 5, Appl1
42	176.2	25.6	832	3	US-08-767-820A-20	Sequence 20, Appl1
43	176.2	25.6	832	3	US-08-622-046B-4	Sequence 4, Appl1
44	176.2	25.6	832	3	US-08-622-046B-15	Sequence 15, Appl1
45	176.2	25.6	832	4	US-08-843-076D-4	Sequence 4, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-944-483-8  
Sequence 8, Application US/08944483  
Patent No. 6232456

GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLAAS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA: 2.0  
APPLICATION NUMBER: US/08/944.483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1192 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear



MOLECULE TYPE: CDNA  
US-08-944-483-8

Query Match 100.0%; Score 687; DB 3; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 2,5e-168;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATCTCAAGGGGTTGAGTGCAGCAACCTTCACCTCCAGCCCTGCGAGGACCCCTTTGAG 60
DB 170 ATCTCAAGGGGTTGAGTGCAGCAACCTTCACCTCCAGCCCTGCGAGGACCCCTTTGAG 229
QY 61 AAGACGGGGCTACTCTGTGGGGGAGCGCTCATGCGCCCGAGATGGCTCTGACAGCAGCC 120
DB 230 AAGACGGGGCTACTCTGTGGGGGAGCGCTCATGCGCCCGAGATGGCTCTGACAGCAGCC 289
QY 121 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGCACAACCTTCAGAGAGAGAG 180
DB 290 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGCACAACCTTCAGAGAGAGAG 349
QY 181 GCGTGTAGCAGACCCGAGACAGCCACTGAGTCTCTCCCGACCCCGGCTTCACACAGC 240
DB 350 GCGTGTAGCAGACCCGAGACAGCCACTGAGTCTCTCCCGACCCCGGCTTCACACAGC 409
QY 241 CTCCCAACAAGAGCAACCGCAATGACATCATGCTGGGAGATGGATGGCCAGTCTCC 300
DB 410 CTCCCAACAAGAGCAACCGCAATGACATCATGCTGGGAGATGGATGGCCAGTCTCC 469
QY 301 ATCACTGGGGCTGTGCGACCCCTCACCCTCTCTCAGCTGTGTCACTGTGCGACAGC 360
DB 470 ATCACTGGGGCTGTGCGACCCCTCACCCTCTCTCAGCTGTGTCACTGTGCGACAGC 529
QY 361 TGCTCTATTTCCGGCTGGGGGAGCAGCTCCAGCCCGCAATGACCTGCTCAGACCTTG 420
DB 530 TGCTCTATTTCCGGCTGGGGGAGCAGCTCCAGCCCGCAATGACCTGCTCAGACCTTG 589
QY 421 CGATCGCCCAACATCATCATATGAGCAGCAGAAAGTGTGAGAACGGCTTACCCGGGAC 480
DB 590 CGATCGCCCAACATCATCATATGAGCAGCAGAAAGTGTGAGAACGGCTTACCCGGGAC 649
QY 481 ATCAGACAGACCATGTGTGTGCCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
DB 650 ATCAGACAGACCATGTGTGTGCCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 709
QY 541 GACTCGGGGGGCGCTCTGTGTCTGTAAACAGTCTTCAAGGCAATATCTCTGGGGCCAG 600
DB 710 GACTCGGGGGGCGCTCTGTGTCTGTAAACAGTCTTCAAGGCAATATCTCTGGGGCCAG 769
QY 601 GATCCGCTGTGAGTCAACCCGAAAGCTGTGTCTACAGAAAGTCTCAAAATATGTGAG 660
DB 770 GATCCGCTGTGAGTCAACCCGAAAGCTGTGTCTACAGAAAGTCTCAAAATATGTGAG 829
QY 661 TGGATCCAGAGAGAGATGAAGAACAT 687
DB 830 TGGATCCAGAGAGAGATGAAGAACAT 856
```

RESULT 2  
US-09-025-059-2  
Sequence 2, Application US/09025059  
Patent No. 6075136

GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,059  
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0481 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1314 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: LUNGUT10

CLONE: 2723646

US-09-025-059-2

Query Match 100.0%; Score 687; DB 3; Length 1314;  
Best Local Similarity 100.0%; Pred. No. 2,6e-168;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATCTCAAGGGGTTGAGTGCAGCAACCTTCACCTCCAGCCCTGCGAGGACCCCTTTGAG 60
DB 287 ATCTCAAGGGGTTGAGTGCAGCAACCTTCACCTCCAGCCCTGCGAGGACCCCTTTGAG 346
QY 61 AAGACGGGGCTACTCTGTGGGGGAGCGCTCATGCGCCCGAGATGGCTCTGACAGCAGC 120
DB 347 AAGACGGGGCTACTCTGTGGGGGAGCGCTCATGCGCCCGAGATGGCTCTGACAGCAGC 406
QY 121 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGCACAACCTTCAGAGAGAGAG 180
DB 407 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGCACAACCTTCAGAGAGAGAG 466
QY 181 GCGTGTAGAGACACCGGAGACAGCCACTGAGTCTTCCCGACCCCGGCTTCACACAGC 240
DB 467 GCGTGTAGAGACACCGGAGACAGCCACTGAGTCTTCCCGACCCCGGCTTCACACAGC 526
QY 241 CTCCCAACAAGAGCAACCGCAATGACATCATGCTGGGAGATGGATGGCCAGTCTCC 300
DB 527 CTCCCAACAAGAGCAACCGCAATGACATCATGCTGGGAGATGGATGGCCAGTCTCC 586
QY 587 ATCACTGGGGCTGTGCGACCCCTCACCCTCTCTCAGCTGTGTCACTGTGCGACAGC 646
DB 647 ATCACTGGGGCTGTGCGACCCCTCACCCTCTCTCAGCTGTGTCACTGTGCGACAGC 706
QY 647 TGCTCTATTTCCGGCTGGGGGAGCAGCTCCAGCCCGCAATGAGCTCTGCTCAGACCTTG 420
DB 706 TGCTCTATTTCCGGCTGGGGGAGCAGCTCCAGCCCGCAATGAGCTCTGCTCAGACCTTG 480
QY 707 CGATCGCCCAACATCATCATATGAGCAGCAGAAAGTGTGAGAACGGCTTACCCGGGAC 766
DB 826 CGATCGCCCAACATCATCATATGAGCAGCAGAAAGTGTGAGAACGGCTTACCCGGGAC 826
QY 826 ATCAGACAGACCATGTGTGTGCCAGGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGG 826
DB 826 ATCAGACAGACCATGTGTGTGCCAGGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGG 826
QY 826 GACTCGGGGGGCGCTCTGTGTCTGTAAACAGTCTTCAAGGCAATATCTCTGGGGCCAG 600
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Db 827 GACTCCGGGGCCCTTGGTCTGTAAACGACTCTCTTCAAGGCAATATCTCTGGGGCCAG 886  
QY 601 GATCCGTGTGCATACACCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAAATATGTGAC 660  
Db 887 GATCCGTGTGCATACACCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAAATATGTGAC 946  
QY 661 TGGATCCAGAGACGATGAAGAACAAT 687  
Db 947 TGGATCCAGAGACGATGAAGAACAAT 973

RESULT 3  
US-09-205-258-189  
Sequence 189, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
EARLIER FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 189  
LENGTH: 1292  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-205-258-189

Query Match 99.9%; Score 686.6; DB 4; Length 1292;  
Best Local Similarity 99.9%; Pred. No. 3,2e-168;  
Matches 686; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATGAAGGGGTTCAGTGAAGCCTCACTCCACCCCTGGAGGACGCTGTTGAG 60  
Db 270 ATCATGAAGGGGTTCAGTGAAGCCTCACTCCACCCCTGGAGGACGCTGTTGAG 329  
QY 61 AAGACGGGCTACTCTGTGGGGGAGCGCATGCGCCCGAGATGGCTCGACAGGCG 120  
Db 330 AAGACGGGCTACTCTGTGGGGGAGCGCATGCGCCCGAGATGGCTCGACAGGCG 389  
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGAGCACAACCTCCAGAAAGAGAG 180  
Db 390 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGAGCACAACCTCCAGAAAGAGAG 449  
QY 181 GGCTGTGACAGACCCGGAGCGCACTGAGTCTTCCCAACCCGGCTTCAACACAGC 240  
Db 450 GGCTGTGACAGACCCGGAGCGCACTGAGTCTTCCCAACCCGGCTTCAACACAGC 509  
QY 241 CTCGCCAACAAGACACCGCAATGACATCATGCTGTGAAGTGGCATGCGAGCTCC 300  
Db 510 CTCGCCAACAAGACACCGCAATGACATCATGCTGTGAAGTGGCATGCGAGCTCC 569  
QY 301 ATCACTGGGCTGTGGAGCCCTCACCTCTCTCAAGCTGTGTCACTGTGGACACAGC 360  
Db 570 ATCACTGGGCTGTGGAGCCCTCACCTCTCTCAAGCTGTGTCACTGTGGACACAGC 629  
QY 361 TGGCTCATTTCCGGGCTGGGGGAGCGAGCTGAGCCCAATGACGCTGCTACACTTG 420  
Db 630 TGGCTCATTTCCGGGCTGGGGGAGCGAGCTGAGCCCAATGAGCTGCTACACTTG 689  
QY 421 CGATGGCCCAACATCACTCATTTGAGACCAAGATGTGAAAGCGCTAACCCGGCAAC 480  
Db 690 CGATGGCCCAACATCACTCATTTGAGACCAAGATGTGAAAGCGCTAACCCGGCAAC 749  
QY 481 ATCAAGACACATGTGTGTGCAAGCTGTGCAAGAAAGGGGGCAAGAGACTCTGCGAGGT 540

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Db 750 ATCAAGACACCAATGCTGTGCAAGCTGCAAGAGGGGCAAGAGCTCTGCGAGGT 809
OY 541 GACTCCGGGGGCGCCCTGTGCTGTACAGCTCTTCAAGCATTATCTGGGGCCAG 600
Db 810 GACTCCGGGGGCGCCCTGTGCTGTACAGCTCTTCAAGCATTATCTGGGGCCAG 869
OY 601 GATCGGTGTGCGATCACCAGGAGCGTGTGTACAGGAAAGTCTGCAATATGTGAC 660
Db 870 GATCGGTGTGCGATCACCAGGAGCGTGTGTGTACAGGAAAGTCTGCAATATGTGAC 929
OY 661 TGGATCCAGAGAGATGAGAGCAAT 687
Db 930 TGGATCCAGAGAGATGAGAGCAAT 956

RESULT 4
US-09-205-258-247
: Sequence 247, Application US/09205258
: Patent No. 6525174
: GENERAL INFORMATION:
: APPLICANT: Young et al.
: TITLE OF INVENTION: 207 Human Secreted Proteins
: FILE REFERENCE: P2007P1
: CURRENT APPLICATION NUMBER: US/09/205,258
: EARLIER FILING DATE: 1998-12-04
: EARLIER APPLICATION NUMBER: PCT/US98/11422
: EARLIER FILING DATE: 1998-06-04
: EARLIER APPLICATION NUMBER: 60/048,885
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/049,375
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,881
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,880
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,896
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/049,020
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,876
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,895
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,884
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,894
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,971
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,964
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,882
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,899
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,893
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,900
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,901
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,892
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,915
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/049,019
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,970
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,972
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,916
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EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/049,373
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,875
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/049,374
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,917
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,949
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,974
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,883
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,897
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,898
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,962
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/070,923
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,877
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,878
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/070,923
: EARLIER FILING DATE: 1997-12-18
: EARLIER APPLICATION NUMBER: 60/092,921
: EARLIER FILING DATE: 1998-07-15
: EARLIER APPLICATION NUMBER: 60/094,657
: EARLIER FILING DATE: 1998-07-30
: NUMBER OF SEQ ID NOS: 1227
: SOFTWARE: Patentln ver. 2.0
: SEQ ID NO 247
: LENGTH: 1146
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (20)
: OTHER INFORMATION: n equals a,t,g, or c
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (35)
: OTHER INFORMATION: n equals a,t,g, or c
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (36)
: OTHER INFORMATION: n equals a,t,g, or c
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (37)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-247

Query Match 99.8%; Score 685.8; DB 4; Length 1146;
Best Local Similarity 99.6%; Pred. No. 5e-168;
Matches 684; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATCATCAAGGGGTTGAGTGCAAGCTTCCAGCCTGGCAGGAGCCCTGTTGAG 60
Db 124 ATCATCAAGGGGTTGAGTGCAAGCTTCCAGCCTGGCAGGAGCCCTGTTGAG 183
OY 61 AAGAGCGGCTACTCTGTGGGCGAGCTCATGCGCCCAAGATGCTCTGACAGAGCC 120
Db 184 AAGAGCGGCTACTCTGTGGGCGAGCTCATGCGCCCAAGATGCTCTGACAGAGCC 243
OY 121 CACTGCTCAAGCCCGCTCATGATGTCACCTGGGGAGAGCAACCTCCAGAGAGAG 180
Db 244 CACTGCTCAAGCCCGCTCATGATGTCACCTGGGGAGAGCAACCTCCAGAGAGAG 303
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OY 181 GGCTGTGACAGACCCGGACAGCCACTGAGTCTTCCCGACCCGGCTTCAACAACAGC 240
DB 304 GGCTGTGACAGACCCGGACAGCCACTGAGTCTTCCCGACCCGGCTTCAACAACAGC 363
OY 241 CTCGCCAACAAGACACCGCAATGATCATGTCTGTGAAGATGTCATGCGAGCTCC 300
DB 364 CTCGCCAACAAGACACCGCAATGATCATGTCTGTGAAGATGTCATGCGAGCTCC 423
OY 301 ATCAGCTGGGCTGTGCGACCCCTACCCCTCTCCAGCTGTCTACTGTCAGCCAGCAGC 360
DB 424 ATCAGCTGGGCTGTGCGACCCCTACCCCTCTCCAGCTGTCTACTGTCAGCCAGCAGC 483
OY 361 TGCCTCATTTCCGGCTGGGGGACAGCAGCTCAGCCCAATTAACGCTGCTCAGACCTTG 420
DB 484 TGTCTCATTTCCGGCTGGGGGACAGCAGCTCAGCCCAATTAACGCTGCTCAGACCTTG 543
OY 421 CGATGGCGCAACATCATCATTTGAGCAGCAGAAAGTGTGAGAACGCTTACCCCGGCAAC 480
DB 544 SGATGGCGCAACATCATCATTTGAGCAGCAGAAAGTGTGAGAACGCTTACCCCGGCAAC 603
OY 481 ATCAGAGACACCATGCTGTGTGCGACCGTGTGAGAGAGGGGGCAAGGACTCTGCCAGGCT 540
DB 604 ATCAGAGACACCATGCTGTGTGCGACCGTGTGAGAGAGGGGGCAAGGACTCTGCCAGGCT 663
OY 541 GACTCCGGGGGCGCTCTGTGTGTATACAGCTCTTTCAAGCAATTAATCTCTGGGGCCAG 600
DB 664 GACTCCGGGGGCGCTCTGTGTGTATACAGCTCTTTCAAGCAATTAATCTCTGGGGCCAG 723
OY 601 GATCCGTGTGCGATACCCGGAAGCCTGTGTCTACAGAAAGTGTGCAAAATATGTGAGC 660
DB 724 GATCCGTGTGCGATACCCGGAAGCCTGTGTCTACAGAAAGTGTGCAAAATATGTGAGC 783
OY 661 TGGATCCAGAGACGATGAGAACAAT 687
DB 784 TGGATCCAGAGACGATGAGAACAAT 810

RESULT 5
US-08-944-483-7
; Sequence 7, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLAS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1166 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-944-483-7

Query Match      99.7%; Score 685.2; DB 3; Length 1166;
Best Local Similarity 99.6%; Pred. No. 7,2e-168;
Matches 684; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 ATCATCAAGGGGTTCAGTGTCAAGCCTCACTCCAGCCCTGGAGGACAGCCGTTGAG 60
DB 166 ATCATCAAGGGGTTCAGTGTCAAGCCTCACTCCAGCCCTGGAGGACAGCCGTTGAG 225
OY 61 AAGACGGGCTACTCTGTGGGGGAGCGCTATGCGCCAGATGGCTCTGACAGCAGCC 120
DB 226 AAGACGGGCTACTCTGTGGGGGAGCGCTATGCGCCAGATGGCTCTGACAGCAGCC 285
OY 121 CACTGCTTAAGCCCGCTTACATATGTTCACTTGGGGACACACAACTCCAGAAAGAGAG 180
DB 286 CACTGCTTAAGCCCGCTTACATATGTTCACTTGGGGACACACAACTCCAGAAAGAGAG 345
OY 181 GGCTGTGACAGACCCGGACAGCCACTGATGCTTCCCGACCCGGCTTCAACAACAGC 240
DB 346 GGCTGTGACAGACCCGGACAGCCACTGATGCTTCCCGACCCGGCTTCAACAACAGC 405
OY 241 CTCGCCAACAAGACACCGCAATGATCATGTCTGTGAAGATGTCATGCGAGCTCC 300
DB 406 CTCGCCAACAAGACACCGCAATGATCATGTCTGTGAAGATGTCATGCGAGCTCC 465
OY 301 ATCAGCTGGGCTGTGCGACCCCTCAACCCCTCTCTACGCTGTGTCTACTGCTGGACAGC 360
DB 466 ATCAGCTGGGCTGTGCGACCCCTCAACCCCTCTCTACGCTGTGTCTACTGCTGGACAGC 525
OY 361 TGCCTCATTTCCGGCTGGGGGACAGCAGCTCAGCCCAATTAACGCTGCTCAGACCTTG 420
DB 526 TGCCTCATTTCCGGCTGGGGGACAGCAGCTCAGCCCAATTAACGCTGCTCAGACCTTG 585
OY 421 CGATGGCGCAACATCATCATTTGAGCAGCAGAAAGTGTGAGAACGCTTACCCCGGCAAC 480
DB 586 CGATGGCGCAACATCATCATTTGAGCAGCAGAAAGTGTGAGAACGCTTACCCCGGCAAC 645
OY 481 ATCAGAGACACCATGCTGTGTGCGACCGTGTGAGAGAGGGGGCAAGGACTCTGCCAGGCT 540
DB 541 ATCAGAGACACCATGCTGTGTGCGACCGTGTGAGAGAGGGGGCAAGGACTCTGCCAGGCT 705
OY 541 GACTCCGGGGGCGCTCTGTGTGTATACAGCTCTTTCAAGCAATTAATCTCTGGGGCCAG 600
DB 706 GACTCCGGGGGCGCTCTGTGTGTATACAGCTCTTTCAAGCAATTAATCTCTGGGGCCAG 765
OY 601 GATCCGTGTGCGATACCCGGAAGCCTGTGTCTACAGAAAGTGTGCAAAATATGTGAGC 660
DB 766 GATCCGTGTGCGATACCCGGAAGCCTGTGTCTACAGAAAGTGTGCAAAATATGTGAGC 825
OY 661 TGGATCCAGAGACGATGAGAACAAT 687
DB 826 TGGATCCAGAGACGATGAGAACAAT 852

RESULT 6
US-09-386-642-10
; Sequence 10, Application US/09386642
; Patent No. 6420157

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GENERAL INFORMATION:  
APPLICANT: Darrow, Andrew  
APPLICANT: Q1, Jensen  
APPLICANT: Andrade-Gordon, Patricia  
TITLE OF INVENTION: Zymogen Activation System  
FILE REFERENCE: ORT-1028  
CURRENT APPLICATION NUMBER: US/09/386,642  
CURRENT FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn ver. 2.0  
SEQ ID NO 10  
LENGTH: 1052  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
OTHER INFORMATION: with homo sapien serine protease catalytic domain  
US-09-386-642-10

Query Match 96.1%; Score 660; DB 4; Length 1052;  
Best Local Similarity 100.0%; Pred. No. 2,2e-161;  
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

28 CACTCCAGCCCTGGCAGGAGCCCTGTGAGAAGAGGGGCTACTCTGTGGGGCAGC 87  
196 CACTCCAGCCCTGGCAGGAGCCCTGTGAGAAGAGGGGCTACTCTGTGGGGCAGC 255  
88 CTCTATGCCCCCAGATGGCTCTGACAGCAGCCCTGCTCAAGCCCGCTACATAGTT 147  
256 CTCTATGCCCCCAGATGGCTCTGACAGCAGCCCTGCTCAAGCCCGCTACATAGTT 315  
148 CACTGGGGGAGCAGCAACTTCAGAGAAGAGAGGGCTGTGAGCAGACCCGAGCAGCACT 207  
316 CACTGGGGGAGCAGCAACTTCAGAGAAGAGAGGGCTGTGAGCAGACCCGAGCAGCACT 375  
208 GAGTCTCTCCCGCCCGCGGCTTACAGAACAGCTCCCAAGAACAGCAGCAATGAC 267  
376 GAGTCTCTCCCGCCCGCGGCTTACAGAACAGCTCCCAAGAACAGCAGCAATGAC 435  
268 ATCATGCTGGTGAAGATGGCATCGCATGCTCATCACTGGGCTGTGCGACCCCTGACC 327  
436 ATCATGCTGGTGAAGATGGCATCGCATGCTCATCACTGGGCTGTGCGACCCCTGACC 495  
328 CTCTCTCAGCGCTGTGCTACTGCTGGCAGCAGCTGCTCATTTCCGGCTGGGGCAGCAGC 387  
496 CTCTCTCAGCGCTGTGCTACTGCTGGCAGCAGCTGCTCATTTCCGGCTGGGGCAGCAGC 555  
388 TCCAGCCCGCAGTATGAGCTGCTCAGACCTTGGATGGCCAGCATCAACATCATGAG 447  
556 TCCAGCCCGCAGTATGAGCTGCTCAGACCTTGGATGGCCAGCATCAACATCATGAG 615  
448 CACAGAGAAGTGTGAAGAGCGCTACCCCGGCAACATCAGACAGCATGCTGTGCGAGC 507  
616 CACAGAGAAGTGTGAAGAGCGCTACCCCGGCAACATCAGACAGCATGCTGTGCGAGC 675  
508 GTGAGAGAAGGGGCAAGGACTCTGCGCAGGGGTACTCCGGGGGCTCTGTGTGTAAAC 567  
676 GTGAGAGAAGGGGCAAGGACTCTGCGCAGGGGTACTCCGGGGGCTCTGTGTGTAAAC 735  
568 CAGTCTCTTCAAGGCAATATCTCTGCGGCGAGGATCGTGTGGATCACCCGAAAGCCT 627  
736 CAGTCTCTTCAAGGCAATATCTCTGCGGCGAGGATCGTGTGGATCACCCGAAAGCCT 795  
628 GGTGTCTACACGAAGTCTGCAGAAATATGTGAGTCAAGTCAAGAGAGCATGAGAAACAT 687  
796 GGTGTCTACACGAAGTCTGCAGAAATATGTGAGTCAAGTCAAGAGAGCATGAGAAACAT 855

RESULT 7  
US-08-790-137-2  
; Sequence 2, Application US/08790137  
; Patent No. 5840871  
; GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.  
APPLICANT: Goli, Surya K.  
TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED  
TITLE OF INVENTION: KALLIKREIN  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Inocyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/790,137  
FILING DATE: Filed Herewith  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0195 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 833 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-790-137-2

Query Match 95.2%; Score 654.2; DB 2; Length 833;  
Best Local Similarity 97.6%; Pred. No. 6,5e-160;  
Matches 662; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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108 GGCTGGAGAGTGTGAGCAGATTCCTCCAGCCCTGGCAGGCGGCTGTTCAGAGAACGCGG 167  
70 CTACTGTGTGGGGGAGGCTCATGCCCCAGATGGCTCTGTGAGCAGCCCACTGCTC 129  
168 CTACTGTGTGGGGGAGGCTCATGCCCCAGATGGCTGTTCAGAGCAGCCCACTGCTC 227  
130 AAGCCCGCTACATAGTTCACTGCGGCGAGCAGCAACCTCCAGAGAGGAGGGCTGAG 189  
228 AAGCCCGCTACATAGTTCACTGCGGCGAGCAGCAACCTCCAGAGAGGAGGGCTGAG 287  
190 CAGACCGCGAGCAGCACTGAGTCTTCCCGCACCCCGGCTTCAACAACAGCTCCCAAC 249  
288 CAGACCGCGAGCAGCACTGAGTCTTCCCGCACCCCGGCTTCAACAACAGCTCCCAAC 347  
250 AAGAGCAGCAGCAATGATCATGCTGTGTAAGTGGCATGCGCAGCTCTCATCTACTGG 309  
348 AAGAGCAGCAGCAATGATCATGCTGTGTAAGTGGCATGCGCAGCTCTCATCTACTGG 407  
310 GCTGTGAGACCCCTCACTCTCTCAAGCTGTGTCACTGCTGGCAGCAGCTGCTCATTT 369  
408 GCTGTGAGACCCCTCACTCTCTCTCAAGCTGTGTCACTGCTGGCAGCAGCTGCTCATTT 467  
370 TCGGCTGGGGCAGCAGCTCCAGGCCCACTTACGCTGCTCAACACTTTCAGATGCGCC 429  
468 TCGGCTGGGGCAGCAGCTCCAGGCCCACTTACGCTGCTCAACACTTTCAGATGCGCC 527  
430 AACATCACTCATTTGAGCAGCAGAGATGTGAGAACCTTACCCCGGCAACATCAGCAGC 489

Db 528 AACATCACCATCATTTGAGCACCAGAAAGTGTGAAACGCCCTACCCCGCAACATCAACAGC 587  
QY 490 ACCATGCTGTGTCCAGCGCTGCAGAGAGGGGCGAAGAGACTCTCCAGGGTACTCCGG 549  
Db 588 ACCATGCTGTGTCCAGCGCTGCAGAGAGGGGCGAAGAGACTCTCCAGGGTACTCCGG 647  
QY 550 GAGCCCTGTGTGTAAACAGTCTCTCAAGGCAATTAATCTCTGGGGCCAGATCCCTGT 609  
Db 648 GAGCCCTGTGTGTAAACAGTCTCTCAAGGCAATTAATCTCTGGGGCCAGATCCCTGT 707  
QY 610 GCGATCACCAGAAAGCTGTGTCTACAGAAAGTCTGCAAAATATGTGTGATGATCCAG 669  
Db 708 GCGATCACCAGAAAGCTGTGTCTACAGAAAGTCTGCAAAATATGTGTGATGATCCAG 767  
QY 670 GAGACGATGAGAACAT 687  
Db 768 GAGACGATGAGAACAT 785

## RESULT 8

US-09-280-116-3  
; Sequence 3, Application US/09280116A  
; Patent No. 6311427  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs  
; FILE REFERENCE: 5800-24, 035800/176965  
; CURRENT APPLICATION NUMBER: US/09/280,116A  
; CURRENT FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 268  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 618  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: trypsin-like serine proteases  
US-09-280-116-3

Query Match 67.6%; Score 464.6; DB 4; Length 618;  
Best Local Similarity 91.8%; Pred. No. 5.4e-111;  
Matches 559; Conservative 0; Mismatches 14; Indels 36; Gaps 5;

QY 66 GCGGTACTCTGTGTGGGGGAGCGCTATGCCCCGAGATGCTCTGACAGACGCCACTG 125  
Db 1 GCGGTACTCTGTGTGGGGGAGC-CITCATCG-CCTCAGATGGCTCTGACAGACGCCACTG 58  
QY 126 COTCAAGCCCGCTACATAGTTACCTGGGGGAGACAAACCTCCAGAGAGAGAGGCTG 185  
Db 59 CCTCAAGCCCGCTACATAGTTACCTGGGGGAGACAAACCTCCAGAGAGAGAGGCTG 118  
QY 186 TGAGCAGACCCGAGACAGCAGTGAATCTCTCCGCCAGCCCGGCTTCAACAAAGCCTCC 245  
Db 119 TGAGCAGACCCGAGACAGCAGTGAATCTCTCCGCCAGCCCGGCTTCAACAAAGCCTCC 178  
QY 246 CAACAAGACCAACCGCAATGACATCATCTGTGTGAAGATGGCAGTCCAGT-CITCATCA 304  
Db 179 CAACAAGACCAACCGCAATGACATCATCTGTGTGAAGATGGCAGTCCAGTCCATCA 238  
QY 305 COTGGGCTGTGGAGCCCTCAACCTCTCTCAAGCTGTGTACAGCTGTGGCAACAGCTCC 364  
Db 239 COTGGGCTGTGGAGCCCTCAACCTCTCTCAAGCTGTGTACAGCTGTGGCAACAGCTCC 298  
QY 365 TCATTTCCGGGTGGGGGAGCAGCTCCAGCCCGCAAGTTAGCTGTGCTCAACCTTGCAT 424  
Db 299 TCATTTCCGGGTGGGGGAGCAGCTCCAGCCCGCAAGTTAGCTGTGCTCAACCTTGCAT 358  
QY 425 GCGCACAATCAATCATTTTGAACACCAAGAGTGTGAGACAGCTTACCCGGCAACATCA 484  
Db 359 GCGCACAATCAATCATTTTGAACACCAAGAGTGTGAGACAGCTTACCCGGCAACATCA 418  
QY 485 CAGACACCATGTGTGTGCGCAGCGTGCAGAAAGGGGCAAGAGTCCCGCAGGGTGACT 544

Db 419 CAGACACCATGGTGTGTGCCAGCGCTGAAGAGAGGGGCGAAGAGACTCTGCCAAGTCTTT 478  
QY 545 CCGGGGGCCCTGTGTGTGTGTAAACAGTCTCTCAAGGCAATTAATCTCTGGGG--CCAGGA 602  
Db 479 C-----AAAGCAATTAATCTCTGGGGGCGAGAGC 507  
QY 603 TCCGTGTGATCACCAGGCTGTGTGTCTACAGAAAGTGTGCAAAATATGTGTGACTG 662  
Db 508 TCCGTGTGATCACCAGGCTGTGTGTCTACAGAAAGTGTGCAAAATATGTGTGACTG 567  
QY 663 GATCCAGGA 671  
Db 568 GATCCAGGA 576

## RESULT 9

US-09-702-705-109  
; Sequence 109, Application US/09702705  
; Patent No. 6504010  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Ranger, Gary  
; APPLICANT: Vedvick, Tom  
; APPLICANT: Carter, Darriack  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.478C14  
; CURRENT APPLICATION NUMBER: US/09/702,705  
; CURRENT FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 1833  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 109  
; LENGTH: 662  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-702-705-109

Query Match 41.8%; Score 287; DB 4; Length 662;  
Best Local Similarity 100.0%; Pred. No. 4.1e-65;  
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 TACGCTGTGTACACCTTGGGATGCGCAACATCAATCATTTGAGCACCAGAAAGTGTG 460  
Db 14 TACGCTGTGTACACCTTGGGATGCGCAACATCAATCATTTGAGCACCAGAAAGTGTG 73  
QY 461 AGAAGCCTTACCCCGCAACATCAAGACACCATGATGTGTGCGACGTCAGAGAGGG 520  
Db 74 AGAAGCCTTACCCCGCAACATCAAGACACCATGATGTGTGCGACGTCAGAGAGGG 133  
QY 521 GCAAGACTCTGTCCAGGGGTGACTCCGGGGGCCCTGTGTGTAAACAGTCTCTTCAAG 580  
Db 134 GCAAGACTCTGTCCAGGGGTGACTCCGGGGGCCCTGTGTGTAAACAGTCTCTTCAAG 193  
QY 581 GCATTAATCTCTGGGGGCGAAGATCCGTGTGATCAACCCGAAAGCTGTGTCTACAGA 640  
Db 194 GCATTAATCTCTGGGGGCGAAGATCCGTGTGATCAACCCGAAAGCTGTGTCTACAGA 253  
QY 641 AAGTGTCAAAATATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687  
Db 254 AAGTGTCAAAATATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 300

## RESULT 10

US-09-736-457-109  
; Sequence 109, Application US/09736457  
; Patent No. 6509448  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong

APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Fanger, Gary  
APPLICANT: Vedlick, Tom  
APPLICANT: Carter, Darlick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
APPLICANT: Fan, Liqun  
APPLICANT: Wang, Aijun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121, DIAGNOSIS OF LUNG CANCER  
CURRENT APPLICATION NUMBER: US/09/736,457  
CURRENT FILING DATE: 2000-12-13  
NUMBER OF SEQ ID NOS: 1864  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 109  
LENGTH: 662  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-736-457-109

Query Match 41.8%; Score 287; DB 4; Length 662;  
Best Local Similarity 100.0%; Pred. No. 4,1e-65;  
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 TAGCCCTGCTCAACCTGCGATGCGCCCAACATCATTCATGAGCACCAGAACTGTG 460  
DB 14 TAGCCCTGCTCAACCTGCGATGCGCCCAACATCATTCATGAGCACCAGAACTGTG 73  
QY 461 AGAAGCCTTACCCCGGCAACATCAGACACACATGTTGTGTCCAGCGTCCAGAGAGGG 520  
DB 74 AGAAGCCTTACCCCGGCAACATCAGACACACATGTTGTGTCCAGCGTCCAGAGAGGG 133  
QY 521 GCAAGGACTCCTGCGAGGAGTACTCCGGGGCCCTGTGTCTGTAACTCTCTTCAAG 580  
DB 134 GCAAGGACTCCTGCGAGGAGTACTCCGGGGCCCTGTGTCTGTAACTCTCTTCAAG 193  
QY 581 GCATTATCTCTGGGGCCAGATCGTGTGCGATCACCCGAAAGCCTGTGTCTACAGA 640  
DB 194 GCATTATCTCTGGGGCCAGATCGTGTGCGATCACCCGAAAGCCTGTGTCTACAGA 253  
QY 641 AAGCTGCAATATATGTGACTGATCCAGAGAGAGATGAAGCAAT 687  
DB 254 AAGCTGCAATATATGTGACTGATCCAGAGAGAGATGAAGCAAT 300

RESULT 11  
US-09-280-116-136  
Sequence 136, Application US/09280116A  
Patent No. 6331427  
GENERAL INFORMATION:  
APPLICANT: Robison, Keith E.  
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs  
FILE REFERENCE: 5800-24, 03800/0176965  
CURRENT APPLICATION NUMBER: US/09/280,116A  
CURRENT FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 268  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 136  
LENGTH: 472  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: trypsin-like serine proteases  
US-09-280-116-136

Query Match 38.2%; Score 262.4; DB 4; Length 472;  
Best Local Similarity 99.6%; Pred. No. 8,2e-59;  
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATCATCAAGGGGTTGAGTCAAGCCTCACTCCAGCCCGGAGAGAGCCCTGTTCAG 60  
|||||

DB 209 ATCATCAAGGGGTTGAGTCAAGCCTCACTCCAGCCCGGAGAGAGCCCTGTTCAG 268  
QY 61 AAGAGCGGCTACTCTGTGGGCGAGCGCTCATGCCGCCAGATGCTCTGACAGCAGCC 120  
DB 269 AAGAGCGGCTACTCTGTGGGCGAGCGCTCATGCCGCCAGATGCTCTGACAGCAGCC 328  
QY 121 CACTGCTCAAGCCCGCTACATATGTTACCTGGGGCAGACACAACCTCCAGAAAGAGAG 180  
DB 329 CACTGCTCAAGCCCGCTACATATGTTACCTGGGGCAGACACAACCTCCAGAAAGAGAG 388  
QY 181 GGCTGTAGAGAGACCGGAGAGAGCAGTACGATCTCTCCCGCAGCCCGGCTTCAACAGC 240  
DB 389 GGCTGTAGAGAGACCGGAGAGAGCAGTACGATCTCTCCCGCAGCCCGGCTTCAACAGC 448  
QY 241 CTCCCAACAAGACACCGCAAT 264  
DB 449 CTCCCAACAAGACACCGCAAT 472

RESULT 12  
US-08-944-483-4  
Sequence 4, Application US/08944483  
Patent No. 6232456  
GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLAAS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROUPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183, US, 01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-944-483-4

Query Match 36.4%; Score 250; DB 3; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1e-55;



Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 GACCAACCGCATGATCATGCTGTGAGATGGATGCCAGTCTCATCATCAGCTGGGCT 312  
|||||  
Db 1 GACCAACCGCATGATCATGCTGTGAGATGGATGCCAGTCTCATCATCAGCTGGGCT 60  
QY 313 GGGCAGACCCCTACCTCTCTCTCAGCCTGTGTACCTGTGGACACAGCTGCTCATTTCC 372  
|||||  
Db 61 GGGCAGACCCCTACCTCTCTCTCAGCCTGTGTACCTGTGGACACAGCTGCTCATTTCC 120  
QY 373 GGGTGGGGGAGCAGCTGACAGCCCGGAGTACGCTCTCAGACCTTGGAGTGGCGGAC 432  
|||||  
Db 121 GGGTGGGGGAGCAGCTGACAGCCCGGAGTACGCTCTCAGACCTTGGAGTGGCGGAC 180  
QY 433 ATCCACCATCATTTGAGCAGCAGAAAGTGTGAAAGCGCTTACCCGGGCAACATCAAGACACC 492  
|||||  
Db 181 ATCCACCATCATTTGAGCAGCAGAAAGTGTGAAAGCGCTTACCCGGGCAACATCAAGACACC 240  
QY 493 ATGGTGTGTG 502  
|||||  
Db 241 ATGGTGTGTG 250

## RESULT 13

US-08-944-483-3  
; Sequence 3, Application US/08944483  
; Patent No. 6232456

## GENERAL INFORMATION:

APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLASS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
TITLE OF INVENTION: OF THE PROSTATE  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-944-483-3

Query Match 34.6%; Score 237.4; DB 3; Length 239;  
Best Local Similarity 99.6%; Pred. No. 1.9e-52;  
Matches 238; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 CCCAGCCCTGGGAGGAGCCCTGTTGAGAAAGAGCGGGCTACTCTGTGTGGGGGAGAGCTCA 91  
|||||  
Db 1 CCCAGCCCTGGGAGGAGCCCTGTTGAGAAAGAGCGGGCTACTCTGTGTGGGGGAGAGCTCA 60  
QY 92 TGGCCCCCAGATGGCTCTGACAGCAGCCCACTGCTCAAGCCCCCTCATATGTTGACC 151  
|||||  
Db 61 TGGCCCCCAGATGGCTCTGACAGCAGCCCACTGCTCAAGCCCCCTCATATGTTGACC 120  
QY 152 TGGGGCAGACAACCTCTCAGAAAGAGAGGGCTGTGAGAGAGCCGGAGAGCCAGT 211  
|||||  
Db 121 TGGGGCAGACAACCTCTCAGAAAGAGAGGGCTGTGAGAGAGCCGGAGAGCCAGT 180  
QY 212 CCTTCCCCCAGCCCGCTTCAACACAGCCTCCCAACAAAGACACCGCAATGACATC 270  
|||||  
Db 181 CCTTCCCCCAGCCCGCTTCAACACAGCCTCCCAACAAAGACACCGCAATGACATC 239

## RESULT 14

US-08-944-483-5  
; Sequence 5, Application US/08944483  
; Patent No. 6232456

## GENERAL INFORMATION:

APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLASS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
TITLE OF INVENTION: OF THE PROSTATE  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 262 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear





XX WPI; 1999-580450/49.  
 DR P-PSDB; AAY42439.  
 XX New human serine protease CASB12, for treatment, prevention and  
 PT diagnosis of cancer and autoimmune diseases -  
 PS Claim 10; Page 47; 58pp; English.  
 XX This is the nucleotide sequence of the CASB12 gene. The nucleotide  
 CC sequence of AA22638 shows homology with neuropilin and the encoded  
 CC protein AAY42439 is structurally related to other proteins of the  
 CC serine protease family, having homology and/or structural similarity  
 CC with neuropilin. It is expected that as well as similar structure, these  
 CC proteins will also share similar biological functions and properties.  
 CC The CASB12 polypeptides and polynucleotides can be used to develop  
 CC methods for identifying agonists and antagonists/inhibitors of these  
 CC molecules, and thereby treating conditions associated with CASB12  
 CC polypeptide imbalance. The invention also provides for diagnostic assays  
 CC for detecting diseases associated with inappropriate CASB12 polypeptide  
 CC activity or levels.  
 CC Since CASB12 is either specifically expressed or highly over-expressed  
 CC in tumors compared to normal cells, the polypeptides and polynucleotides  
 CC of the invention are believed to be important immunogens for specific  
 CC prophylactic or therapeutic immunization against tumors. The  
 CC polypeptides and polynucleotides can therefore be targeted by antigen  
 CC specific immune reactions (which result in the destruction of the tumor  
 CC cell) or they can be used to diagnose the occurrence of tumor cells.  
 SQ Sequence 1106 BP; 247 A; 348 C; 287 G; 224 T; 0 other;  
 Query Match 100.0%; Score 687; DB 20; Length 1106;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-137;  
 Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATCATCAAGGGGCTTCAGTGAAGCCCTACCTCCAGCCCTGGGAGGCGCTGTGGAG 60  
 Db 173 ATCTTCAAGGGGCTTCAGTGAAGCCCTACCTCCAGCCCTGGGAGGCGCTGTGGAG 232  
 QY 61 AAGACGGGCTACTCTGTGGGGGAGCGCTCATGCCCCAGATGGCTCTGACAGCACC 120  
 Db 233 AAGACGGGCTACTCTGTGGGGGAGCGCTCATGCCCCAGATGGCTCTGACAGCACC 292  
 QY 121 CACTGCTTCAAGCCCGCTTCATATGTTACCTGGGGGAGACAACTCCAGAGGAGAG 180  
 Db 293 CACTGCTTCAAGCCCGCTTCATATGTTACCTGGGGGAGACAACTCCAGAGGAGAG 352  
 QY 181 GGGTGTAGAGACCGGAGAGCCACTGAGTCTCCCGACCCCGGCTTCAACAGAGC 240  
 Db 353 GGGTGTAGAGACCGGAGAGCCACTGAGTCTCCCGACCCCGGCTTCAACAGAGC 412  
 QY 241 CTGCCCAAAAGACACCGCAATGACATCATGCTGTGAAGATGGCATGCCAGTCTCC 300  
 Db 413 CTGCCCAAAAGACACCGCAATGACATCATGCTGTGAAGATGGCATGCCAGTCTCC 472  
 QY 301 ATACACCTGGGCTGTGGAGCCCTTCACCTCTCTCAGCGTGTGTCACTGTGGACACG 360  
 Db 473 ATACACCTGGGCTGTGGAGCCCTTCACCTCTCTCAGCGTGTGTCACTGTGGACACG 532  
 QY 361 TGCTCTATTTCCGGCTGTGGGAGAGCTCCAGCCCGGCTTCAACAGCTTG 420  
 Db 533 TGCTCTATTTCCGGCTGTGGGAGAGCTCCAGCCCGGCTTCAACAGCTTG 592  
 QY 421 CGATGGCCCAACATACCATCATTTGAGACACAGAAAGTGTGAAGACGGCTTACCCGGAC 480  
 Db 593 CGATGGCCCAACATACCATCATTTGAGACACAGAAAGTGTGAAGACGGCTTACCCGGAC 652  
 QY 481 ATACAGACACCATGTGTGTGTCCAGGCTGACAGAGAGGGGCAAGAGCTCTGCGACAGGT 540  
 Db 653 ATACAGACACCATGTGTGTGTGTCCAGGCTGACAGAGAGGGGCAAGAGCTCTGCGACAGGT 712  
 QY 541 GACTCCGGGGGCGCTGTGTGTGTGAACAGTCTTTAAAGCAATATCTCTGGGGCCAG 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 713 GACTCCGGGGGCGCTGTGTGTGTGAACAGTCTTTCAAGGCAATATCTCTGGGGCCAG 772  
 QY 601 GATCCGTGTGGATACACCCGAAAGCCTGTGTGTACAGAAAGTGTCAATATGTGAC 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 773 GATCCGTGTGGATACACCCGAAAGCCTGTGTGTGTACAGAAAGTGTCAATATGTGAC 832  
 QY 661 TGGATCCAGAGACGATGAAGACAAT 687  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 833 TGGATCCAGAGACGATGAAGACAAT 859  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 RESULT 2  
 AA22639  
 ID AA22639 standard; cDNA; 1158 BP.  
 XX  
 AC AA22639;  
 XX  
 DT 08-DEC-1999 (first entry)  
 XX  
 DE CASB12 derived from Expressed Sequence Tag sequences.  
 XX  
 KW neuropilin; cancer; assay; inhibitor; serine protease; immunogenic;  
 KW autoimmune disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 84..932  
 FT /\*tag= a  
 FT /product= CASB12  
 XX  
 XX W09949055-A1.  
 FN  
 XX  
 XX 30-SEP-1999.  
 PD  
 XX  
 PF 17-MAR-1999; 99WO-EP01894.  
 XX  
 PR 20-MAR-1998; 98GB-0006095.  
 XX  
 PA (SWIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA  
 XX  
 PI Bruck CEM, Cassart J, Coche T, Vinals-Bassols C;  
 XX  
 DR WPI; 1999-580450/49.  
 DR P-PSDB; AAY42440.  
 XX  
 DR New human serine protease CASB12, for treatment, prevention and  
 PT diagnosis of cancer and autoimmune diseases -  
 PS Claim 26; Page 49; 58pp; English.  
 XX This is the nucleotide sequence of the CASB12 gene derived from  
 CC Expressed Sequence Tag (EST) search for tumor-specific and  
 CC tumor-associated antigens. The nucleotide sequence of AA22638 shows  
 CC homology with neuropilin and the encoded protein AAY42439 is structurally  
 CC related to other proteins of the serine protease family, having homology  
 CC and/or structural similarity with neuropilin. It is expected that as well  
 CC as similar structure, these proteins will also share similar biological  
 CC functions and properties.  
 CC The CASB12 polypeptides and polynucleotides can be used to develop  
 CC methods for identifying agonists and antagonists/inhibitors of these  
 CC molecules, and thereby treating conditions associated with CASB12  
 CC polypeptide imbalance. The invention also provides for diagnostic assays  
 CC for detecting diseases associated with inappropriate CASB12 polypeptide  
 CC activity or levels.  
 CC Since CASB12 is either specifically expressed or highly over-expressed  
 CC in tumors compared to normal cells, the polypeptides and polynucleotides  
 CC of the invention are believed to be important immunogens for specific  
 CC prophylactic or therapeutic immunization against tumors. The  
 CC polypeptides and polynucleotides can therefore be targeted by antigen  
 CC specific immune reactions (which result in the destruction of the tumor  
 CC cell) or they can be used to diagnose the occurrence of tumor cells

Sequence 1158 BP; 274 A; 359 C; 306 G; 219 T; 0 other;

Query Match 100.0%; Score 687; DB 20; Length 1158;  
Best Local Similarity 100.0%; Pred. No. 7.1e-137;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTGAGTGAAGGCTTCACTCCAGACCTGGCAGGACCCCTGTTCCAG 60  
DB 243 ATCATCAAGGGGTGAGTGAAGGCTTCACTCCAGACCTGGCAGGACCCCTGTTCCAG 302  
QY 61 AAGAGCGGGCTACTGTGTGGGGGAGAGGCTATCGCCCCAGATGGCTCTGACAGAGGC 120  
DB 303 AAGAGCGGGCTACTGTGTGGGGGAGAGGCTATCGCCCCAGATGGCTCTGACAGAGGC 362  
QY 121 CACTGCTTCAGACCCCGCTACATAGTTCACTGAGGAGCAGACACCTCCAGAGAGAG 180  
DB 363 CACTGCTTCAGACCCCGCTACATAGTTCACTGAGGAGCAGACACCTCCAGAGAGAG 422  
QY 181 GGCTGTGAGCAGACCCGGAGACGCACTAGTCTTCCCGGCTTCAACAGACG 240  
DB 423 GGCTGTGAGCAGACCCGGAGACGCACTAGTCTTCCCGGCTTCAACAGACG 482  
QY 241 CTCCCAACAAAGACACCGCAATGACATCATGCTGTGAAGATGAGCATCGCAGCTCC 300  
DB 483 CTCCCAACAAAGACACCGCAATGACATCATGCTGTGAAGATGAGCATCGCAGCTCC 542  
QY 301 ATCACTGGGCTGTGAGACCCCTCACTCTCTCACTGCTGCTGCTGCTGCTGCTGCTG 360  
DB 543 ATCACTGGGCTGTGAGACCCCTCACTCTCTCACTGCTGCTGCTGCTGCTGCTGCTG 602  
QY 361 TGGCTCATTTCCGGGTGGGGGAGCAGCTCAGCCCGGAGTTACGCTTGCCTCAGACCTTG 420  
DB 603 TGGCTCATTTCCGGGTGGGGGAGCAGCTCAGCCCGGAGTTACGCTTGCCTCAGACCTTG 662  
QY 421 CGATCGCCCAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 480  
DB 663 CGATCGCCCAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 722  
QY 481 ATCAAGACACCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
DB 723 ATCAAGACACCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 782  
QY 541 GACTCGGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
DB 783 GACTCGGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 842  
QY 601 GATCGGTGCTGATCAACCGAAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
DB 843 GATCGGTGCTGATCAACCGAAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 902  
QY 661 TGGATTCAGAGAGCATGAGAACAT 687  
DB 903 TGGATTCAGAGAGCATGAGAACAT 929

## RESULT 3

ABK92131  
ID ABK92131 standard; DNA; 1186 BP.

AC ABK92131;

XX 15-AUG-2002 (first entry)

DE Prostate cancer-associated DNA sequence #17.

KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;

XX gene therapy; gene; ds.

OS Mammalia.

XX WO200230268-A2.

PN 18-APR-2002.

PD

XX 12-OCT-2001; 2001WO-US32045.  
PF 13-OCT-2000; 2000US-0687576.  
PR 08-DEC-2000; 2000US-0733288.  
PR 08-DEC-2000; 2000US-0733742.  
PR 24-JAN-2001; 2001US-263957P.  
PR 16-MAR-2001; 2001US-276791P.  
PR 16-MAR-2001; 2001US-276888P.  
PR 06-APR-2001; 2001US-281922P.  
PR 24-APR-2001; 2001US-286214P.  
PR 30-APR-2001; 2001US-0847046.  
PR 04-MAY-2001; 2001US-288589P.  
XX (EOSB-) EOS BIOTECHNOLOGY INC.  
XX Gish KC, Mack DH, Wilson KE, Afar D, Hvezzi P;  
DR WPI; 2002-471335/50.  
DR P-PSDB; AB61816.  
XX  
PT Detecting a prostate cancer-associated transcript in a cell in a  
PT patient, useful for diagnosing prostate cancer (PC) or screening  
PT modulators of PC, by determining if prostate cancer-associated genes  
PT are expressed in a prostate tissue  
XX  
PS Claim 22; Page 313; 436pp; English.  
XX  
CC The present invention relates to methods of detecting a prostate  
CC cancer-associated transcript in a cell from a patient. The method  
CC comprises contacting a biological sample from the patient with  
CC prostate cancer-associated polynucleotides (designated PC genes)  
CC selectively hybridize to a sequence that is at least 80% identical  
CC to them. The prostate cancer-associated polynucleotide sequences  
CC are differentially expressed in prostate tumour tissue or in  
CC prostate cancer and are derived from the tissues of various  
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).  
CC The methods of the invention are useful for diagnosing and treating  
CC prostate cancer in mammals. The prostate cancer-associated genes are  
CC useful for diagnosing or treating prostate cancer, as well as for  
CC identifying modulators of prostate cancer or agents that inhibit  
CC prostate cancer. The nucleic acid sequences are particularly useful  
CC in gene therapy, as a vaccine or in antisense applications.  
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide  
CC sequences.  
XX  
SQ Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 other;

Query Match 100.0%; Score 687; DB 24; Length 1186;  
Best Local Similarity 100.0%; Pred. No. 7.1e-137;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTGAGTGAAGGCTTCACTCCAGACCTGGCAGGACCCCTGTTCCAG 60  
DB 185 ATCATCAAGGGGTGAGTGAAGGCTTCACTCCAGACCTGGCAGGACCCCTGTTCCAG 244  
QY 61 AAGAGCGGGCTACTGTGTGGGGGAGAGGCTATCGCCCCAGATGGCTCTGACAGAGGC 120  
DB 245 AAGAGCGGGCTACTGTGTGGGGGAGAGGCTATCGCCCCAGATGGCTCTGACAGAGGC 304  
QY 121 CACTGCTTCAGACCCCGCTACATAGTTCACTGAGGAGCAGACACCTCCAGAGAGAG 180  
DB 305 CACTGCTTCAGACCCCGCTACATAGTTCACTGAGGAGCAGACACCTCCAGAGAGAG 364  
QY 181 GGCTGTGAGCAGACCCGGAGACGCACTAGTCTTCCCGGCTTCAACAGACG 240  
DB 365 GGCTGTGAGCAGACCCGGAGACGCACTAGTCTTCCCGGCTTCAACAGACG 424  
QY 241 CTCCCAACAAAGACACCGCAATGACATCATGCTGTGAAGATGAGCATCGCAGCTCC 300  
DB 425 CTCCCAACAAAGACACCGCAATGACATCATGCTGTGAAGATGAGCATCGCAGCTCC 484  
QY 301 ATCACTGGGCTGTGAGACCCCTCACTCTCTCACTGCTGCTGCTGCTGCTGCTGCTG 360



ID	ADL4842	standard: DNA; 1192 BP.
XX	ADL4842;	
XX	01-NOV-2001	(first entry)
XX	Human PS133 gene contig.	
XX	Human; PS133; prostate disease; cancer; immunogen; gene therapy; EST;	
XX	expressed sequence tag; cytosolic; ds.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	CDS	107..859
XX	FT	/*tag= a
XX	FT	/product= "Human PS133 protein"
XX	FT	/transl_except= (pos:188..196, aa:Cys-Pro)
XX	FT	/transl_except= (pos:224..232, aa:Phe-Lys)
XX	US6232456-B1.	
XX	15-MAY-2001.	
XX	06-OCT-1997;	97US-09444483.
XX	06-OCT-1997;	97US-09444483.
XX	(ABBO ) ABBOTT LAB.	
XX	Cohen M, Colpitts TL, Friedman PN, Granados E, Klass MR;	
XX	Russell JC, Stewart KD, Stroupe SD;	
XX	WPI: 2001-366357/38.	
XX	P-PSDB; AAE08017.	
XX	New PS133 polynucleotides, useful for detecting, diagnosing, staging,	
XX	monitoring, prognosing, preventing, treating or determining the	
XX	predisposition of an individual to a prostate disease, e.g. cancer -	
XX	Claim 1; Column 71-74; 93pp: English.	
XX	The patent discloses PS133 polynucleotides and polypeptides which	
XX	are indicative of prostate disease. The patent also provides a method	
XX	for detecting PS133 protein in a test sample. The polynucleotides of	
XX	the invention are useful for detecting, diagnosing, staging, monitoring,	
XX	prognosing, preventing, treating or determining the predisposition of	
XX	an individual to prostate diseases such as cancer. PS133-derived	
XX	polynucleotides are used for the detection of normal or altered gene	
XX	expression, in assays for detecting, amplifying or quantifying genes	
XX	or nucleic acids relating to prostate tissue diseases and conditions,	
XX	and to produce probes which can be used in the detection of nucleic	
XX	acids in a sample. PS133 proteins are used as immunogens for the	
XX	production of antibodies. PS133 sequences are also used in gene	
XX	therapy. The present sequence is human PS133 gene contig.	
XX	Sequence 1192 BP; 279 A; 385 C; 290 G; 238 T; 0 other;	
XX	Query Match	100.0%; Score 687; DB 22; Length 1192;
XX	Best Local Similarity	100.0%; Pred. No. 7.1e-137;
XX	Matches	687; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX	1 ATCATCAAGGGGTTGAGTGCAGAGCCTCACTCCAGCCCTGGACAGCCCTGTTTCAG	60
XX		
XX	170 ATCATCAAGGGGTTGAGTGCAGAGCCTCACTCCAGCCCTGGACAGCCCTGTTTCAG	229
XX		
XX	61 AAGACGGGGCTACTGCTGTGGGGCGACGCTCAATCCGCCCAAGTGGCTCCTGTGACAGAGCC	120
XX		
XX	230 AAGACGGGGCTACTGCTGTGGGGCGACGCTCAATCCGCCCAAGTGGCTCCTGTGACAGAGCC	289

OY	121	CACCTGCCTCAAGCCCGCTACATAGTTCACCTGGGGGACAGACAACTCCGAAGGGAG	180
Db	230	CACCTGCCTCAAGCCCGCTACATAGTTCACCTGGGGGACAGACAACTCCGAAGGGAG	349
OY	181	GCGTGTGAGCAGACCCGGACAGCCACCTGAGTCTTCCCGCACCCCGGCTTCAACACAGC	240
Db	350	GCGTGTGAGCAGACCCGGACAGCCACCTGAGTCTTCCCGCACCCCGGCTTCAACACAGC	409
OY	241	CTCCCAACAAAGACCACCGCATGATGATGCTGGTGAAGATGGCATTCGCCAGTCTCC	300
Db	410	CTCCCAACAAAGACCACCGCATGATGATGCTGGTGAAGATGGCATTCGCCAGTCTCC	469
OY	301	ATCACCTGGGGGTGGGAGACCCGTCACCCCTCTCCAGCGTGTCACTGCTGGCACCAGC	360
Db	470	ATCACCTGGGGGTGGGAGACCCGTCACCCCTCTCCAGCGTGTGTCACTGCTGGCACCAGC	529
OY	361	TGCCCTCAATTTCCGGCTGGGGGACAGCAGTCCACGCCCAATTAAGCCTGGCTCACACTTG	420
Db	530	TGCCCTCAATTTCCGGCTGGGGGACAGCAGTCCACGCCCAATTAAGCCTGGCTCACACTTG	589
OY	421	CGATGCGGCCACATATACCATTCATTGAGCACCCAGAGTGTGAGAGACCTTACCCGGCAAC	480
Db	590	CGATGCGGCCACATATACCATTCATTGAGCACCCAGAGTGTGAGAGACCTTACCCGGCAAC	649
OY	481	ATTCACAGACACCATGATGTGTGTCCACAGCGTGCAGGAAGGGGGCAAGGACATCTCCAGGGT	540
Db	650	ATTCACAGACACCATGATGTGTGTCCACAGCGTGCAGGAAGGGGGCAAGGACATCTCCAGGGT	709
OY	541	GACTCGGGGGGCCCTCTGGTCTGTACACAGTCTCTTCAAGGCAATTAATCTCTGGGCCAG	600
Db	710	GACTCGGGGGGCCCTCTGGTCTGTACACAGTCTCTTCAAGGCAATTAATCTCTGGGCCAG	769
OY	601	GATCGGTGTGGCATTCACCCGGAAGCCTGGTGTCTACAGAAAGTCTGCAATATGTGGAC	660
Db	770	GATCGGTGTGGCATTCACCCGGAAGCCTGGTGTCTACAGAAAGTCTGCAATATGTGGAC	829
OY	661	TGGATCCAGAGACGATGAGAACAAT 687	
Db	830	TGGATCCAGAGACGATGAGAACAAT 856	
RESULT 6			
AAA37072			
ID	AAA37072 standard; cDNA; 1204 BP.		
XX	AAA37072;		
AC			
XX	08-AUG-2000 (first entry)		
DT			
DE	Human PRO1279 (UNQ649) cDNA sequence SEQ ID NO:169.		
XX			
KW	Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;		
KW	transmembrane; secretion; Immunoadhesion; pharmaceutical; screening;		
RS	ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200012708-A2.		
XX			
PD	09-MAR-2000.		
XX			
PF	01-SEP-1999; 99WO-US20111.		
XX			
PR	01-SEP-1998;	98US-0098716	
PR	01-SEP-1998;	98US-0098749	
PR	01-SEP-1998;	98US-0098750	
PR	02-SEP-1998;	98US-0098803	
PR	02-SEP-1998;	98US-0098821	
PR	02-SEP-1998;	98US-0098843	
PR	09-SEP-1998;	98US-0099536	
PR	09-SEP-1998;	98US-0099596	
PR	09-SEP-1998;	98US-0099598	



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PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.
PR 10-SEP-1998; 98US-0099741.
PR 10-SEP-1998; 98US-0099754.
PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 15-SEP-1998; 98US-0099816.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100390.
PR 16-SEP-1998; 98US-0100394.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 16-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100930.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102685.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104967.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.

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PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106052.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0106500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106934.
PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.
PR 17-NOV-1998; 98US-0108867.
PR 17-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108848.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108858.
PR 18-NOV-1998; 98US-0108904.

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(GETH ) GENENTECH INC.

Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI,

WPI: 2000-237871/20.

P-PSDB; AAY9390.

PT New mammalian DNA sequences encoding transmembrane, receptor or  
PT secreted PRO polypeptides; useful for screening of potential peptide or  
PT small molecule inhibitors of the relevant receptor/ligand interactions  
XX  
XX Claim 2; Fig 101; 773pp; English.

CC AAA37022 to AAA37144 encode the new isolated human transmembrane,  
CC receptor or secreted PRO polypeptides given in AAY9340 to AAY9462. The  
CC transmembrane and receptor PRO proteins can be used for screening of  
CC potential peptide or small molecule inhibitors of the relevant  
CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
CC encoding them have various industrial applications, including uses as  
CC pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent  
CC PCR primers and hybridisation probes used in the isolation of the PRO  
CC polypeptides from the present invention.  
XX

SO Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Query Match 100.0%; Score 687; DB 21; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 7.2e-137;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTCCAGTGCAGCAAGCTTCACTCCACAGCCCTGCAGGACAGCCCTGTTCGAG 60  
DB 169 ATCATCAAGGGGTTCCAGTGCAGCAAGCTTCACTCCACAGCCCTGCAGGACAGCCCTGTTCGAG 228









QY 481 ATCAGACACCATGTTGTGTGTCAGACGTCGAGGAAGGGGCGACGCTCTGCCAGGCT 540  
|||||  
Db 649 ATCAGACACCATGTTGTGTGTCAGACGTCGAGGAAGGGGCGACGCTCTGCCAGGCT 708  
|||||  
QY 541 GACTCGGGGGCCCTGTGTCGTATACAGTCCTTCAAGGCAATTTCTCTGGGGCCAG 600  
|||||  
Db 709 GACTCGGGGGCCCTGTGTCGTATACAGTCCTTCAAGGCAATTTCTCTGGGGCCAG 768  
|||||  
QY 601 GATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACACGAAGTCTGCAATATATGTGAC 660  
|||||  
Db 769 GATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACACGAAGTCTGCAATATATGTGAC 828  
|||||  
QY 661 TGGATCCAGAGACCATGTAAGAACAT 687  
|||||  
Db 829 TGGATCCAGAGACCATGTAAGAACAT 855  
|||||  
RESULT 11  
ID ABR33628 standard; cDNA; 1204 BP.  
XX  
AC ABR33628;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE cDNA encoding human PRO protein, Seq ID No 185.  
XX  
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
KW pericyte cell proliferation; chondrocyte cell proliferation;  
KW tumour necrosis factor-alpha; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200208288-A2.  
XX  
PD 31-JAN-2002.  
XX  
PE 29-JUN-2001; 2001WO-US21066.  
XX  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220585P.  
PR 25-JUL-2000; 2000US-220605P.  
PR 25-JUL-2000; 2000US-220607P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220638P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 25-JUL-2000; 2000US-220666P.  
PR 26-JUL-2000; 2000US-220893P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 15-SEP-2000; 2000US-000000P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 28-NOV-2000; 2000US-253646P.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001WO-US17092.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Desnoyers L, Gerlitsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
XX  
DR MPI; 2002-172001/22.  
DR P-PSDB; AA083684.  
XX  
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for treating a PRO related disorder and for diagnosing tumours  
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal

PT tumour or liver tumour -  
XX  
PS Claim 2; Figure 185; 359pp; English.  
XX  
CC The invention relates to one hundred and twenty two nucleic acids  
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
CC agonists and antagonists are useful for treating a PRO related disorder.  
CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
CC liver tumour. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression, in pericyte cells, for stimulating  
CC the proliferation or differentiation of chondrocyte cells, for  
CC stimulating the release of tumour necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal  
CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes,  
CC and in chromosome and gene mapping. ABR33536-ABR33657 represent human  
CC PRO protein coding sequences of the invention.  
XX  
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;  
XX  
Query Match. 100.0%; Score 687; DB 24; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 7.2e-137;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATCATCAAGGGGTTGAGTGAAGCCTCACTCCAGCCTTGCGAGGACCCGTTGCGAG 60  
|||||  
Db 169 ATCATCAAGGGTGTGAGTGAAGCCTCACTCCAGCCTTGCGAGGACCCGTTGCGAG 228  
|||||  
QY 61 AAGAGCGGCTACTCTGTGTGGGCGACGCTCATGCCCCAGATGCTCTGACAGACGC 120  
|||||  
Db 229 AAGAGCGGCTACTCTGTGTGGGCGACGCTCATGCCCCAGATGCTCTGACAGACGC 288  
|||||  
QY 121 CACTGCTTAAGCCCCCGCTACATAGTTACCTTGGGGACACAACTCCAGAAAGGAG 180  
|||||  
Db 289 CACTGCTTAAGCCCCCGCTACATAGTTACCTTGGGGACACAACTCCAGAAAGGAG 348  
|||||  
QY 181 GCGTGTGACAGACCCGAGACGCACTGATGCTTCCCGCCGCGCTTCAACAGACG 240  
|||||  
Db 349 GCGTGTGACAGACCCGAGACGCACTGATGCTTCCCGCCGCGCTTCAACAGACG 408  
|||||  
QY 241 CTCGCCAACAAAGACACCGCAATGACATCATGTGTGTAAGATGGCATGCGCAGTCTCC 300  
|||||  
Db 409 CTCGCCAACAAAGACACCGCAATGACATCATGTGTGTAAGATGGCATGCGCAGTCTCC 468  
|||||  
QY 301 ATCACTGTGGGTGTGAGACCCCTCACCCCTCTCTACGCTGTGTACTGCTGGACACG 360  
|||||  
Db 469 ATCACTGTGGGTGTGAGACCCCTCACCCCTCTCTACGCTGTGTACTGCTGGACACG 528  
|||||  
QY 361 TGCCTCATTTCCGGGCGGGGAGACAGTCCAGCCCCCAATTAAGCGCTGACTACACCTTG 420  
|||||  
Db 529 TGCCTCATTTCCGGGCGGGGAGACAGTCCAGCCCCCAATTAAGCGCTGACTACACCTTG 588  
|||||  
QY 421 CGATGGCCCAACATCAATCATATTGAGCACAGAAAGTGTAGAAAGCGCTTACCCCGGCAAC 480  
|||||  
Db 589 CGATGGCCCAACATCAATCATATTGAGCACAGAAAGTGTAGAAAGCGCTTACCCCGGCAAC 648  
|||||  
QY 481 ATCAGACACCATGTTGTGTGTCAGACGTCGAGGAAGGGGCGACGCTCTGCCAGGCT 540  
|||||  
Db 649 ATCAGACACCATGTTGTGTGTCAGACGTCGAGGAAGGGGCGACGCTCTGCCAGGCT 708  
|||||  
QY 541 GACTCGGGGGCCCTGTGTCGTATACAGTCCTTCAAGGCAATTTCTCTGGGGCCAG 600  
|||||  
Db 709 GACTCGGGGGCCCTGTGTCGTATACAGTCCTTCAAGGCAATTTCTCTGGGGCCAG 768  
|||||  
QY 601 GATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACACGAAGTCTGCAATATATGTGAC 660  
|||||  
Db 769 GATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACACGAAGTCTGCAATATATGTGAC 828  
|||||  
QY 661 TGGATCCAGAGACCATGTAAGAACAT 687  
|||||

DB 829 TGGATCCAGACGATGACACAT 855

RESULT 12

ACA03855

ID ACA03855 standard; cDNA; 1204 BP.

XX

AC ACA03855;

XX

DT 23-MAY-2003 (first entry)

XX

DE cDNA encoding human PRO polypeptide #253.

XX

KW Human; PRO polypeptide; secreted and transmembrane protein;

KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;

KW differentiation; chondrocyte; tumour; genetic disorder;

KW cytosolic; gene; ss.

XX

OS Homo sapiens.

XX

FN US2003036180-A1.

XX

PD 20-FEB-2003.

XX

PE 09-MAY-2002; 2002US-0143114.

XX

PR 31-MAR-1997; 97WO-US05230.

PR 12-JUN-1998; 98WO-US12456.

PR 14-JUL-1998; 98WO-US14552.

PR 28-AUG-1998; 98WO-US17888.

PR 10-SEP-1998; 98WO-US18824.

PR 14-SEP-1998; 98WO-US19093.

PR 14-SEP-1998; 98WO-US19094.

PR 16-SEP-1998; 98WO-US19177.

PR 17-SEP-1998; 98WO-US19330.

PR 07-OCT-1998; 98WO-US19437.

PR 29-OCT-1998; 98WO-US21141.

PR 29-OCT-1998; 98WO-US22992.

PR 29-OCT-1998; 98WO-US22992.

PR 20-NOV-1998; 98WO-US24855.

PR 01-DEC-1998; 98WO-US25108.

PR 05-JAN-1999; 99WO-US00106.

PR 08-MAR-1999; 99WO-US05028.

PR 10-MAR-1999; 99WO-US05190.

PR 20-APR-1999; 99WO-US08615.

PR 14-MAY-1999; 99WO-US10733.

PR 02-JUN-1999; 99WO-US12252.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 05-OCT-1999; 99WO-US23089.

PR 29-NOV-1999; 99WO-US28214.

PR 30-NOV-1999; 99WO-US28313.

PR 30-NOV-1999; 99WO-US28409.

PR 01-DEC-1999; 99WO-US28301.

PR 02-DEC-1999; 99WO-US28634.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28564.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 20-DEC-1999; 99WO-US30999.

PR 22-DEC-1999; 99WO-US30720.

PR 30-DEC-1999; 99WO-US31243.

PR 30-DEC-1999; 99WO-US31274.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00277.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.

PR 01-MAR-2000; 2000WO-US05601.

PR 02-MAR-2000; 2000WO-US05746.

PR 02-MAR-2000; 2000WO-US05841.

PR 10-MAR-2000; 2000WO-US06319.

PR 15-MAR-2000; 2000WO-US06884.

PR 20-MAR-2000; 2000WO-US07377.

PR 21-MAR-2000; 2000WO-US07532.

PR 30-MAR-2000; 2000WO-US08439.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 28-JUL-2000; 2000WO-US20710.

PR 11-AUG-2000; 2000WO-US22031.

PR 23-AUG-2000; 2000WO-US23522.

PR 24-AUG-2000; 2000WO-US23328.

PR 08-NOV-2000; 2000WO-US30952.

PR 10-NOV-2000; 2000WO-US30873.

PR 01-DEC-2000; 2000WO-US32678.

PR 20-DEC-2000; 2000WO-US34956.

PR 28-FEB-2001; 2001WO-US06520.

PR 01-MAR-2001; 2001WO-US06666.

PR 25-MAY-2001; 2001WO-US17092.

PR 01-JUN-2001; 2001WO-US17800.

PR 20-JUN-2001; 2001WO-US19692.

PR 22-JUN-2001; 2001WO-US20116.

PR 29-JUN-2001; 2001WO-US21066.

PR 09-JUL-2001; 2001WO-US21735.

PR 20-DEC-2000; 2000US-0747259.

PR 28-FEB-2001; 2001US-076498.

PR 09-MAR-2001; 2001US-0802706.

PR 14-MAR-2001; 2001US-0808689.

PR 22-MAR-2001; 2001US-0816744.

PR 05-APR-2001; 2001US-0828366.

PR 10-MAY-2001; 2001US-0834208.

PR 10-MAY-2001; 2001US-0854280.

PR 18-MAY-2001; 2001US-0860216.

PR 25-MAY-2001; 2001US-086028.

PR 25-MAY-2001; 2001US-0866034.

PR 01-JUN-2001; 2001US-0872035.

PR 05-JUN-2001; 2001US-0874503.

PR 14-JUN-2001; 2001US-0882636.

PR 19-JUN-2001; 2001US-0886342.

PR 21-JUN-2001; 2001US-0887879.

PR 18-JUL-2001; 2001US-0908827.

PR 06-AUG-2001; 2001US-0924419.

PR 09-AUG-2001; 2001US-0927796.

PR 16-AUG-2001; 2001US-0931836.

PR 19-DEC-2001; 2001US-0028072.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,

PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tamas D, Watanabe CK, Wood WL, Zhang Z;

XX

DR WPL; 2003-332040/31.

DR P-PDSB; AB068822.

XX

PT New secreted and transmembrane PRO nucleic acids, useful for gene

PT therapy, in chromosome and gene mapping, as chromosome markers, in

PT tissue typing, and in chromosome identification

XX

PS Claim 2; Fig 505; 660pp; English.

XX

CC The present invention relates to the isolation of novel human PRO

CC polypeptides, and the polynucleotide sequences encoding them. The

CC PRO polypeptides are secreted and transmembrane proteins. The PRO

CC polypeptides are useful for detecting other PRO polypeptides, for

CC linking bioactive molecules to cells expressing PRO polypeptides,



CC for modulating biological activities of cells expressing PRO  
 CC polypeptides, and for identifying agonists or antagonists.  
 CC The PRO polypeptides are useful for stimulating the release of  
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating  
 CC the proliferation or differentiation of chondrocytes, and detecting the  
 CC presence of tumours. The polynucleotide sequences encoding PRO  
 CC polypeptides are useful as hybridisation probes, in chromosome and  
 CC gene mapping, in the generation of antisense RNA and DNA, in the  
 CC preparation of PRO polypeptides, for generating transgenic animals or  
 CC knockout animals, for the genetic analysis of individuals with genetic  
 CC disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs  
 CC encoding the human PRO polypeptides of the invention.  
 CC Note: The sequence data for this patent was obtained in electronic  
 CC format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipspidentry.html.

xx Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Query Match 100.0%; Score 687; DB 25; Length 1204;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-137;  
 Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTGAGTGCAGCCCTCCAGCCCTGGCAGGACCCCTGTTGAG 60  
 DB 169 ATCATCAAGGGGTTGAGTGCAGCCCTCCAGCCCTGGCAGGACCCCTGTTGAG 228  
 QY 61 AAGAGCGGGCTACTGTGGGGGCGAGCGTATCGCCCCAGATGGCTCTGACAGAGCC 120  
 DB 229 AAGAGCGGGCTACTGTGGGGGCGAGCGTATCGCCCCAGATGGCTCTGACAGAGCC 288  
 QY 121 CACTGCTTAAGCCCGCTGACTAGTTCACCTGGGGGACACACCTCCAGAGAGAG 180  
 DB 289 CACTGCTTAAGCCCGCTGACTAGTTCACCTGGGGGACACACCTCCAGAGAGAG 348  
 QY 181 GCGTGTGAGACAGCCGCGAGCAGCACTGATGCTTCCCGCCGGCTTCAACAACAGC 240  
 DB 349 GCGTGTGAGACAGCCGCGAGCAGCACTGATGCTTCCCGCCGGCTTCAACAACAGC 408  
 QY 241 CTCGCCAACAAGACACCGCAATGACATGCTGTGTGAAGATGGCATCGCCAGTCC 300  
 DB 409 CTCGCCAACAAGACACCGCAATGACATGCTGTGTGAAGATGGCATCGCCAGTCC 468  
 QY 301 ATCACTGGGCTGTGCGACCCCTCAACCTCTCTCAAGCTGTGTACCTGTGGACAC 360  
 DB 469 ATCACTGGGCTGTGCGACCCCTCAACCTCTCTCAAGCTGTGTACCTGTGGACAC 528  
 QY 361 TGCCTCATTTCCGGCTGGGGGAGCAGCTGACGCCCCCAAGTTACGCTGCTCAACCTTG 420  
 DB 529 TGCCTCATTTCCGGCTGGGGGAGCAGCTGACGCCCCCAAGTTACGCTGCTCAACCTTG 588  
 QY 421 CGATCGGCCAATCATCATCATTTGAGCAGCAGAAAGTGTGAGAACGGCTACCCCGGCAAC 480  
 DB 589 CGATCGGCCAATCATCATCATTTGAGCAGCAGAAAGTGTGAGAACGGCTACCCCGGCAAC 648  
 QY 481 ATCAAGACACCATGTTGTGTGCGACGCTGTGAGAAAGGGGGGCAAGAGTCTCTGCGCAGGT 540  
 DB 649 ATCAAGACACCATGTTGTGTGCGACGCTGTGAGAAAGGGGGGCAAGAGTCTCTGCGCAGGT 708  
 QY 541 GACTCGGGGGGCTCTGCTGTAAACAGTCTTTCAGGAGTATATCTGCGGGCCAG 600  
 DB 709 GACTCGGGGGGCTCTGCTGTAAACAGTCTTTCAGGAGTATATCTGCGGGCCAG 768  
 QY 601 GATCGGTGTGCGATACCCGGAAGCGTGTCTACAGCAAGTGTGCAAAATATGTGAC 660  
 DB 769 GATCGGTGTGCGATACCCGGAAGCGTGTCTACAGCAAGTGTGCAAAATATGTGAC 828  
 QY 661 TGGATCCAGAGACGATGAAGAACAT 687  
 DB 829 TGGATCCAGAGACGATGAAGAACAT 855

RESULT 13  
 ACA04276

ID	ACA04276 standard; cDNA: 1204 BP.
XX	
AC	ACA04276;
XX	
DT	27-MAY-2003 (first entry)
XX	
DE	Human cDNA encoding a secreted/transmembrane protein, SEQ ID 505.
XX	
KW	Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW	Inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW	infertility; birth defects; premature aging; AIDS; biosensor;
KW	acquired immunodeficiency syndrome; cancer; diabetic complication;
KW	bioreactor; tumour.
XX	
OS	Homo sapiens.
XX	
PN	US2003032155-A1.
XX	
PD	13-FEB-2003.
XX	
PF	03-MAY-2002; 2002US-0137865.
XX	
PR	31-MAR-1997; 97WO-US05230.
PR	12-JUN-1998; 98WO-US12456.
PR	14-JUL-1998; 98WO-US14552.
PR	28-AUG-1998; 98WO-US17888.
PR	10-SEP-1998; 98WO-US18824.
PR	14-SEP-1998; 98WO-US19093.
PR	14-SEP-1998; 98WO-US19094.
PR	14-SEP-1998; 98WO-US19177.
PR	16-SEP-1998; 98WO-US19330.
PR	17-SEP-1998; 98WO-US19437.
PR	07-OCT-1998; 98WO-US21141.
PR	29-OCT-1998; 98WO-US22991.
PR	20-NOV-1998; 98WO-US24855.
PR	01-DEC-1998; 98WO-US25108.
PR	05-JAN-1999; 99WO-US00106.
PR	08-MAR-1999; 99WO-US05028.
PR	10-APR-1999; 99WO-US05190.
PR	20-APR-1999; 99WO-US08615.
PR	14-MAY-1999; 99WO-US10733.
PR	02-JUN-1999; 99WO-US12252.
PR	01-SEP-1999; 99WO-US20111.
PR	08-SEP-1999; 99WO-US20594.
PR	13-SEP-1999; 99WO-US20944.
PR	15-SEP-1999; 99WO-US21090.
PR	05-OCT-1999; 99WO-US23089.
PR	15-SEP-1999; 99WO-US21547.
PR	29-NOV-1999; 99WO-US28214.
PR	30-NOV-1999; 99WO-US28313.
PR	30-NOV-1999; 99WO-US28409.
PR	01-DEC-1999; 99WO-US28301.
PR	01-DEC-1999; 99WO-US28634.
PR	02-DEC-1999; 99WO-US28551.
PR	02-DEC-1999; 99WO-US28564.
PR	16-DEC-1999; 99WO-US30095.
PR	20-DEC-1999; 99WO-US30911.
PR	20-DEC-1999; 99WO-US30999.
PR	22-DEC-1999; 99WO-US30720.
PR	30-DEC-1999; 99WO-US31243.
PR	05-JAN-2000; 2000WO-US00219.
PR	06-JAN-2000; 2000WO-US00277.
PR	06-JAN-2000; 2000WO-US00376.
PR	11-FEB-2000; 2000WO-US03565.
PR	18-FEB-2000; 2000WO-US04341.
PR	22-FEB-2000; 2000WO-US04342.
PR	24-FEB-2000; 2000WO-US04914.
PR	01-MAR-2000; 2000WO-US05004.
PR	01-MAR-2000; 2000WO-US05601.

02-MAR-2000; 2000WO-US05746.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23322.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US34956.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 22-JUN-2001; 2001WO-US20116.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 20-DEC-2000; 2000US-0747259.  
PR 28-FEB-2001; 2001US-0796498.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854280.  
PR 18-MAY-2001; 2001US-0860216.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 01-JUN-2001; 2001US-0872035.  
PR 05-JUN-2001; 2001US-0874503.  
PR 14-JUN-2001; 2001US-0882636.  
PR 19-JUN-2001; 2001US-0886342.  
PR 21-JUN-2001; 2001US-0887879.  
PR 18-JUL-2001; 2001US-0908827.  
PR 06-AUG-2001; 2001US-0924419.  
PR 09-AUG-2001; 2001US-0927796.  
PR 16-AUG-2001; 2001US-0931836.  
PR 19-DEC-2001; 2001US-0028072.  
XX  
PA (GENE) GENENTECH INC.  
XX  
PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
PI Geriltsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX  
DR WPI: 2003-331925/31.  
DR P-PSDB; AB067096.  
XX  
PT New secreted and transmembrane nucleic acids and polypeptides,  
PT designated as PRO, useful for treating inflammation, organ failure,  
PT atherosclerosis, cardiac injury, infertility, birth defects, premature  
PT aging, AIDS, or cancer -  
XX  
PS  
PS Claim 2; Fig 505; 659pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising, or which is  
CC at least 80% identical to, or the full-length coding sequence of, any of  
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide  
CC (one of 275 secreted or transmembrane proteins). The nucleic acid  
CC further comprises the full-length coding sequence of the DNA deposited  
CC under American Type Culture Collection (ATCC) accession number in a list  
CC given in the specification. Also included are vectors and host  
CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO

CC antibodies, PRO extracellular domains and mature sequences, methods  
CC of detecting PRO proteins, methods for stimulating the release of  
CC TNF-alpha (tumour necrosis factor alpha) from human blood,  
CC (and the proliferation of differentiation of chondrocyte cells, the  
CC proliferation of, or gene expression in pericyte cells, the release or  
CC proteoglycans from cartilage, proliferation of inner ear utricular  
CC supporting cells, the proliferation of T-lymphocyte cells, the release  
CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the  
CC proliferation of endothelial cells), a method for modulating the uptake  
CC of glucose or free fatty acid (FFA) by skeletal muscle cells,  
CC a method for inhibiting the binding of A-peptide to factor VIIa,  
CC or the differentiation of adipocyte cells, a method for detecting the  
CC presence of a tumour in a mammal and an oligonucleotide probe derived  
CC from any of the nucleotide sequences cited above. The nucleic acids and  
CC polypeptides are useful for treating inflammatory diseases, organ  
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,  
CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or  
CC diabetic complications. The nucleic acids are useful as hybridisation  
CC probes, in chromosome and gene mapping, and in generating antisense RNA  
CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
CC biosensors or bioreactors. Both are useful in tissue typing.  
CC The present sequence encodes a PRO protein of the invention.  
XX

SO Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Query Match 100.0%; Score 687; DB 25; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 7.2e-137;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTTCAGTGCAGACCTTCCAGCCCTGGAGAGAGCCCTGTTGAG 60  
DB 169 ATCATCAAGGGGTTTCAGTGCAGACCTTCCAGCCCTGGAGAGAGCCCTGTTGAG 228  
QY 61 AAGAGCGGGCTACTCTGTGGGGGAGAGCTATGATGCGCCCGAGATGGCTCTGACAGAGCC 120  
DB 229 AAGAGCGGGCTACTCTGTGGGGGAGAGCTATGATGCGCCCGAGATGGCTCTGACAGAGCC 288  
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGAGAGAGAGAGAGAG 180  
DB 289 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGAGAGAGAGAGAGAGAGAGAG 348  
QY 181 GCGTGTAG 240  
DB 349 GCGTGTAG 408  
QY 241 CTCGCCAAG 300  
DB 409 CTCGCCAAG 468  
QY 301 ATCACTGGGCTGTGGAG 360  
DB 469 ATCACTGGGCTGTGGAG 528  
QY 361 TGGCTCATTTTCGGGCTGGGAG 420  
DB 529 TGGCTCATTTTCGGGCTGGGAG 588  
QY 421 CGATGCGCAACATCATCATATTTAG 480  
DB 589 CGATGCGCAACATCATCATATTTAG 648  
QY 481 ATCAAG 540  
DB 649 ATCAAG 708  
QY 541 GACTCGGGGGGCGCTGTGTCTGTACCAATCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
DB 709 GACTCGGGGGGCGCTGTGTCTGTACCAATCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 768  
QY 601 GATCCGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
DB 769 GATCCGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828

QY 661 TGGATCCAGAGACGATGAGACAAAT 687  
 DB 829 TGGATCCAGAGACGATGAGACAAAT 855  
 RESULT 14  
 ID ABX89393 standard; cDNA, 1204 BP.  
 AC ABX89393;  
 XX 13-MAY-2003 (first entry)  
 DE DNA encoding novel secreted and transmembrane protein PRO1279.  
 XX  
 KM Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KM cardiac insufficiency disorder; cancer; tumour; immune response;  
 KM adrenal cortical capillary endothelial growth; c-fos induction;  
 KM vascular endothelial growth factor inhibition; VEGF inhibition;  
 KM endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KM retinal neurons cell survival; rod photoreceptor cell survival;  
 KM retinal disorder; retinitis pigmentosa; kidney disorder;  
 KM mammalian kidney mesangial cell proliferation; Berger disease;  
 KM dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
 KM chondrocyte redifferentiation; sports injury; arthritis; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PM US2003017563-A1.  
 XX  
 PD 23-JAN-2003.  
 XX  
 PF 07-MAY-2002; 2002US-0140808.  
 XX  
 XX 31-MAR-1997; 97WO-US05230.  
 PR 12-JUN-1998; 98WO-US12456.  
 PR 14-JUL-1998; 98WO-US14532.  
 PR 28-AUG-1998; 98WO-US17888.  
 PR 10-SEP-1998; 98WO-US18824.  
 PR 14-SEP-1998; 98WO-US19093.  
 PR 14-SEP-1998; 98WO-US19094.  
 PR 14-SEP-1998; 98WO-US19177.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 29-OCT-1998; 98WO-US22991.  
 PR 29-OCT-1998; 98WO-US22992.  
 PR 20-NOV-1998; 98WO-US24855.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 10-MAR-1999; 99WO-US05190.  
 PR 20-APR-1999; 99WO-US08615.  
 PR 14-MAY-1999; 99WO-US10733.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 22-DEC-1999; 99WO-US30999.  
 PR 22-DEC-1999; 99WO-US30720.

PR 30-DEC-1999; 99WO-US31243.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05746.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 22-JUN-2001; 2001WO-US20116.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 18-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 05-JUN-2001; 2001US-0874503.  
 PR 14-JUN-2001; 2001US-0882636.  
 PR 19-JUN-2001; 2001US-0886342.  
 PR 21-JUN-2001; 2001US-0887879.  
 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Flyvareff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PU, Guirney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;  
 XX WPI; 2003-148238/14.  
 DR P-PSDB; AB059903.  
 XX  
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer

PT treatments  
 XX  
 PS Claim 2, Fig 505; 659pp; English.  
 CC The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
 CC PRO948, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1256,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
 CC immune response. PRO828, PRO1068 or PRO1312 enhance survival of  
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and  
 CC are thus useful for treating sports injuries, and arthritis. This  
 CC sequence encodes a novel human PRO protein.  
 XX  
 SQ Sequence 1204 BP; 364 A; 364 C; 294 G; 240 T; 0 other:  
 Query Match 100.0%; Score 687; DB 25; Length 1204;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-137;  
 Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATCATCAAGGGGTTGAGTGCAGAGCTTCCAGCCCTGCGAGGAGCCCTGTTGAG 60  
 DB 169 ATCATCAAGGGGTTGAGTGCAGAGCTTCCAGCCCTGCGAGGAGCCCTGTTGAG 228  
 QY 61 AAGACGGGCTACTCTGTGGGGCGAGCCTATGCCCCAGANGGCTCTGACAGACCC 120  
 DB 229 AAGACGGGCTACTCTGTGGGGCGAGCCTATGCCCCAGANGGCTCTGACAGACCC 288  
 QY 121 CACGCGCTCAAGCCCGCTACATAGTTCACTGGGGGAGAGCAACCTCCGAAGGAGAG 180  
 DB 289 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGAGCAACCTCCGAAGGAGAG 348  
 QY 181 GGCTGTAGAGAGAGCCCGAGAGCCACTAGTCTCTCCCGACCCCGGCTTCAACAGAGC 240  
 DB 349 GGCTGTAGAGAGAGCCCGAGAGCCACTAGTCTCTCCCGACCCCGGCTTCAACAGAGC 408  
 QY 241 CTGCCCCAAGAACCCGCAATGACATATGCTGTGAAGATGGCATGCCAGTCTCC 300  
 DB 409 CTGCCCCAAGAACCCGCAATGACATATGCTGTGAAGATGGCATGCCAGTCTCC 468  
 QY 301 ATACACGTGGGCTGTGAGACCCCTACCCCTCTCCCTCAAGCTGTGTGACACACAGC 360  
 DB 469 ATACACGTGGGCTGTGAGACCCCTACCCCTCTCCCTCAAGCTGTGTGACACACAGC 528  
 QY 361 TGCCCTATTTCGAGCTGGGAGACAGTCCAGCCCGAGTTAGAGCTGCTCAACCTTG 420  
 DB 529 TGCCCTATTTCGAGCTGGGAGACAGTCCAGCCCGAGTTAGAGCTGCTCAACCTTG 588  
 QY 421 CGATGGCCCAACATACATCATTTAGAGACAGAGTGTGAAGAGGCTTACCCGGGAC 480  
 DB 589 CGATGGCCCAACATACATCATTTAGAGACAGAGTGTGAAGAGGCTTACCCGGGAC 648  
 QY 481 ATCAGAGACACATGATGTGTGCGACAGCTGCGAGGAAGGGGCAAGAGACTCTCCAGG 540

DB 649 ATCAGAGACACATGATGTGTGCGACAGTCCAGGAAGGGGCAAGGACTCTCCAGG 708  
 QY 541 GACTCCGGGGAGCCCTGTGCTGTGAACCACTCTTCAAGCATATATCTCTGGGGCAG 600  
 DB 709 GACTCCGGGGAGCCCTGTGCTGTGAACCACTCTTCAAGCATATATCTCTGGGGCAG 768  
 QY 601 GATCCGTGTGCGATACCCGAAAGCCCTGTGTACACGAAGTGTGCAATATGTGGAC 660  
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 DB 829 TGGATCCAGAGAGCATGAAGAACAT 855  
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 ID AAA61763 standard; cDNA: 1301 BP.  
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 AC AAA61763;  
 XX  
 DT 23-OCT-2000 (first entry)  
 XX  
 DE cDNA encoding human serine protease BSSP6 (hbSSP6) SEQ ID NO:1.  
 XX  
 KW BSSP6; serine protease; human; hbSSP6; mouse; mbSSP6; brain;  
 KW diagnostic marker; antibody; transgenic animal; Alzheimer's disease;  
 KW epilepsy; cancer; inflammation; infertility; pancreatitis;  
 KW prostatic hypertrophy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200031257-A1.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 19-NOV-1999; 99WO-JP06476.  
 XX  
 PR 20-NOV-1998; 98JP-0347802.  
 XX  
 PA (FUSO ) FUSO PHARM IND LTD.  
 XX  
 PI Uemura H, Okui A, Komimami K, Yamaguchi N, Mitsui S;  
 XX  
 DR WPI: 2000-40067/34.  
 DR P-PSDB; AAB11712.  
 XX  
 PT Serine protease BSSP6, useful in detecting homologs, mutants and  
 PT polymorphic variants as markers for diagnosis of Alzheimer's disease,  
 PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,  
 PT using blood or other tissues  
 XX  
 PS Claim 2; Page 67-69; 94pp; Japanese.  
 XX  
 CC The invention relates to novel serine proteases designated BSSP6  
 CC (AAB11712-B11714), and to nucleic acids encoding them (AAA61763-61765).  
 CC The invention also relates to vectors and transformants comprising BSSP6  
 CC nucleic acids; transgenic animals in which the expression level of BSSP6  
 CC can be varied; and an mbSSP6 knockout mouse. The invention additionally  
 CC encompasses anti-BSSP6 antibodies and methods of production of such  
 CC antibodies, methods of BSSP6 detection using the antibodies, and the  
 CC use of BSSP6 proteins or fragments as diagnostic markers for certain  
 CC medical conditions. Nucleotides encoding BSSP6 were initially  
 CC isolated in a human brain cDNA library using degenerate PCR primers  
 CC (AAA61795-A61796) based on conserved regions of serine proteases. The  
 CC BSSP6 serine proteases and nucleotides encoding them are useful in  
 CC detecting homologues, mutants and polymorphic variants in biological  
 CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis  
 CC and spleen) as diagnostic markers for conditions such as Alzheimer's  
 CC disease, epilepsy, cancer, inflammation, infertility and prostatic  
 CC hypertrophy. Sequences AAA61763 and AAA61765 represent cDNAs encoding  
 CC human BSSP6 variants (hbSSP6), and sequence AAA61764 represents cDNA

CC encoding murine BSSP6 (mBSP6).  
 XX Sequence 1301 BP; 332 A; 387 C; 330 G; 252 T; 0 other;  
 SQ

Query Match 100.0%; Score 687; DB 21; Length 1301;  
 Best local Similarity 100.0%; Pred. No. 7.2e-137;  
 Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATCATCAAGGGGCTTCAGTGCACAGCCTCCTCAGCCCTGGCAGGAGCCCTGTTGAG	60
DB	272	ATCATCAAGGGGCTTCAGTGCACAGCCTCCTCAGCCCTGGCAGGAGCCCTGTTGAG	331
QY	61	AAGAGCGGGCTACTGTGGGGGAGCGCATGSCCCAGATGGCTCCTGAGAGAGCC	120
DB	332	AMAGCGGCTACTGTGGGGGAGCGCATGSCCCAGATGGCTCCTGAGAGAGCC	391
QY	121	CACTGCTCAAGCCCGCTACATAGTTCACTGGGGAGCACAACCTCCAGAGAGAG	180
DB	392	CACTGCTCAAGCCCGCTACATAGTTCACTGGGGAGCACAACCTCCAGAGAGAG	451
QY	181	GGCTGTAGACAGACCCGAGAGGCACTGAGTCTTCCCAACCCGCGCTTCAACAAGC	240
DB	452	GGCTGTAGACAGACCCGAGAGGCACTGAGTCTTCCCAACCCGCGCTTCAACAAGC	511
QY	241	CTCCCAACAAGAGACCGCAATGACATCATGCTGTGAAGATGGCATGCCAGTCTCC	300
DB	512	CTCCCAACAAGAGACCGCAATGACATCATGCTGTGAAGATGGCATGCCAGTCTCC	571
QY	301	ATCACCTGGGCTGTGGAGACCCCTCACCTCTCTCAGGCTGTGCTCACTGGTGGACAGC	360
DB	572	ATCACCTGGGCTGTGGAGACCCCTCACCTCTCTCAGGCTGTGCTCACTGGTGGACAGC	631
QY	361	TGCTCATTTCCGGCTGGGGGAGCAGCTCAGGCCCAAGTTAGCCTGCTCAGACCTTG	420
DB	632	TGCTCATTTCCGGCTGGGGGAGCAGCTCAGGCCCAAGTTAGCCTGCTCAGACCTTG	691
QY	421	CGATGGGCAACATCAACATCAATGAGCAGCAAGTGAAGAAGCCCTAACCCGGCAAC	480
DB	692	CGATGGGCAACATCAACATCAATGAGCAGCAAGTGAAGAAGCCCTAACCCGGCAAC	751
QY	481	ATCACAGACACCATGCTGTGTGCCAGCGTGCAGAGAGGGGCAAGGACTCTGCCAGGCT	540
DB	752	ATCACAGACACCATGCTGTGTGCCAGCGTGCAGAGAGGGGCAAGGACTCTGCCAGGCT	811
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DB	932	TGATCCAGAGAGAGTGAAGAACAAT	958

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 11:00:23 ; Search time 3358.63 Seconds

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Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	687	100.0	1106	6	BD137019
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4	687	100.0	1158	6	BD137020
5	687	100.0	1181	9	AB013730
6	687	100.0	1186	9	AB012917
7	687	100.0	1192	6	AR152174
8	687	100.0	1204	6	AX358932
9	687	100.0	1204	6	AX362425
10	687	100.0	1204	6	AX454622
11	687	100.0	1204	6	AX464372
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16	687	100.0	1301	6	AB041036
17	687	100.0	1314	6	AR098430
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19	685.2	99.7	1166	6	AR152173
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21	660	96.1	1052	6	AR219287
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23	654.2	95.2	833	6	BD082136
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25	600.4	87.4	930	9	AB078780
26	514.2	74.8	1213	10	AB016226
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29	464.6	67.6	618	6	AR263825
30	462.2	67.3	1164	6	AX661915
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38	267.2	38.9	230000	9	AF243527
39	264	38.4	178504	2	AC140096
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41	262.4	38.2	472	6	AR263958
42	252.8	36.8	176647	2	AC130188
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DEFINITION	Sequence 1 from Patent WO949055.				
ACCESSION	AX016287				
VERSION	AX016287.1 GI:10041854				
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
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	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1	Bruck C.E., Coche T., Cassart J.P. and Vinals-Bassols C.			
AUTHORS		Human casb12 polypeptide, a serine protease			
TITLE		Patent: WO 9949055-A I 30-SEP-1999;			
JOURNAL					

Pred. No. is the number of results predicted by chance to have a



BRUCK CLAUDINE ELVIRE MARIE (BE); SMITHKLINE BEECHAM BIOLOG (BE);  
COACHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTA  
(BE)

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Db 833 TGGATCCAGAGACGATGAAGAACAAT 859

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Bruck,C.E., Coche,T., Cassart,J.P. and Vinals-Bassols,C.
TITLE Human casb12 polypeptide, a serine protease
JOURNAL Patent: WO 9949055-A 3 30-SEP-1999;
BRUCK CLAUDELINE ELVIRE MARIE (BE); SMITHKLINE BEECHAM BIOLOG (BE);
COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTA
(BE)
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BASE COUNT 274 a 359 c 306 g 219 t
ORIGIN

Query Match 100.0%; Score 687; DB 6; Length 1158;
Best Local Similarity 100.0%; Pred. No. 2,1e-139;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATCATCAAGGGGTTTGAGTGTGCAAGCCTCACTCCAGCCCTGGCAAGCCTGTTCAG 60
Db 243 ATCATCAAGGGGTTTGAGTGTGCAAGCCTCACTCCAGCCCTGGCAAGCCTGTTCAG 302
Oy 61 AAGAGCGGGCTACTGTGTGGGGCGAGCTCATGCCGCCAGATGGCTCTCTGACAGACCC 120
Db 303 AAGAGCGGGCTACTGTGTGGGGCGAGCTCATGCCGCCAGATGGCTCTCTGACAGACCC 362
Oy 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGAGCAACACCTCCAGAAAGAGAG 180
Db 363 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGAGCAACACCTCCAGAAAGAGAG 422
Oy 181 GCGTGTGAGCAGACCCGAGACCACTGAGTCTTCCCCACCCGGCTTCAACAACAGC 240
Db 423 GCGTGTGAGCAGACCCGAGACCACTGAGTCTTCCCCACCCGGCTTCAACAACAGC 482
Oy 241 CTCCCAACAAGACACCGCAATGATCATGCGGTGGGAAGATGGCATCGCAAGTCTCC 300
Db 483 CTCCCAACAAGACACCGCAATGATCATGCGGTGGGAAGATGGCATCGCAAGTCTCC 542
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Db 543 ATCACTGTGGCTGTGCGACCCCTCAACCTCTCTACAGCTGTGTACAGTGTGACACAGC 602
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Oy 421 CGATGCGCAACATCAACCATCATTTGAGACAGAAAGTGTGAAGAGCTTACCCGGGAGC 480
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Oy 661 TGGATCCAGAGACGATGAAGAACAAT 687
Db 903 TGGATCCAGAGACGATGAAGAACAAT 929

RESULT 4
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LOCUS Human CASB 12 polypeptide, a serine protease.
DEFINITION BD137020
ACCESSION BD137020.1 GI:23231965
VERSION BD137020.1 GI:23231965
KEYWORDS JP 2002507425-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1158)
AUTHORS Bruck,C.E.M., Cassart,J.P., Coche,T. and Bassols,C.V.
TITLE Human CASB 12 polypeptide, a serine protease
JOURNAL Patent: JP 2002507425-A 2 12-MAR-2002;
SMITHKLINE BEECHAM BIOLOGICALS SA
COMMENT OS Homo sapiens (human)
PN JP 2002507425-A/2
PD 12-MAR-2002
PF 17-MAR-1999 JP 2000538015
PR 20-MAR-1998 GB 9806095.7
PI CLAUDELINE ELVIRE MARIE BRUCK,JEAN POL CASSART,THIERRY COCHE, PI
CARLOTA VINALS BASSOLS
PC C12N15/09,A61K31/70,A61K38/00,A61P35/00,A61P37/02,C07K16/40,
PC C12N1/15,
PC C12N1/19,C12N1/21,C12N5/10,C12N9/64,C12P21/02,C12Q1/02,C12Q1/
PC 68,G01N33/15,
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ORIGIN

Query Match 100.0%; Score 687; DB 6; Length 1158;
Best Local Similarity 100.0%; Pred. No. 2,1e-139;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATCATCAAGGGGTTTGAGTGTGCAAGCCTCACTCCAGCCCTGGCAAGCCTGTTCAG 60
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Oy 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGAGCAACAACCTTCCAGAGAGAG 180
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 AB013730  
 ACCESSION  
 AB013730.1 GI:6681453  
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 Hippostasin.  
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 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Eumetazoa; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 1 (sites)  
 Mitsuhashi, S., Yamada, T., Okui, A., Komihama, K., Nemura, H. and  
 Yamaguchi, N.  
 A novel isoform of a kallikrein-like protease, TLSP/Hippostasin,  
 (PRSS20), is expressed in the human brain and prostate  
 Biochem. Biophys. Res. Commun. 272 (1), 205-211 (2000)  
 JOURNAL MEDLINE  
 PUBMED  
 10872828  
 2 (bases 1 to 1181)  
 Yamaguchi, N. and Mitsuhashi, S.  
 Direct Submission  
 Submitted (08-MAY-1998) Nozomi Yamaguchi, Kyoto Prefectural  
 University of Medicine, Res. Ins. Geriatrics; Kawarimachi Hiroko1,  
 Kyoto, Kyoto 602-8566, Japan (E-mail: nozomi@koto.kpu-m.ac.jp,  
 Tel:81-75-251-5848, Fax:81-75-251-5848)  
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 ACCESSION  
 AB012917.1 GI:3649790  
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 TLSP, serine protease (TLSP).  
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polya\_site

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ORIGIN

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100.0%; Score 687; DB 9; Length 1181;

Best Local Similarity 100.0%; Pred. No. 2e-139;

Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
 AUTHORS Yoshida,S., Taniguchi,M., Suemoto,T., Oka,T., He,X. and Shiozaka,S.  
 TITLE cDNA cloning and expression of a novel serine protease, TLSP  
 JOURNAL Biochim. Biophys. Acta 1399 (2-3), 225-228 (1998)  
 MEDLINE 98438738  
 PUBMED 9765601

REFERENCE  
 AUTHORS Yoshida,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-APR-1998) Shigetaka Yoshida, Department of Anatomy 1, Asahikawa Medical College, Midorigaoka Higashi 2-1-1, Asahikawa, Hokkaido 078-8510, Japan (E-mail: syoshida@asahikawa-med.ac.jp, Tel:81-166-68-2300, Fax:81-166-68-2309)

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 ACCESSION AR152174  
 VERSION AR152174.1 GI:15118224  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE  
 1 (bases 1 to 1192)  
 Cohen,M., Colpitts,T.L., Friedman,P.N., Granados,E., Klass,M.R.,  
 Russell,J.C., Stewart,K.D. and Stroupe,S.D.  
 Serine protease reagents and methods useful for detecting and  
 treating diseases of the prostate  
 Patent: US 6232456-A 8 15-MAY-2001;  
 Location/Qualifiers  
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BASE COUNT 279 a 385 c 290 g 238 t  
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ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent: WO 0193983-A 185 13-DEC-2001;		
JOURNAL	Genentech Inc. (US)		
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REFERENCE			
AUTHORS	1 Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,		
	Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,		
	Watanabe,C.K. and Wood,W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding		
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JOURNAL	Patent: WO 0208288-A 185 31-JAN-2002;		
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ACCESSION AX454622.1 GI:21713935  
KEYWORDS  
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REFERENCE  
AUTHORS 1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,  
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.  
and Ye,W.  
TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
JOURNAL Patent: WO 0208284-A 207 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)

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QY 361 TGCCTCATTTCCGGCTGGGGGACAGCATGTCACCCCAATTCAGCTGCTCAACCTTG 420  
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Db 649 ATACAGACACCATGCTGTGTGACAGCGTGCAGAGAGGGGGCAAGGACTCTGCCAGGCT 708  
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Db 709 GACTCCGGGGGCGCTCTGTGTGTAAACGATCTCTTCAAGGCAATATCTCTGGGGCCAG 768  
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| | | | |  
Db 769 GATCCGTGTGCGATACCCGGAAGCCTGTGTCTACAGAAAGTGTGCAATATATGTGAC 828  
QY 661 TGGATCCAGAGACGATGAAGAACAT 687  
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Db 829 TGGATCCAGAGACGATGAAGAACAT 855

RESULT 11  
AX464372 1204 bp DNA linear PAT 16-JUL-2002  
LOCUS Sequence 505 from Patent WO0140466.  
DEFINITION AX464372  
ACCESSION AX464372.1 GI:21899202  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
REFERENCE  
AUTHORS 1 Baker,K.P., Beresini,M., DeForge,L., Desnoyers,L., Filvaroff,E.,  
Gao,W.O., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,  
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,  
Wood,W.L. and Zhang,Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
same  
JOURNAL Patent: WO 0140466-A 505 07-JUN-2001;  
Genentech Inc. (US)  
FEATURES  
source 1. 1204  
Location/Qualifiers



/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 306 a 364 c 294 g 240 t

ORIGIN

Query Match 100.0%; Score 687; DB 6; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 2e-139;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTGAGTGCAGAGCTCAGCTCCAGCCCTGGAGGAGGAGCCCTGTTCAG 60  
DB 169 ATCATCAAGGGGTTGAGTGCAGAGCTCAGCTCCAGCCCTGGAGGAGGAGCCCTGTTCAG 228

QY 61 AAGAGGGGCTACTCTGTGGGGCGAGCTCATATGCCCCAGATGGCTCTGACAGAGCC 120  
DB 229 AAGAGGGGCTACTCTGTGGGGCGAGCTCATATGCCCCAGATGGCTCTGACAGAGCC 288

QY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGAGGAGCAACCTCCAGAAAGAGAG 180  
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QY 181 GCGTGTAGAGAGAGCCCGAGAGCCATGAGTCTCTCCAGCCCGGCTTCAACAGAGC 240  
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QY 241 CTCGCCCAAAAGACACCCGCAATGACATCATGCTGTGAAGATGGCATGCCAGTCTCC 300  
DB 409 CTCGCCCAAAAGACACCCGCAATGACATCATGCTGTGAAGATGGCATGCCAGTCTCC 468

QY 301 ATCACTGGGGCTGTGGAGCCCTCAGCTCTCCAGAGTGTGACGTGGGAGCAGC 360  
DB 469 ATCACTGGGGCTGTGGAGCCCTCAGCTCTCCAGAGTGTGACGTGGGAGCAGC 528

QY 361 TGCCTCATTTCCGGCTGGGGAGAGCAGCTCCAGCCCAAGTACCTCTCAGACCTTG 420  
DB 529 TGCCTCATTTCCGGCTGGGGAGAGCAGCTCCAGCCCAAGTACCTCTCAGACCTTG 588

QY 421 CGATGGCCCAACATCACCATCATTTGAGCAGCAGAAAGTGTGAAGAGCCCTTACCCGGCAAC 480  
DB 589 CGATGGCCCAACATCACCATCATTTGAGCAGCAGAAAGTGTGAAGAGCCCTTACCCGGCAAC 648

QY 481 ATCAGACAGACCATGATGTGTGCCAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGT 540  
DB 649 ATCAGACAGACCATGATGTGTGCCAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGT 708

QY 541 GACTCCGGGGCCCTCTGTGTCTGTACAGCTCTTCAAGGCAATATCTCTGGGGCAG 600  
DB 709 GACTCCGGGGCCCTCTGTGTCTGTACAGCTCTTCAAGGCAATATCTCTGGGGCAG 768

QY 601 GATCCGTGTGCGATCAGCCGAAAGCCTGTGTCTACAGAAAGTCTGCAAAATATGTGGAC 660  
DB 769 GATCCGTGTGCGATCAGCCGAAAGCCTGTGTCTACAGAAAGTCTGCAAAATATGTGGAC 828

QY 661 TGGATCCAGGAGAGCATGAAGAACAAT 687  
DB 829 TGGATCCAGGAGAGCATGAAGAACAAT 855

RESULT 12  
AX491100 1204 bp DNA linear PAT 16-AUG-2002  
LOCUS  
DEFINITION Sequence 207 from Patent WO0200690.  
ACCESSION AX491100  
VERSION AX491100.1 GI:22323887  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 Baker, K. P., Ferrara, N., Gerber, H., Gerltzen, M. E., Goddard, A.,  
Godowski, P. J., Gurney, A. L., Hillan, K. J., Marsters, S. A., Pan, J.,

Paoni, N. F., Stephan, J. P., Watanabe, C. K., Williams, P. M., Wood, W. I.  
and Ye, W.  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
Patent: WO 0200690-A 207 03-JAN-2002;  
Genentech, Inc. (US)  
Location/Qualifiers  
1..1204  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 306 a 364 c 294 g 240 t

ORIGIN

Query Match 100.0%; Score 687; DB 6; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 2e-139;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCATCAAGGGGTTGAGTGCAGAGCTCAGCTCCAGCCCTGGAGGAGGAGCCCTGTTCAG 60  
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QY 61 AAGAGGGGCTACTCTGTGGGGCGAGCTCATATGCCCCAGATGGCTCTGACAGAGCC 120  
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QY 181 GCGTGTAGAGAGAGCCCGAGAGCCATGAGTCTCTCCAGCCCGGCTTCAACAGAGC 240  
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QY 241 CTCGCCCAAAAGACACCCGCAATGACATCATGCTGTGAAGATGGCATGCCAGTCTCC 300  
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QY 301 ATCACTGGGGCTGTGGAGCCCTCAGCTCTCCAGAGTGTGACGTGGGAGCAGC 360  
DB 469 ATCACTGGGGCTGTGGAGCCCTCAGCTCTCCAGAGTGTGACGTGGGAGCAGC 528

QY 361 TGCCTCATTTCCGGCTGGGGAGAGCAGCTCCAGCCCAAGTACCTCTCAGACCTTG 420  
DB 529 TGCCTCATTTCCGGCTGGGGAGAGCAGCTCCAGCCCAAGTACCTCTCAGACCTTG 588

QY 421 CGATGGCCCAACATCACCATCATTTGAGCAGCAGAAAGTGTGAAGAGCCCTTACCCGGCAAC 480  
DB 589 CGATGGCCCAACATCACCATCATTTGAGCAGCAGAAAGTGTGAAGAGCCCTTACCCGGCAAC 648

QY 481 ATCAGACAGACCATGATGTGTGCCAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGT 540  
DB 649 ATCAGACAGACCATGATGTGTGCCAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGT 708

QY 541 GACTCCGGGGCCCTCTGTGTCTGTACAGCTCTTCAAGGCAATATCTCTGGGGCAG 600  
DB 709 GACTCCGGGGCCCTCTGTGTCTGTACAGCTCTTCAAGGCAATATCTCTGGGGCAG 768

QY 601 GATCCGTGTGCGATCAGCCGAAAGCCTGTGTCTACAGAAAGTCTGCAAAATATGTGGAC 660  
DB 769 GATCCGTGTGCGATCAGCCGAAAGCCTGTGTCTACAGAAAGTCTGCAAAATATGTGGAC 828

QY 661 TGGATCCAGGAGAGCATGAAGAACAAT 687  
DB 829 TGGATCCAGGAGAGCATGAAGAACAAT 855

RESULT 13  
AX697101 1204 bp DNA linear PAT 02-APR-2003  
LOCUS  
DEFINITION Sequence 169 from Patent WO0078961.  
ACCESSION AX697101  
VERSION AX697101.1 GI:29498066



KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L., Eaton, D.L., Gao, W.Q., Pan, J., Botstein, D., Fong, S., Goddard, A., Godwin, P.J., Gueney, A.L., Smith, V., Tumas, D., Wood, W.I., Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A. and Watanabe, C.K. Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0078961-A 169 28-DEC-2000;

FEATURES Location/Qualifiers

source 1..1204

mol\_type="genomic DNA"

db\_xref="taxon:9606"

BASE COUNT 306 a 364 c 294 g 240 t

ORIGIN

Query Match 100.0%; Score 687; DB 6; Length 1204;

Best Local Similarity 100.0%; Pred. No. 2e-139;

Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATCATCAAGGGGTTCAGTGAAGCTCCTCACTCCAGCCCTGGCAGCAGCCCTGTTCCAG 60

169 ATCATCAAGGGGTTCAGTGAAGCTCCTCACTCCAGCCCTGGCAGCAGCCCTGTTCCAG 228

61 AAGACGGGCTACTCTGTGGGGGCGAGCTCATGCCCCAGATGGCTCTGACAGAGCC 120

229 AAGACGGGCTACTCTGTGGGGGCGAGCTCATGCCCCAGATGGCTCTGACAGAGCC 288

121 CACTGCTCAACGCCCGCTACATAGTTCACCTGGGGGACACACCTCCAGAGAGGAG 180

289 CACTGCTCAACGCCCGCTACATAGTTCACCTGGGGGACACACCTCCAGAGAGGAG 348

181 GCGCTGAGCAGACCCGCGACAGCCAGTCTCTCCCGCCCGCTTCAACAACAGC 240

349 GCGCTGAGCAGACCCGCGACAGCCAGTCTCTCCCGCCCGCTTCAACAACAGC 408

241 CTCCTCCCAACAGACCCGCGACAGCCAGTCTCTCCCGCCCGCTTCAACAACAGC 300

409 CTCCTCCCAACAGACCCGCGACAGCCAGTCTCTCCCGCCCGCTTCAACAACAGC 468

301 ATCACTGGGGCTGTGCGAGACCCCTCACTCTCTCACTGTGTCACTGCTGGACAGC 360

469 ATCACTGGGGCTGTGCGAGACCCCTCACTCTCTCACTGTGTCACTGCTGGACAGC 528

361 TGCCTCATTTCCGGCTGGGGGACAGCTCCAGCCCGCCAGTTACGCTGCTCAGACCTTG 420

529 TGCCTCATTTCCGGCTGGGGGACAGCTCCAGCCCGCCAGTTACGCTGCTCAGACCTTG 588

421 CGATCGGCCAATCATCATCATGTGAGCAGCCAGAAAGTGTGAGAGAGCCCTACCCGGCAGC 480

589 CGATCGGCCAATCATCATCATGTGAGCAGCCAGAAAGTGTGAGAGAGCCCTACCCGGCAGC 648

481 ATCAAGAGACACCATGTTGTGCCAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

649 ATCAAGAGACACCATGTTGTGCCAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 708

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709 GACTCGGGGGGCTCTGTGTGTAAACAGTCTCTTCAAGGATTAATCTCTGGGGCCAG 768

601 GATCGGTGTGATCAACCCGAAAGCTGTGTACAGAGAAAGTCTGCAATATGTGAGC 660

769 GATCGGTGTGATCAACCCGAAAGCTGTGTGTACAGAGAAAGTCTGCAATATGTGAGC 828

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829 TGGATCCAG 855

RESULT 14

BC022068

LOCUS BC022068

DEFINITION Homo sapiens, kallikrein 11, clone MGC:33060 IMAGE:4824387, mRNA.

ACCESSION BC022068

VERSION BC022068.1 GI:18314497

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1213)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (22-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

COMMENT Contact: MGC help desk

Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

Contact: [amadan@systemsbiology.org](mailto:amadan@systemsbiology.org)

Anup Madan, Jessica Fahy, Erin Helton, Mark Keltman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLIN at: <http://image.lnl.gov>

Series: IRAP Plate: 46 Row: m Column: 6

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5803198.

Location/Qualifiers

1..1213

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mol\_type="mRNA"

db\_xref="LocusID:11012"

db\_xref="taxon:9606"

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BASE COUNT 290 a 376 c 296 g 251 t

ORIGIN

Query Match 100.0%; Score 687; DB 9; Length 1213;

Best Local Similarity 100.0%; Pred. No. 2e-139;

Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATCATCAAGGGGTTCAGTGAAGCTCCTCACTCCAGCCCTGGCAGCAGCCCTGTTCCAG 60

196 ATCATCAAGGGGTTCAGTGAAGCTCCTCACTCCAGCCCTGGCAGCAGCCCTGTTCCAG 255

61 AAGACGGGCTACTCTGTGGGGGCGAGCTCATGCCCCAGATGGCTCTGACAGAGCC 120

Db 256 AAGAGGGGCTACTCTGTGGGGGCGACGCTCATCGCCGCCAGATGGCTCTGACAGCAGCC 315  
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QY 181 GGCCTGTAGAGAGAGCCCGGAGAGCCAGTGAAGTCTTCCCGGAGAGAGAGAGAGAGC 240  
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QY 241 CTCGCCAACAAGAGAGCCCGGAGAGCCAGTGAAGTCTTCCCGGAGAGAGAGAGAGAGC 300  
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QY 661 TGGATCCAGAGAGAGATGAAGAACAAT 687  
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RESULT 15  
BD091587 1301 bp DNA linear PAT 27-AUG-2002  
LOCUS Novel serine protease BSSP6.  
DEFINITION BD091587  
ACCESSION BD091587.1 GI:22637198  
VERSION WO 0031257-A/1.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1301)  
AUTHORS Uemura,H., Okui,A., Kominami,K., Yamaguchi,N. and Mitsui,S.  
TITLE Novel serine protease BSSP6  
JOURNAL Patent: WO 0031257-A 1 02-JUN-2000;  
FUSO PHARMACEUTICAL INDUSTRIES LTD, HIDEOTOSHI UEMURA, AKIRA OKUI,  
KATSUYA KOMINAMI, NOZOMI YAMAGUCHI, SHINICHI MITSUI  
COMMENT OS Homo sapiens (human)  
PN WO 0031257-A/1  
PD 02-JUN-2000  
PF 19-NOV-1999 WO 1999JP006476  
PR 20-NOV-1998 JP 98P 347802  
PI HIDEOTOSHI UEMURA, AKIRA OKUI, KATSUYA KOMINAMI, NOZOMI YAMAGUCHI,  
SHINICHI MITSUI  
PC C12N15/12, C12N9/64, C12N5/06, C12N1/21, C07K16/40, C12P21/08, PC  
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FH Key Location/Qualifiers.

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Best Local Similarity 100.0%; Pred. No. 2e-139;  
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 332 AAGAGGGGCTACTCTGTGGGGGAGAGCTATCGCCCGGAGAGAGAGAGAGAGAGAGC 391  
QY 121 CACTGCTCAAGCCCGCTACATAGTTCCACTGGGGGAGAGAGAGAGAGAGAGAGAGAG 180  
Db 392 CACTGCTCAAGCCCGCTACATAGTTCCACTGGGGGAGAGAGAGAGAGAGAGAGAGAG 451  
QY 181 GGCCTGTAGAGAGAGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 240  
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QY 241 CTCGCCAACAAGAGAGCCCGGAGAGCCAGATGATGCTGTGTGAAGAGAGAGAGAGAGC 300  
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QY 301 ATCACTGGGGCTGTGGAGACCCCTCACCCTCTCTCAAGCTGTGTGTGTGTGTGTGTGT 360  
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QY 361 TGCCTCATTTCCGGCTGTGGGGGAGAGAGTCCAGAGCCCGGAGAGAGAGAGAGAGAGC 420  
Db 632 TGCCTCATTTCCGGCTGTGGGGGAGAGAGTCCAGAGCCCGGAGAGAGAGAGAGAGAGC 691  
QY 421 CGATGCCCAACATCAGATCATATGAGCAGACAGAAAGTGTGAAGAGAGAGAGAGAGC 480  
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Job time : 3361.13 secs

GenCore version 5.1.6  
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(without alignments)  
2468.773 Million cell updates/sec

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Delop 6.0 , Delext 7.0

Searched: 600653 seqs, 161128416 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

1	1258	98.7	250	11	US-09-946-374-170	Sequence 170, App
2	1258	98.7	250	12	US-10-015-387A-170	Sequence 170, App
3	1258	98.7	250	12	US-10-137-870-506	Sequence 506, App
4	1258	98.7	250	12	US-10-140-018-506	Sequence 506, App
5	1258	98.7	250	12	US-10-140-021-506	Sequence 506, App
6	1258	98.7	250	12	US-10-140-274-506	Sequence 506, App
7	1258	98.7	250	12	US-10-140-471-506	Sequence 506, App
8	1258	98.7	250	12	US-10-140-807-506	Sequence 506, App
9	1258	98.7	250	12	US-10-140-922-506	Sequence 506, App
10	1258	98.7	250	12	US-10-140-924-506	Sequence 506, App
11	1258	98.7	250	12	US-10-140-926-506	Sequence 506, App
12	1258	98.7	250	12	US-10-141-688-506	Sequence 506, App
13	1258	98.7	250	12	US-10-141-702-506	Sequence 506, App
14	1258	98.7	250	12	US-10-141-704-506	Sequence 506, App
15	1258	98.7	250	12	US-10-142-421-506	Sequence 506, App
16	1258	98.7	250	12	US-10-142-432-506	Sequence 506, App
17	1258	98.7	250	12	US-10-142-467-506	Sequence 506, App
18	1258	98.7	250	12	US-10-143-033-506	Sequence 506, App
19	1258	98.7	250	12	US-10-144-994-506	Sequence 506, App
20	1258	98.7	250	12	US-10-144-628-506	Sequence 506, App
21	1258	98.7	250	12	US-10-145-631-506	Sequence 506, App
22	1258	98.7	250	12	US-10-145-633-506	Sequence 506, App
23	1258	98.7	250	12	US-10-145-746-506	Sequence 506, App
24	1258	98.7	250	12	US-10-145-748-506	Sequence 506, App
25	1258	98.7	250	12	US-10-145-823-506	Sequence 506, App
26	1258	98.7	250	12	US-10-145-826-506	Sequence 506, App
27	1258	98.7	250	12	US-10-145-870-506	Sequence 506, App
28	1258	98.7	250	12	US-10-145-876-506	Sequence 506, App
29	1258	98.7	250	12	US-10-145-959-506	Sequence 506, App
30	1258	98.7	250	12	US-10-146-724-506	Sequence 506, App
31	1258	98.7	250	12	US-10-146-725-506	Sequence 506, App
32	1258	98.7	250	12	US-10-146-795-506	Sequence 506, App
33	1258	98.7	250	12	US-10-147-495-506	Sequence 506, App
34	1258	98.7	250	12	US-10-147-511-506	Sequence 506, App
35	1258	98.7	250	12	US-10-147-504-506	Sequence 506, App
36	1258	98.7	250	12	US-10-147-506-506	Sequence 506, App
37	1258	98.7	250	12	US-10-147-509-506	Sequence 506, App
38	1258	98.7	250	12	US-10-147-510-506	Sequence 506, App
39	1258	98.7	250	12	US-10-147-511-506	Sequence 506, App
40	1258	98.7	250	12	US-10-147-529-506	Sequence 506, App
41	1258	98.7	250	12	US-10-153-397-506	Sequence 506, App
42	1258	98.7	250	12	US-10-153-586-506	Sequence 506, App
43	1258	98.7	250	12	US-10-158-783-506	Sequence 506, App
44	1258	98.7	250	12	US-10-158-786-506	Sequence 506, App
45	1258	98.7	250	12	US-10-006-130A-170	Sequence 170, App

## ALIGNMENTS

RESULT 1  
US-09-946-374-170  
; Sequence 170, Application US/09946374  
; Publication No. US20030073129A1  
GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fond, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C1  
CURRENT APPLICATION NUMBER: US/09/946,374  
PRIOR FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
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PRIOR APPLICATION NUMBER: 60/099536  
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PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
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PRIOR APPLICATION NUMBER: 60/099763  
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PRIOR APPLICATION NUMBER: 60/099808  
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PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
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PRIOR FILING DATE: 1998-09-10  
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PRIOR FILING DATE: 1998-09-15  
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PRIOR FILING DATE: 1998-09-15  
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PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627  
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PRIOR APPLICATION NUMBER: 60/100684  
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PRIOR APPLICATION NUMBER: 60/100710  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100711  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18

PRIOR APPLICATION NUMBER: 60/100849  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
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PRIOR FILING DATE: 1998-09-17  
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PRIOR FILING DATE: 1998-09-24  
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PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102207  
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PRIOR APPLICATION NUMBER: 60/102330  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102487  
PRIOR FILING DATE: 1998-09-30  
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PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102571  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102684  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102687  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102965  
PRIOR FILING DATE: 1998-10-02  
PRIOR APPLICATION NUMBER: 60/103258  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103314  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103315  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103328  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103395  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103396

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; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
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; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

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## Alignment Scores:

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Pred. No.: 6,09e-87 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 11 Gaps: 0

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US-09-856-320a-1\_copy\_272\_958 (1-687) x US-09-946-374-170 (1-250)

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QY 1 ATCATCAAGGGGTGAGTGCAGCAAGCCTCACTCCCAAGCCTGGAGGAGCAGCCTGTTCGAG 60
DB 22 IIEIIEIYSGIYPHEGLUCYSIYLAATHTLEUIIEAIAIROAGTGTPTLEUHTHRAIAIA 41
QY 61 AAGAGCGGGCTACTGTGTGGGGGAGCGGTCATCGCCCGGAGATGGCTCTGTGACAGAGCC 120
DB 42 LYSTHTARGLEUCISGSIYLAATHTHTLEUIIEAIAIROAGTGTPTLEUHTHRAIAIA 61
QY 121 CACTGCTTCAGAGCCCGGTACATAGTTCACSTGTGGGAGACACAACTCCAGAGAGAG 180
DB 62 HISCYSLEULYSPROATGTGTTLIEVALHISLEUGIYGLINHISASINLEUGIYSGIUGIU 81
QY 181 GGCCTGTGAGACAGCCGGAGACAGCCACSTGAGTCTTCCCGGAGCCCGGGCTTCAACAAGAGC 240
DB 82 GLYCYSGLUGIHTHTARGTHRAIATHTHTGUSERPHERTONIAIROGLYRHEASINSNSER 101
QY 241 CTCGCCCAACAAAGACCCGCGATGATCATGCTGTGGTAAATGGCATGCCAGTCTGC 300
DB 102 ILEUPROASNIYASPHISATGASNSPRIEMELLEVALIYMETALISERPROVALISER 121
QY 301 ATCACTGGGGGTGTGGAGCCCTCAAGCCTTCCTGACGGTGTGTGACAGTGGAGCCAGC 360
DB 122 IIEHTHTPRALIAVALATRGPROLEUHTHTLEUSERSEHAGCYVALHTHRAIAIATHTHRSER 141
QY 361 TGCCTCATTTCCGGGTGGGGGAGACAGCTGCAGCCCGGAGTACAGCTGGCTGCAGACCTTG 420
DB 142 CYSLEUIIESERGIYTPROLYSERHTHTSERHTSERPROGLINLEUATRGLEUHTHROHISHRIE 161
QY 421 CGATGCGGCACATACCATCTATTGAGACAGCAAGAGTGTGAGAGAGCCTACCCGGGAGAGC 480

```

```

DB 162 ARGYSALIASNIIEHTHTLEIIEGLIHISGLINLYSCYSGIULASNAIAATYRPROGLIYASN 181
QY 481 ATCAAGACACACATGAGTGTGTGCAGCGTGCAGAGAGGGGGAGAGACTCTGCGAGGGT 540
DB 182 IIEHTHASPHTHMETALICYSALASERVALGIMGLIGIYGLIYUSASPERCYSGIUGIU 201
QY 541 GACTCGGGGGCCCTGTGTGTGTATACAGTCTTTCAGAGCATTAATCTCTGGGGCCAG 600
DB 202 ASPSERGIYGLYPROLEUVALCYASANGINSERLEUGIYGLIIELESERTPTGLIYGIN 221
QY 601 GATCCCTGTGCGATCAACCCGGAAGCCTGGTGTGTATACAGAAAGTCTGCAATATGTGAGC 660
DB 222 ASPPTCYSAIATIEHTHARGIYSPROGLIYVALTYHTHTLYVALCYSLYSTYRVALIASP 241
QY 661 TCGATCCAGAGACAGCATGAAGAACAT 687
DB 242 TPTLIEGLINGIHTHTMETIYSAASNA 250

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## RESULT 2

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US-10-015-387A-170
; Sequence 170, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:

```

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 170
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-387A-170

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## Alignment Scores:

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Pred. No.: 6,09e-87 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 12 Gaps: 0

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US-09-856-320a-1\_copy\_272\_958 (1-687) x US-10-015-387A-170 (1-250)

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QY 1 ATCATCAAGGGGTGAGTGCAGCAAGCCTCACTCCCAAGCCTGGAGGAGCAGCCTGTTCGAG 60
DB 22 IIEIIEIYSGIYPHEGLUCYSIYSPRONHISERGINPROTPTGLIAIAIAIATHTHRAIAIA 41
QY 61 AAGAGCGGGCTACTGTGTGGGGGAGACAGCTATCGCCCGGAGATGGCTCTGTGACAGAGCC 120
DB 42 LYSTHTARGLEUCISGSIYLAATHTHTLEUIIEAIAIROAGTGTPTLEUHTHRAIAIA 61
QY 121 CACTGCTTCAGAGCCCGGTACATAGTTCACSTGTGGGAGACACAACTCCAGAGAGAGAG 180
DB 62 HISCYSLEULYSPROATGTGTTLIEVALHISLEUGIYGLINHISASINLEUGIYSGIUGIU 81
QY 181 GGCCTGTGAGACAGCCGGAGACAGCCACSTGAGTCTTCCCGGAGCCCGGGCTTCAACAAGAGC 240

```



; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3330R1C158  
 ; CURRENT APPLICATION NUMBER: US/10/140,018  
 ; CURRENT FILING DATE: 2002-05-06  
 ; Prior Application removed - See Palm or File Wrapper  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 506  
 ; LENGTH: 250  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 ; US-10-140-018-506

## Alignment Scores:

Pred. No.:	6,09e-87	Length:	250
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.67%	Indels:	0
DB:	12	Gaps:	0

US-09-856-320a-1\_copy\_272\_958 (1-687) x US-10-140-018-506 (1-250)

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OY 1 ATCATCAGAGGGGTGGAGTGCAGAGCCTCCAGCCCTGGACAGAGCCCTGTTGAG 60
DB 22 ILEILEYSGLYPHEGLUCYSLSYSPROHISSEGINPOTRPGILALALALEUPHEGU 41
OY 61 AAGAGCGGGCTACTGTGTGGGGGAGAGCTCATGCCCCAGATGGCTCTGACAGAGCC 120
DB 42 LYSTHARGLEULEUCYSGLYALATHRLEUILEALPROARGTRPLEUETHRALALA 61
OY 121 CACTGCTCAGAGCCCCGCTACATAGTTCACCTGGGGGAGACAACTCCAGAGAGAG 180
DB 62 HISCYSLEULYSPTARGTRTYRILEVALHISLEUGLYGINHISASNLEUINLSGLUGU 81
OY 181 GGCTGTGAGCAGACCCGGAGACGCACTGAGTCTTCCCGCCGCTTCAACAAGAGC 240
DB 82 GLYCSGLUGINTHARGTHRLEUHRGUSERPHEPROHISPROGLYPHEASNANSER 101
OY 241 CTCGCCAACAAGACCCAGCAGATGATCATGTGTGAGAGATGGCATGCCAGCTTCC 300
DB 102 LEUPROASNLYSASPHISARGASNAPRIEMELLEVALLYSMETALASERPROVALSER 121
OY 301 ATCAGCTGGGTGGTGGAGCCCTCAGCCTCTCTACAGCTGTGTACGTGGACAGCAG 360
DB 122 ILEHTRTPALAVALARGPPOLEUHRLEUSERSERARGCYSAITHRALAGLYTHSER 141
OY 361 TGCCATATTTCCGGCTGGGGGAGCAGCTGACAGCCCGGATTAGGCTGGCTCAGACCTTG 420
DB 142 CYSLEUILESERGLYTRIGLYSERTHRSESRPROGLINLEUARGLEUPROHISTHREU 161
OY 421 CGATGCGCAACATCAGCATATGAGACAGCAAGAGTGTGAGACAGCTACCCCGGCAAC 480
DB 162 ARGYSALASASNIIEFTHRIEILEGINHISGLINLYSCYSLUASNALATYRPROGLYSN 181
OY 481 ATCAAGACACCATGTGTGTGCCAGCTGCGAGGAAGGGGGAGAGAGATCTCCGCAAGGT 540
DB 102 ILEHTRAPTHMEVALCYSALESERVALGINGLUGLYLYSASPSECTCYSGINGLY 201
OY 541 GACTCGGGGGCCCTGCTGTGTAAACAGTCTTCAAGGATATATCTCCGGGGGCGAG 600
DB 202 ASPSERGLYGLYPROLEUVALCYASNINLSERLEUGINGLYILEIESERTIPOLYGIN 221
OY 601 GATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACAGCAAGTGTGCAATATGTGGAGC 660
DB 222 ASPPROCYSALEIIEFTHARGLYSPROGLYVALTYRTHLYSVALCYLYSTYVALASP 241
OY 661 TGGATCCGAGAGAGATGAAGAACAAT 687
  
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DB 242 TRPILGLINLUTHRMELYSASN 250

## RESULT 5

US-10-140-021-506  
 ; Sequence 506 Application US/10140021  
 ; Publication No. US20030138886A1  
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: Deforge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerlitsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3330R1C167  
 ; CURRENT APPLICATION NUMBER: US/10/140,021  
 ; CURRENT FILING DATE: 2002-05-06  
 ; Prior Application removed - See Palm or File Wrapper

; SEQ ID NO 506  
 ; LENGTH: 250  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 ; US-10-140-021-506

US-09-856-320a-1\_copy\_272\_958 (1-687) x US-10-140-021-506 (1-250)

## Alignment Scores:

Pred. No.:	6,09e-87	Length:	250
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.67%	Indels:	0
DB:	12	Gaps:	0

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OY 1 ATCATCAGAGGGGTGGAGTGCAGAGCCTCCAGCCCTGGACAGAGCCCTGTTGAG 60
DB 22 ILEILEYSGLYPHEGLUCYSLSYSPROHISSEGINPOTRPGILALALALEUPHEGU 41
OY 61 AAGAGCGGGCTACTGTGTGGGGGAGAGCTCATGCCCCAGATGGCTCTGACAGAGCC 120
DB 42 LYSTHARGLEULEUCYSGLYALATHRLEUILEALPROARGTRPLEUETHRALALA 61
OY 121 CACTGCTCAGAGCCCCGCTACATAGTTCACCTGGGGGAGACAACTCCAGAGAGAG 180
DB 62 HISCYSLEULYSPTARGTRTYRILEVALHISLEUGLYGINHISASNLEUINLSGLUGU 81
OY 181 GGCTGTGAGCAGACCCGGAGACGCACTGAGTCTTCCCGCCGCTTCAACAAGAGC 240
DB 82 GLYCSGLUGINTHARGTHRLEUHRGUSERPHEPROHISPROGLYPHEASNANSER 101
OY 121 CACTGCTCAGAGCCCCGCTACATAGTTCACCTGGGGGAGACAACTCCAGAGAGAG 180
DB 62 HISCYSLEULYSPTARGTRTYRILEVALHISLEUGLYGINHISASNLEUINLSGLUGU 81
OY 181 GGCTGTGAGCAGACCCGGAGACGCACTGAGTCTTCCCGCCGCTTCAACAAGAGC 240
DB 82 GLYCSGLUGINTHARGTHRLEUHRGUSERPHEPROHISPROGLYPHEASNANSER 101
OY 241 CTCGCCAACAAGACCCAGCAGATGATCATGTGTGAGAGATGGCATGCCAGCTTCC 300
DB 102 LEUPROASNLYSASPHISARGASNAPRIEMELLEVALLYSMETALASERPROVALSER 121
OY 301 ATCAGCTGGGTGGTGGAGCCCTCAGCCTCTCTACAGCTGTGTACGTGGACAGCAG 360
DB 122 ILEHTRTPALAVALARGPPOLEUHRLEUSERSERARGCYSAITHRALAGLYTHSER 141
OY 361 TGCCATATTTCCGGCTGGGGGAGCAGCTGACAGCCCGGATTAGGCTGGCTCAGACCTTG 420
  
```





```

; TYPE: PRF
; ORGANISM: Homo Sapien
US-10-140-471-506

Alignment Scores:
Pred. No.: 6,09e-87 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-1_copy_272_958 (1-687) x US-10-140-471-506 (1-250)

QY 1 ATCATCAAGGGGTTCAGTGCAGAGCCCTCACTCCAGCCCTGGACAGACCCCTGTTGAG 60
DB 22 IlettllysGlyPheglucylsAllysProhlsSerGlnProtrpGlnAlaIalaIeuhbeglu 41
QY 61 AAGAGCGGCTACTCTGTGGGGGAGCGTCAATCGCCCGCCAGATGGCTCTGACAGACGCC 120
DB 42 LysThrArgLeuLeuCyseGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaIa 61
QY 121 CACTGCTCAAGCCCGGTACATGTTCACTGAGGGGACAGACACCTCCAGAGAGAG 180
DB 62 HiscysLeuLysProhArgTrpIleValHnIsleuGlyGlnHnIsaHnleuGlnLysGluGln 81
QY 181 GCGTGTGACAGACCCGGACAGACCCAGTCCCTTCCCGCCAGCCCGGCTTCAACAACAGC 240
DB 82 GlyCysGluGlnThrArgThrAlaThrGlnSerPheProhlsProGlyPheAsnAsnSer 101
QY 241 CTCCCAACAAAGACCCAGCCGAATGACATCATGCTGTGGAAGATGGCATCCGCACTGCC 300
DB 102 LeuProhAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121
QY 301 ATCACTGGGCTGTGCGAGACCCCTCACTCCCTGACCTGTGCTGACCTGGACAGAC 360
DB 122 IlettlrtrpAlaValAlaArgProleuThrLeuSerSerArgCysValThrAlaIeIyhrSer 141
QY 361 TGCTCATATTTCCGGCTGGGGGACAGACGTCACAGCCCGCCAGTTACGCTCGCTCAACACTTG 420
DB 142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProhIsThrLeu 161
QY 421 CGATCGCGCAACATACCATATCTTGAAGACAGAAAGTGTGAAGAGCTTACCCCGGCAAC 480
DB 162 ArgCysAlaAsnIleThrIleIleGlnHnIsGlnLysCysGlnAsnAlaIyTrpGlyAsn 181
QY 481 ATCAGACAGACCATGCTGTGTGCCAGCTGCAGAAAGGGGGGACAGACCTCCAGAGGT 540
DB 182 IlettlrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 201
QY 541 GACTCCGGGGGGCCCTGTGCTGTGAACAGTCTTCAAGGCAATTAATCTCGGGGGCCAG 600
DB 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221
QY 601 GATCGGTGTGCGATACCCGGAAGCCCTGGTGTCAACAGAAAGTGTGCAATATATGTGAC 660
DB 222 AspProCysAlaIleThrArgLysProGlyValIyTrpHnLysValCysLysTrpValAsp 241
QY 661 TGGATCCAGAGAGAGATGAGAAACAAT 687
DB 242 TrpIleGlnGlnThrMetLysAsnAsn 250

```

```

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C1/74
; CURRENT APPLICATION NUMBER: US/10/140,807
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRF
; ORGANISM: Homo Sapien
US-10-140-807-506

Alignment Scores:
Pred. No.: 6,09e-87 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-1_copy_272_958 (1-687) x US-10-140-807-506 (1-250)

QY 1 ATCATCAAGGGGTTCAGTGCAGAGCCCTCACTCCAGCCCTGGACAGACCCCTGTTGAG 60
DB 22 IlettllysGlyPheglucylsAllysProhlsSerGlnProtrpGlnAlaIalaIeuhbeglu 41
QY 61 AAGAGCGGCTACTCTGTGGGGGAGCGTCAATCGCCCGCCAGATGGCTCTGACAGACGCC 120
DB 42 LysThrArgLeuLeuCyseGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaIa 61
QY 121 CACTGCTCAAGCCCGGTACATGTTCACTGAGGGGACAGACACCTCCAGAGAGAG 180
DB 122 IlettlrtrpAlaValAlaArgProleuThrLeuSerSerArgCysValThrAlaIeIyhrSer 141
QY 361 TGCTCATATTTCCGGCTGGGGGACAGACGTCACAGCCCGCCAGTTACGCTCGCTCAACACTTG 420
DB 142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProhIsThrLeu 161
QY 421 CGATCGCGCAACATACCATATCTTGAAGACAGAAAGTGTGAAGAGCTTACCCCGGCAAC 480
DB 162 ArgCysAlaAsnIleThrIleIleGlnHnIsGlnLysCysGlnAsnAlaIyTrpGlyAsn 181
QY 481 ATCAGACAGACCATGCTGTGTGCCAGCTGCAGAAAGGGGGGACAGACCTCCAGAGGT 540
DB 182 IlettlrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 201
QY 541 GACTCCGGGGGGCCCTGTGCTGTGAACAGTCTTCAAGGCAATTAATCTCGGGGGCCAG 600
DB 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221

```

QY 601 GATCCGTGTGGATCACCAGCCGCTGTGTACACGAAAGTTCGAATFATGTGGAC 660  
DB 222 AspProCysAlaIleThrAlaGlySPProGlyValIleThrIlySValCysIyValAsp 241  
QY 661 TGGATCCAGAGACGATGAAGAACAT 687  
DB 242 TriPleGIInIuThrMetIySaSn 250

## RESULT 9

US-10-922-506  
Sequence 506, Application US/10140922  
Publication No. US20030138889A1

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Matanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C179  
CURRENT APPLICATION NUMBER: US/10/140,922  
CURRENT FILING DATE: 2002-05-07  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-140-922-506

## Alignment Scores:

Pred. No.: 6,09e-87 Length: 250  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.67% Indels: 0  
DB: 12 Gaps: 0

US-09-856-320a-1\_COPY\_272\_958 (1-687) x US-10-140-922-506 (1-250)

QY 1 ATATCAAGGGGTTGCGATGCAAGCCCTACCTCCAGCCCGGAGCGAGCCCTTTGGAG 60  
DB 22 IleIleIlySAlPProGlyCysIySPProHISerGInPProItrPgiAlaIleuPheGlu 41  
QY 61 AAGACGGGCTACTGTGTGGGGGAGCGCTATCGSCCCCAAGATGGCTCTGACAGCAGCC 120  
DB 42 IyStHrAlrGleuIeuCysGlyAlaIthLeuIleAlaItrProIgrItrPleuIeuThrAlaAla 61  
QY 121 CACTGCCTCAAGCCCGGCTACATAGTTCACTGGGGGAGCACAACCTCGAAGAGAGAG 180  
DB 62 HIsCysIeuIySPProIgrIyIleValHISleuGlyInHISAsnIleuGInIySglu 81  
QY 181 GGGTGTGAGAGACCGCGAGCGACGATGCTCTCCCAAGCCCGGCTTCACACAGC 240  
DB 82 GLySGeIuGInIthrAlrGInIthrGInIthrGInIthrGInIthrGInIthrGInIthr 101  
QY 241 CTCGCCAACAAGACGACGCAATGACATCATCTGGTGAAGATGGCATGCCAGTCTCC 300  
DB 102 IeuProAsnIySaSPHISrAlrGAsnAspIleMetIeuValIySmetAlaISerProValSer 121

QY 301 ATCAGCTGGGGCTGTGCGACCCCTCAGCCCTGTCTACAGCTGTGTCTACTGTGTGCGAC 360  
DB 122 IleIthrItrAlaValAlrProIeuThrIeuSerSerArgCysValIthrAlaGlyThrSer 141  
QY 361 TGGCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCAAGTTCAGCTGCTCTACACTTG 420  
DB 142 CysIeuIleSerGlyItrPglYSerThrSerSerProGInIeuArGleuProHISrIleu 161  
QY 421 CGATGCGCAACATCACCATTATGACACCCAGCAAGTGTGAGAACGCCCTACCCCGCAC 480  
DB 162 ArgCysAlaAsnIleIthrIleIleGInHISGInIySgluSAlaIyItrProGlyAsn 181  
QY 481 ATCAGACACACCATGTGTGTGCCAGCTGCGAGAGAGGGGCAAGACCTCTCGCAGGT 540  
DB 182 IleIthrAsPthrMetValCysAlaSerValGInIuGInIyGlyIySaSPSerCysGInIy 201  
QY 541 GACTCGGGGGCCCTGTGTGTGTAACCACTGTCTTCAAGCATTAATCTCTGGGGCAG 600  
DB 202 AspSerIyGlyProIeuValCysAsnGInSerIeuIeuGInIyIleIleSerItrPglYGl 221  
QY 601 GATCCGTGTGGATCACCAGCCGCTGTGTCTACACGAAAGTTCGAATFATGTGGAC 660  
DB 222 AspProCysAlaIleThrAlaGlySPProGlyValIleThrIlySValCysIyValAsp 241  
QY 661 TGGATCCAGAGACGATGAAGAACAT 687  
DB 242 TriPleGIInIuThrMetIySaSn 250

## RESULT 10

US-10-924-506  
Sequence 506, Application US/10140924  
Publication No. US20030134355A1

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Matanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C177  
CURRENT APPLICATION NUMBER: US/10/140,924  
CURRENT FILING DATE: 2002-05-07  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-140-924-506

## Alignment Scores:

Pred. No.: 6,09e-87 Length: 250  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.67% Indels: 0  
DB: 12 Gaps: 0

US-09-856-320a-1\_COPY\_272\_958 (1-687) x US-10-140-924-506 (1-250)

```

QY      1 ATCATCAAGGGGTTCGAGTGCAGACCTCACTCCACGCTGGCAGGACGCTGTTCGAG 60
      |||
      22 IleIleIySGlyPheGluCysLysProHISerGlnProTgPglInAlaIaleuPheGlu 41
QY      61 AAGACGGGGCTACTGTGTGGGGGAGGCGCATCGGCGCCAGATGGGTCTCTGACAGAGCC 120
      |||
      42 LysThrArgLeuIleuGlyAlaThrLeuIleAlaProArgTrpLeuIleuThrAlaIa 61
QY      121 CACTGCTTCACGCCCCGCTACATAGTTCACCTGGGGCAGACACCTCCAGAGAGAG 180
      |||
      62 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 81
QY      181 GGCCTGTAGACAGACCCGGAGACGCACTGAGCTCTCCGCCACCCGGCTTCAACAACAGC 240
      |||
      82 GlyCysGluGlnThrArgThrAlaThrGlnSerPheProHISerProGlyPheAsnAsnSer 101
QY      241 CTCGCCCAACAAGACACCGCAATGACATGACGTCGTCGTAAGATGGCAATGGCAGCTTCC 300
      |||
      102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121
QY      301 ATCACTGGGCTGTGTCGACCCCTCACTCTCCACGCTGTGTCACCTGTGGCAGCAGC 360
      |||
      122 IleThrTrpAlaValArgProLeuThrIleuSerSerArgCysValThrAlaGlyThrSer 141
QY      361 TGCCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCCAGTTACGCTGCTCAGACCTTG 420
      |||
      142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHISerThrLeu 161
QY      421 CGATCGGCCAACATCAACATCATTTGAGCAGCCAGAGTGTGAGAGGCGCTAACCCGGCAGC 480
      |||
      162 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn 181
QY      481 ATCAGACAGACCATGCTGTGTGCCAGCGTGCAGAGAGGGGGCAGAGACTCTGCCAGGCT 540
      |||
      182 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 201
QY      541 GACTCCGGGGGCGCTCTGTGTTAACAGTCTCTTCAAGGATATATCTCTGGGGCCAG 600
      |||
      202 AspSerGlyGlyProLeuValCysAsnGlnSerIleuGlnGlyIleIleSerTrpGlyGln 221
QY      601 GATCGGTGTGGCATACCGGAAAGCTGTGTCTACAGAAAGTGTGCAAAATATGTGAGC 660
      |||
      222 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpValAsp 241
QY      661 TGGATCCAGAGACGATGAGAACAAT 687
      |||
      242 TrpIleGlnGluThrMetLysAsnAsn 250

```

## RESULT 11

```

US-10-140-926-506
; Sequence 506, Application US/10140926
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Olang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME

```

```

; FILE REFERENCE: P3330R1C187
; CURRENT APPLICATION NUMBER: US/10/140,926
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRF
; ORGANISM: Homo Sapien
; US-10-140-926-506

```

## Alignment Scores:

```

Pred. No.: 6,09e-87 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 12 Gaps: 0

```

US-09-856-320a-1\_copy\_272\_958 (1-687) x US-10-140-926-506 (1-250)

```

QY      1 ATCATCAAGGGGTTCGAGTGCAGACCTCACTCCACGCTGGCAGGACGCTGTTCGAG 60
      |||
      22 IleIleIySGlyPheGluCysLysProHISerGlnProTgPglInAlaIaleuPheGlu 41
QY      61 AAGACGGGGCTACTGTGTGGGGGAGGCGCATCGGCGCCAGATGGGTCTCTGACAGAGCC 120
      |||
      42 LysThrArgLeuIleuGlyAlaThrLeuIleAlaProArgTrpLeuIleuThrAlaIa 61
QY      121 CACTGCTTCACGCCCCGCTACATAGTTCACCTGGGGCAGACACACCTCCAGAGAGAG 180
      |||
      62 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 81
QY      181 GGCCTGTAGACAGACCCGGAGACGCACTGAGCTCTCCGCCACCCGGCTTCAACAACAGC 240
      |||
      82 GlyCysGluGlnThrArgThrAlaThrGlnSerPheProHISerProGlyPheAsnAsnSer 101
QY      241 CTCGCCCAACAAGACACCGCAATGACATGACGTCGTCGTAAGATGGCAGCTTCC 300
      |||
      102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121
QY      301 ATCACTGGGCTGTGTCGACCCCTCACTCTCCACGCTGTGTCACCTGTGGCAGCAGC 360
      |||
      122 IleThrTrpAlaValArgProLeuThrIleuSerSerArgCysValThrAlaGlyThrSer 141
QY      361 TGCCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCCAGTTACGCTGCTCAGACCTTG 420
      |||
      142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHISerThrLeu 161
QY      421 CGATCGGCCAACATCAACATCATTTGAGCAGCCAGAGTGTGAGAGGCGCTAACCCGGCAGC 480
      |||
      162 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn 181
QY      481 ATCAGACAGACCATGCTGTGTGCCAGCGTGCAGAGAGGGGGCAGAGACTCTGCCAGGCT 540
      |||
      182 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 201
QY      541 GACTCCGGGGGCGCTCTGTGTTAACAGTCTCTTCAAGGATATATCTCTGGGGCCAG 600
      |||
      202 AspSerGlyGlyProLeuValCysAsnGlnSerIleuGlnGlyIleIleSerTrpGlyGln 221
QY      601 GATCGGTGTGGCATACCGGAAAGCTGTGTCTACAGAAAGTGTGCAAAATATGTGAGC 660
      |||
      222 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpValAsp 241
QY      661 TGGATCCAGAGACGATGAGAACAAT 687
      |||
      242 TrpIleGlnGluThrMetLysAsnAsn 250

```

## RESULT 12

```

US-10-141-698-506
; Sequence 506, Application US/10141698
; Publication No. US20030134357A1

```

```

GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C206
: CURRENT FILING DATE: 2002-05-08
: Prior Application removed - See Palm or File Wrapper
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 506
: LENGTH: 250
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-141-698-506

Alignment Scores:
Pred. No.: 6,09e-87 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-1_copy_272_958 (1-687) x US-10-141-698-506 (1-250)
OY 1 ATCATCAAGGGGTTGAGTGCAGGCTCAGTCCAGGCGGAGGAGCCCTGTGGAG 60
Db 22 lIeIleIySglYpHeIglucYsIySPronISerGIProItrpGlnAlaIaleuPheGlu 41
OY 61 AAGAGGGGCTACTCTGTGGGGGAGCGCTCATCGCCCGGAGATGCTCTGACAGCACC 120
Db 42 lYsthrArgIeuIeuCysGlyAlaIthrIleuIlAlaIProArgrIleuIthrAlaIa 61
OY 121 CACTGCCTCAAGCCCGGCTACATAGTTCACCTGGGGGAGACAACTCCAGAAAGAGAG 180
Db 62 HIsCysIeuIySProArgrIYrIleValHIsIleuIyGlnHIsAsnIeuIySgluGlu 81
OY 181 GGGGTGAGGAGAGAGCGGAGGAGCGAGCTGCTCCCGAGCCCGGCTTCAACAAGAGC 240
Db 82 GlYCysIeuIuInHrAlaIthrAlaIthrIleuIleuIleuIleuIleuIleuIleu 101
OY 241 CTCGCCAACAAGACACCGCAATGACATCATGCTGGTGAAGATGGCATGCCAGTCTCC 300
Db 102 leuIProAsnIySPHIsArGaAsnAspRIleMeIeuValIySMeIaIAserProValSer 121
OY 301 ATGACCTGGGCTGTGAGCCCTCACCCTCTCTCAGCGCTGTCTACCTGTGGAGCAGC 360
Db 122 lIeIthrAlaIValAlaIArgProIleuIthrIleuIleuIleuIleuIleuIleu 141
OY 361 TGCGCTATTTCGGGCTGGGAGAGAGCTCAAGCCCGGAGTTAGCGCTGTGACAGCTTG 420
Db 142 CysIeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 161
OY 421 CGATGGCCCAACATCAGCATCATGAGCAGACAGAAAGTGTGAAGCGCTTACCGGAGAC 480
Db 162 ArgCysAlaAsnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 181

```

```

OY 481 ATCAGAGACACCATGTGTGTGCCAGGCTGACAGAGGGGGCAAGAGACTCTGCCAGGCT 540
Db 182 lIeIthrAspIhrMeIValIcysAlaIserValGlnIleuIyGlyIySAspserCysGlnGly 201
OY 541 GACTCCGGGGGCGCTCTGGTCTGTACCAAGTCTTTCAAGCATATCTCTGGGGCCAG 600
Db 202 AspserIyGlyIProIleuValIcysAsnGlnIserIleuIleuIleuIleuIleuIleu 221
OY 601 GATCCGTTGGGATCACCCGAAAGCTGTGTCTACAGAAAGTCTCAATATGTGGAG 660
Db 222 AspProCysAlaIleuIhrAlaIArgIySProGlyValIyIthrIySValIcysIyIyValAsp 241
OY 661 TGGATCCAGAGAGACGATGAAGACAAAT 687
Db 242 TrpIleGlnIuIthrMeIySAsnAsn 250

RESULT 13
US-10-141-702-506
: Sequence 506, Application US/101411702
: Publication No. US20030134358A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P330R1C208
: CURRENT FILING DATE: 2002-05-08
: Prior Application removed - See Palm or File Wrapper
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 506
: LENGTH: 250
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-141-702-506

Alignment Scores:
Pred. No.: 6,09e-87 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-1_copy_272_958 (1-687) x US-10-141-702-506 (1-250)
OY 1 ATCATCAAGGGGTTGAGTGCAGGCTCAGTCCAGGCGGAGGAGCCCTGTGGAG 60
Db 22 lIeIleIySglYpHeIglucYsIySPronISerGIProItrpGlnAlaIaleuPheGlu 41
OY 61 AAGAGGGGCTACTCTGTGGGGGAGCGCTCATCGCCCGGAGATGCTCTGACAGCACC 120
Db 42 lYsthrArgIeuIeuCysGlyAlaIthrIleuIlAlaIProArgrIleuIthrAlaIa 61
OY 121 CACTGCCTCAAGCCCGGCTACATAGTTCACCTGGGGGAGACAACTCCAGAAAGAGAG 180
Db 62 HIsCysIeuIySProArgrIYrIleValHIsIleuIyGlnHIsAsnIeuIySgluGlu 81

```



APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Malanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C218  
CURRENT APPLICATION NUMBER: US/10/142,421  
CURRENT FILING DATE: 2002-05-09  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-142-421-506

Alignment Scores:  
Pred. No.: 6.09e-87 Length: 250  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best local Similarity: 100.00% Mismatches: 0  
Query Match: 98.67% Indels: 0  
DB: 12 Gaps: 0

US-09-856-320a-1\_COPY\_272\_958 (1-687) x US-10-142-421-506 (1-250)

QY 1 ATCATCAAGGGGTTGAGTCAAGCTCTACTCCAGCCCTGGAGCAGCCCTGTTCAG 60  
DB 22 ILETLEYSGLYPRHEGLUCYSLYSPROHISERCLNPROTPGILNLAIALALEUPHEGLU 41  
QY 61 AAGACGGGCTACTCTGTGGGGGAGCGCTCATCGCCCCAGATGGCTCTGACAGCAGCC 120  
DB 42 LYSHTARGLLEUCYSGLYALATHRLEULLEALAPROARGLTRLEULTHRLEULALALA 61  
QY 121 CACGAGCCTCAAGCCCGCTCATAGTACCTGACCTGGGGAGACACACCTCCAGAGGAGAG 180  
DB 62 HISCYSLLEUYSPPROARGLYRILEVALHISLEUGLYINHISASNLEUGLNLYSGLUGLU 81  
QY 181 GGGTGTGAGCAGACCCGAGAGCCACTGAGTCCCTCCACCCCGGCTTCACACAGC 240  
DB 82 GLYCSGLUGLINFHTARGTHRALATHRGLUSERPHEROHSIPROGLYPHEASNASNSER 101  
QY 241 CTCCCAACAAGACACCCGCAATGACATGATGCTGGTGAAGATGGCATGCCAGTCTCC 300  
DB 102 LEUPROASNLYSPHISARGASNASPILAEWETLEUVALIYSMETALASERPROVALSER 121  
QY 301 ATCACTGGGCTGTGGAGCCCTGACCTCTCCAGCTGCTGACATGCTGGGACACAGC 360  
DB 122 ILETHTRPALAYALARGPROLEUTHRLEUSERSERARGCYVALTHRALAGLYTHRSE 141  
QY 361 TGCCCTATTCCGGCTGGGCGAGCAGCTCCAGCCCGGAGTTACGCTGCTCACACCTTG 420  
DB 142 CYSLLEULIESERGLYTRPGLYSERTHRSESRPROGLINLEUARGLEUPROHISTHLEU 161  
QY 421 CGATGGCCCAACATCACATCATTTGAGCACACAGAAGTGTGAGAAAGCCCTAACCCGGCAAC 480  
DB 162 ARGCYSLALASNSLETHTRIETLEGLNHISGLNLYSYSGILUNSNALATYRPROGLYASN 181  
QY 481 ATCAGAGACACACATGGTGTGGCAGCGTCAGGAAGGGGCAAGGACCTCCGTCAGAGGT 540  
DB 182 ILETHTRASPHTMETVALCYSLASERVALGELNGLYGLYLSASPSECYSGNLGLY 201  
QY 541 GACTCGGGGGCCCTGTGTCTGTAAACAGTCTTTCAGGCATTATCTCTGGGGCCAG 600  
DB 202 ASPSERGLYGLYPROLEUVALCYSSASNGLSERLEUENGLYILETIESERTPGLYGLN 221  
QY 601 GATCCGTGTGCGATCACCCGAAAGCTGTGTCTACACGAAAGTGTGCAAAATATGTGGAC 660  
DB 222 ASPPROCYSLALATLETHTRARGLYSPROGLYVALTYRTHRLYSVALCYSLYSTYRVALASP 241  
QY 661 TGGATCCAGAGACGATGAAGAACAAT 687

DB 242 TRIPLEGLINGLUTRIMETLYSASNASN 250

Search completed: October 15, 2003, 20:55:06  
Job time : 93.6763 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 15, 2003, 17:31:30 ; Search time 32.3111 Seconds  
(without alignments)  
6749.699 Million cell updates/sec

Title: US-09-856-320a-1\_copy\_272\_958

Perfect score: 1275  
Sequence: 1 atcatcaagggttcgagtg.....aggagacatgaagaacaat 687

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1107863 segs, 158726573 residues

Total number of hits satisfying chosen parameters: 2215726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-O=/cgn2.1/USPRO\_SPOOL\_P/US09856320/runtat\_15102003.105638.8500/app\_query.fasta\_1.2318  
-DB=A\_Geneseq\_19jun03 -OPMT=fastan -SUFFIT=rag -MINMATCH=0.1 -LOOPTC=0  
-LOOPTXT=0 -UNITS=bits -STARF=1 -END=1 -MATRIX=blomsm62 -TRANS=human40.cdl  
-LIST=45 -DOCLALIGN=200 -THR.SCORE=pcot -THR.MAX=100 -THR.MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09856320.ecgn.1.1-140.ecrnat.15102003.105638.8500 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEREQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A\_Geneseq\_19jun03:\*  
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2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*  
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19: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\*  
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22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	98.7	250	21	Human TLSP. Homo
2	1258	98.7	250	21	Human PRO1279 (UNQ)
3	1258	98.7	250	22	Human secreted pro
4	1258	98.7	250	22	Human PRO1279 poly
5	1258	98.7	250	22	Protein of the inv
6	1258	98.7	250	23	Prostate cancer-as
7	1258	98.7	250	23	Human angiogenesis
8	1258	98.7	250	23	Human PRO1279 prot
9	1258	98.7	250	23	Human PRO protein,
10	1258	98.7	250	24	Human PRO polypept
11	1258	98.7	250	24	Human secreted/Lra
12	1258	98.7	250	24	Novel secreted and
13	1258	98.7	250	24	Lung cancer-associ
14	1258	98.7	282	21	CASB12 amino acid
15	1258	98.7	282	21	Human serine prote
16	1258	98.7	282	21	A human prostate-a
17	1252	98.2	281	20	CASB12 polypeptide
18	1235.5	96.9	275	21	Human serine prote
19	1231	96.5	228	21	Human TLSP. Homo
20	1228	96.3	250	20	Extended human sec
21	1227	96.2	248	22	Human PS133 consen
22	1219.5	95.6	289	22	Fusion gene with h
23	1219.5	95.6	289	22	Amino acid sequenc
24	1182	92.7	228	20	Polypeptide fragme
25	1182	92.7	228	20	Human secreted pro
26	1182	92.7	246	20	Polypeptide fragme
27	1182	92.7	246	21	Human secreted pro
28	1062	83.3	276	21	Mouse serine prote
29	1014.5	79.6	247	23	Human Serine Prote
30	736	57.7	250	21	Human KLR-L3 prote
31	736	57.7	250	21	Human KLR-L3 prote
32	736	57.7	251	22	Human novel secret
33	734	57.6	247	22	Human novel enzyme
34	733.5	57.4	296	21	Human KLR-L3 prote
35	716	56.2	247	22	Novel human connec
36	716	56.2	247	22	Novel human enzyme
37	716	56.2	247	22	Novel human enzyme
38	688	54.0	275	21	Human neurotrophin
39	684	53.6	260	17	Human recombinant
40	684	53.6	260	18	Mouse neurotrophin pr
41	684	53.6	256	23	Mouse ischaemic co
42	682	53.5	256	23	Novel human Kallik
43	682	53.5	320	23	Human protease, PR
44	682	53.5	320	23	Amino acid sequenc
45	681	53.4	260	20	Human PRO322 prote

## ALIGNMENTS

RESULT 1	
AA021325	AA021325 standard; Protein; 250 AA.
XX	
AC	AA021325;
XX	
XX	
DT	02-FEB-2001 (first entry)
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DE	Human TLSP.
XX	
XX	
KW	Human; KLR-L1; KLR-L2; KLR-L3; KLR-L4; KLR-L5; KLR-L6; TLSP;
KM	trypsin-like serine protease; Kallikrein-like protein; serine protease;
KW	cytostatic; cancer; prostate cancer.
XX	
OS	Homo sapiens.
XX	
PN	WO200053776-A2.
XX	



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PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102695.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104287.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106062.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106028.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0106500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106933.
PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.

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PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.
PR 17-NOV-1998; 98US-0108867.
PR 18-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108858.
PR 18-NOV-1998; 98US-0108904.
XX
XX (GENENTECH INC.
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;
XX WPI: 2000-237871/20.
XX N-PSDB: AAA37072.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or
XX secreted PRO polypeptides, useful for screening of potential peptide or
XX small molecule inhibitors of the relevant receptor/ligand interactions
XX
XX Claim 12, Fig 102, 773pp: English.
XX
XX AAA37072 to AAA37144 encode the new isolated human transmembrane,
XX receptor or secreted PRO polypeptides given in AAY9340 to AAY93462. The
XX transmembrane and receptor PRO proteins can be used for screening of
XX potential peptide or small molecule inhibitors of the relevant
XX receptor/ligand interactions. The polypeptides and nucleotide sequences
XX encoding then have various industrial applications, including uses as
XX pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
XX PCR primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention.
XX
XX Sequence 250 AA:
XX
XX Alignment Scores:
XX Pred. No.: 1.4e-94 Length: 250
XX Score: 1258.00 Matches: 229
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 98.67% Indels: 0
XX DB: 21 Gaps: 0
XX
XX US-09-856-320A-1_COPY_272_958 (1-687) x AAY9390 (1-250)
XX
XX QY 1 ATCATCAAGGGGTTGAGTGCAGAGCTCAGCCCTGACAGAGCCCTGTTCCAG 60
XX |||||||
XX Db 22 lletlellysglyphnecilucyslyspriohlsertglnptotrglnalaleuuehgu 41
XX |||||||
XX QY 61 AAGACGCGGCTACTGTGTGGGCGAGGCTCATGCCGCCAGATGAGCTCCTGCAGACGCC 120
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XX Db 42 lylsthrargleuleucysglyalathrlleuleialaiproargtrpleuuehrlalala 61
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XX |||||||
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XX |||||||
XX Db 82 Glycysgluglnthrlartrhlalathrgluserpneprohlsprogllypneasnnsr 101
XX |||||||
XX QY 241 CTCCCAACAAGACACCGCATGATCATGTGTGAAGATGCGATCGCACTGCC 300
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XX |||||||
XX QY 301 ATCACTGGCGTGTGCGACCCCTCACCTCTCTACGCTGTGTACTGTGCGACACGCG 360
XX |||||||

```

Db 122 IIEthrrpAlaValaArgProLeuThLeuSerSerArgCysValThrAlaGlyThrSer 141  
 QY 361 TGGCTATTTCGGGCTGGGAGCAGCAGCTCCAGCCCGAGTACGCTGCTCACACCTTG 420  
 Db 142 CysLeuLeuSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161  
 QY 421 CGATGCGCCCAACATCACCATCATTTAGACACACAGAGTGTGAGAACGCCCTACCCGCAAC 480  
 Db 162 ArgCysAlaAsnIleThrIleIleGlnHisGlnIleGlnIleGlnIleGlnIleGlnIle 181  
 QY 481 ATCAGACAGACAGATGATGTGTGCGAGCTGAGAGAGGGGAGAGAGAGCTGCGAGAGT 540  
 Db 182 IIEthrrpThrMetValCysAlaSerValGlnIleGlnIleGlnIleGlnIleGlnIle 201  
 QY 541 GACTCGGGGGGCTGTGTCTGTACACAGTCTCTTACAGGATTAATCTCTGGGGCCAG 600  
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 QY 601 GATCCGCTGCGATGATGACCCGAAAGCCGTGTCTACACGAAAGTCTGCAATATGTGGAC 660  
 Db 222 AsperCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpValAsp 241  
 QY 661 TGGATCCAGAGAGAGATGAGAACAAAT 687  
 Db 242 TrpIleGlnIleThrMetLysAsnAsn 250

RESULT 3  
 ABB50479 ID ABB50479 standard; Protein; 250 AA.  
 AC ABB50479;  
 DT 07-FEB-2002 (first entry)  
 DE Human secreted protein encoded by gene 179 SEQ ID NO:427.

XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;  
 KW dermatological; immunosuppressive; anti-inflammatory; immunostimulant;  
 KW cytostatic; cardiac; vascular; anti-angiogenic; ophthalmological;  
 KW neuroprotective; neotropic; anticonvulsant; antialzheimer's; vulnary;  
 KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;  
 KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;  
 KW human immunodeficiency virus; hyperproliferative disorder; wound healing;  
 KW Gaucher's disease; cardiovascular disease; scleritis; rheumatoid arthritis;  
 KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiotensin disorder;  
 KW corneal graft neovascularization; diabetic retinopathy; regeneration;  
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;  
 KW Parkinson's disease; infectious disease.

OS Homo sapiens.  
 XX  
 XX WO200162891-A2.  
 XX  
 XX 30-AUG-2001.  
 XX  
 XX 21-FEB-2001; 2001WO-US05614.  
 XX  
 XX 24-FEB-2000; 2000US-184836P.  
 XX  
 XX 29-MAR-2000; 2000US-193170P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX NI J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;  
 PI Ruben SM, Sopet DR, Young PE, Shi Y, Florence KA, Wei Y;  
 PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferris AM, Fan P;  
 PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;  
 PI Zeng Z, Greene JM;  
 XX  
 XX WPI: 2001-625724/72.  
 DR N-PSDB; ABA63372.  
 XX  
 XX Nucleic acids encoding 207 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's

PT disease and diabetic retinopathy -  
 XX  
 PS Claim 11; Page 1181-1182; 1533pp; English.  
 XX  
 CC ABB50301 to ABB51267 and ABA83194 to ABA83441 represent human secreted  
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various  
 CC activities based on the tissues and cells the genes are expressed in.  
 CC Example of these activities include: immunomodulatory; antisclerotic;  
 CC dermatological; immunosuppressive; anti-inflammatory; immunostimulant;  
 CC anti-HIV; cytostatic; cardiac; anti-angiogenic; ophthalmological;  
 CC neuroprotective; neotropic; anticonvulsant; antialzheimer's; vascular;  
 CC antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;  
 CC in gene therapy and vaccine production. (I) and (II) can be used in the  
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple  
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus  
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and  
 CC Gaucher's disease), cardiovascular diseases (e.g. scleritis, rheumatoid  
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiotensin  
 CC disorders (e.g. corneal graft neovascularization and diabetic  
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,  
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or  
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to  
 CC ABA83193 and ABB50300 represent sequences used in the exemplification of  
 CC the present invention.  
 CC  
 XX  
 SQ Sequence 250 AA;  
 Alignment Scores:  
 Pred. No.: 1,4e-94 Length: 250  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.67% Indels: 0  
 DB: 22 Gaps: 0

US-09-856-320A-1\_COPY\_272\_958 (1-687) x ABB50479 (1-250)

QY 1 ATCATCAAGGGGTTGAGTGCAGAGCTTACCTCCAGCCCTGGAGAGCCCTGTTCAG 60  
 Db 22 IIEthrrpAlaValaArgProLeuThLeuSerSerArgCysValThrAlaGlyThrSer 141  
 QY 61 AAGAGCGGCTACTCTGTGGGGGAGCCCTGATGCGCCCGAGAGGCTCTGACAGCACC 120  
 Db 42 LysThrArgLeuLeuGlyValAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 61  
 QY 121 CACTGCTCAAGCCCGCTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 180  
 Db 62 HisCysLeuLysProArgGlyTrpIleValHisLeuGlyGlnHisAsnLeuGlnIleGln 81  
 QY 181 GCGTGTGAGCAGACCCGAGCAGCCAGTGAATGCTGTAAGATGCGATGCCAGCTCC 240  
 Db 82 GlySerGlnIleThrArgTrpAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 101  
 QY 241 CTCGCCAACAAGACCCGCAATGACATGATGCTGTGTAAGATGCGATGCCAGCTCC 300  
 Db 102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121  
 QY 301 ATCAGCTGGGCTGTGACCCCTTACCCCTCTCTGATGATGATGATGATGATGATGATGAT 360  
 Db 122 IIEthrrpAlaValaArgProLeuThLeuSerSerArgCysValThrAlaGlyThrSer 141  
 QY 361 TGGCTATTTCGGGCTGGGAGCAGCAGCTCCAGCCCGAGTACGCTGCTCACACCTTG 420  
 Db 142 CysLeuLeuSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161  
 QY 421 CGATGCGCCCAACATCACCATCATTTAGACACACAGAGTGTGAGAACGCCCTACCCGCAAC 480  
 Db 162 ArgCysAlaAsnIleThrIleIleGlnHisGlnIleGlnIleGlnIleGlnIleGlnIle 181  
 QY 481 ATCAGACAGACAGATGATGTGTGCGAGCTGAGAGAGGGGAGAGAGAGCTGCGAGAGT 540  
 Db 182 IIEthrrpThrMetValCysAlaSerValGlnIleGlnIleGlnIleGlnIleGlnIle 201

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QY 541 GACTCGGGGGCCCTGTGTTACACAGCTCTTCAAGCATATCTCTGGGGCCAG 600
Db 202 ASPTSGELYLProleuValICysasnGlnSerLeuGlnGlyLeIleSerTrpGlyGln 221
QY 601 GATCCGTGTGCATCACCAGCAAGCTGTCTACACAGAAAGTCTGCAATATATGAC 660
Db 222 ASPTGCGYAlaIleThrArgLysProGlyValIYrThrLysValICysLysIYrValAsp 241
QY 661 TGGATCCAGAGACATGAGAAACAT 687
Db 242 TPTIleGlnGluThrMetLysAsn 250

RESULT 4
AAU12424
ID AAU12424 standard; Protein; 250 AA.
XX
AC AAU12424;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO1279 polypeptide sequence.
XX
KM Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KM breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KM cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KM adipocyte; A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32678.
XX
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 11-JAN-2000; 2000WO-US00376.
PR 18-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
PA (GENTECH ) GENENTECH INC.
XX
PI Baker KP, Beresini M, DeForge L, Desnoyers L, Flivaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
PI Smith V, Stewart JA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
XX
XX WPI; 2001-408281/43.
XX
XX N-PSDB; AAS21496.
XX
PI Isolated, secretory and transmembrane PRO polypeptide used to detect

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PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
XX lung, breast, prostate, cervical
XX
XX Claim 12; Fig 506; 813bp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
XX
SQ Sequence 250 AA:
XX
XX
Alignment Scores:
Pred. No.: 1.4e-94 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 22 Gaps: 0

US-09-856-320A-1_COPY_272_958 (1-687) x AAU12424 (1-250)
QY 1 ATCATCAAGGGGGTGGAGTCAAGGCTTCCTCCAGCCCTGGCAGGACGCTGTTGAG 60
Db 22 IIEIIEIYSGIYPheGInUCysLysProHisSerGlnProTrpGlnAlaLeuPheGln 41
QY 61 AAGACGGGCTACTGTGTGGGGGAGCGCTCATCGCCCCAGATGGCTCTGACAGAGCC 120
Db 42 LYSThrArgLeuLeuCysGlyAlaThrIleuAlaProArgTrpLeuThrAlaAla 61
QY 121 CACTGCTCAAGCCCCGCTACATGACTTCACTGGGGGACACACACCTCCAGAGAGAG 180
Db 62 HISCysLeuLysProArgTrpIleValIHisLeuGlnHisAsnLeuGlnLysGln 81
QY 181 GGGTGGAGACAGCCGGGACAGCAGCTGAGTCCCTCCCGCCGGGCTTCAACAAGCC 240
Db 82 GIIYcysGlnGlnThrArgThrAlaThrIleuSerPheProHisProGlyIYpHeAsnSer 101
QY 241 CTCCCAACAAGACACCGCAATGACATCATGTGTGAGATGGCATCGCCAGCTTCC 300
Db 102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValIYMetAlaSerProValSer 121
QY 301 ATCACTGGGCTGTGCGACCCCTCACTCTCTCAACGCTGTGTACTGTGACACAGC 360
Db 122 IIErThrPAlaValArgProLeuThrIleuSerArgCysValIYrThrAlaGlyThrSer 141
QY 361 TGCCCTATTTCGGCTGGGGGAGCAGCTGCACGCCCGCATGGCTGGCTGCACACCTG 420
Db 142 CysLeuIleSerGlyTrpGlySerThrIleuSerProGlnLeuAlaLeuProHisThrLeu 161
QY 421 CGATCGCCCAACATCACCATCATTTAGACACAGAAAGTGTGAGAACGCTTACCCGGCAAC 480
Db 162 ArgCysAlaAsnIleThrIleGlnHisGlnLysCysGlnAsnAlaIYrProLysAsn 181
QY 481 ATCACAGACACCATGTGTGTGCCAGGCTGCAGGAAGGGGGCAGAGCATCTCGCCAGGGT 540

```

Db 182 ILeThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 201  
 QY 541 GACTCCGGGGGCCCTGTGTCGTGAACAGTCCTTCAAGGCAATTATCTCTGGGGCCAG 600  
 Db 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuInGlyIleIleSerTrpGlyGln 221  
 QY 601 GATCCGCTGTCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTCAAAATATGTGAC 660  
 Db 222 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrValAsp 241  
 QY 661 TGGATCCAGAGAGAGATGAAGAACAAAT 687  
 Db 242 TrpIleGlnGlnThrMetLysAsnAsn 250  
 RESULT 5  
 AAB66139  
 ID AAB66139 standard; protein; 250 AA.  
 AC AAB66139;  
 XX 02-APR-2001 (first entry)  
 DT Protein of the invention #51.  
 DE Secreted; transmembrane; gene therapy.  
 XX  
 KM  
 XX  
 OS Unidentified.  
 PN WO200078961-A1.  
 PD 28-DEC-2000.  
 XX 18-FEB-2000; 2000WO-US04342.  
 PE 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145688.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 XX  
 PA (GENENTECH INC.  
 XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan MJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;  
 PI Watanabe CK, Williams PM, Wood WI;  
 XX WPI; 2001-071395/08.  
 DR  
 XX  
 PT Secreted and transmembrane proteins and nucleic acids designated PRO,  
 PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy -  
 XX  
 PS Claim 1; Fig 102; 787pp; English.  
 XX  
 CC The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of  
 CC anti-sense RNA and DNA. They may also be used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents.  
 CC The nucleic acids may also be used in gene therapy.  
 XX  
 SO Sequence 250 AA;  
 Alignment Scores:  
 Pred. No.: 1,4e-94 Length: 250  
 Score: 1258.00 Matches: 229

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.67% Indels: 0  
 DB: 22 Gaps: 0  
 US-09-856-320a-1\_COPY\_272\_958 (1-687) x AAB66139 (1-250)  
 QY 1 ATCATCAAGGGGTTGAGTGCAGAGCCCTCACTCCAGCCCTGGAGGAGCCCTGTTGAG 60  
 Db 22 IleIleLysGlyPheGlnGlyCysProHisSerGlnProIleTrpGlnAlaIlePheGln 41  
 QY 61 AAGACGGGCTACTCTGTGGGGGAGCCCTGATGCCCCAGATGGCTCTGACAGAGCC 120  
 Db 42 LysThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 61  
 QY 121 CACTGACCTCAAGCCCCGCTCATATGATTCACCTGGGGGAGAGACAACCTCCAGAGAGAGAG 180  
 Db 62 HisCysLeuLysProAlaGlyTrpIleValHisLeuGlyGlnHisAsnLeuGlnGlyGln 81  
 QY 181 GGCTGTGAGAGAGAGAGCCGAGAGCCAGTGAAGTCTCCCGCCAGCCGCTTCAACAGAGC 240  
 Db 82 GlyGlyGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 101  
 QY 241 CTCCCCACAAAGACACCCGCAATGACATGCTGTGTAAGATGGCATGCCAGTCTCC 300  
 Db 102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121  
 QY 301 ATCACCTGGGCTGTGGAGCCCTCAACCTGCTGACAGTGTGACATGCTGGAGAGAGC 360  
 Db 122 IleThrTrpAlaValAlaGProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 141  
 QY 361 TGCCTCATTTCCGGCTGGGGGAGAGCAGCTCCAGCCCCAGTGAAGCTGCTCAACAGCTTG 420  
 Db 142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161  
 QY 421 CGATGGCCCAACATCACCATCATGAGCACCAGAGAGTGAAGAGCCCTACCCGGAGAC 480  
 Db 162 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysSerGlnAsnAlaTyrProGlyLysn 181  
 QY 481 ATCAGAGACACCATGCTGTGTGCAGCGTCAGAGAGGGGAGAGAGACTCTCCAGAGGT 540  
 Db 182 ILeThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly 201  
 QY 541 GACTCCGGGGGCCCTGTGTCGTGAACAGTCCTTCAAGGCAATTATCTCTGGGGCCAG 600  
 Db 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuInGlyIleIleSerTrpGlyGln 221  
 QY 601 GATCCGCTGTCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTCAAAATATGTGAC 660  
 Db 222 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrValAsp 241  
 QY 661 TGGATCCAGAGAGAGATGAAGAACAAAT 687  
 Db 242 TrpIleGlnGlnThrMetLysAsnAsn 250  
 RESULT 6  
 AAB61816  
 ID AAB61816 standard; protein; 250 AA.  
 AC AAB61816;  
 XX 15-AUG-2002 (first entry)  
 DT Prostate cancer-associated protein #17.  
 DE Prostate cancer-associated protein #17.  
 XX  
 KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.  
 XX  
 OS Mammalia.  
 OS  
 XX  
 PN WO200230268-A2.  
 PD 18-APR-2002.  
 XX

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PF 12-OCT-2001; 2001WO-US32045.
XX
PR 13-OCT-2000; 2000US-0687576.
PR 08-DEC-2000; 2000US-0733288.
PR 08-DEC-2000; 2000US-0733742.
PR 24-JAN-2001; 2001US-263957P.
PR 16-MAR-2001; 2001US-276791P.
PR 16-MAR-2001; 2001US-276888P.
PR 06-APR-2001; 2001US-281922P.
PR 24-APR-2001; 2001US-286214P.
PR 30-APR-2001; 2001US-0847046.
PR 04-MAY-2001; 2001US-286589P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Gish KC, Mack DH, Wilson KE, Afar D, Heyezi P;
XX WPI: 2002-471335/50.
DR N-PSDB; ABR92131.
XX
XX Detecting a prostate cancer-associated transcript in a cell in a
PI patient, useful for diagnosing prostate cancer (PC) or screening
PI modulators of PC, by determining if prostate cancer-associated genes
PI are expressed in a prostate tissue
XX
XX Claim 27; Page 314; 436pp; English.
XX
XX The present invention relates to methods of detecting a prostate
CC cancer-associated transcript in a cell from a patient. The method
CC comprises contacting a biological sample from the patient with
CC prostate cancer-associated polynucleotides (designated PC genes) that
CC selectively hybridise to a sequence that is at least 80% identical
CC to them. The prostate cancer-associated polynucleotide sequences
CC are differentially expressed in prostate tumour tissue or in
CC prostate cancer and are derived from the tissues of various
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC The methods of the invention are useful for diagnosing and treating
CC prostate cancer in mammals. The prostate cancer-associated genes are
CC useful for diagnosing or treating prostate cancer, as well as for
CC identifying modulators of prostate cancer or agents that inhibit
CC prostate cancer. The nucleic acid sequences are particularly useful
CC in gene therapy, as a vaccine or in antisense applications.
CC AB61800-AB61944 represent prostate cancer-associated proteins.
XX
XX SQ Sequence 250 AA;
XX
XX Alignment Scores:
XX Pred. No.: 1,4e-94 Length: 250
XX Score: 1258.00 Matches: 229
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 98.67% Indels: 0
XX DB: Gaps: 0
XX
XX US-09-856-320a-1_COPY_272_958 (1-687) x AB61816 (1-250)
XX
XX 1 ATCATCAAGGGGTTGAGTGCAGGCTTCCAGCCCTGGGAGGAGCCCTGTTGAG 60
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 22 lletlelsglypnehlucylslyspromisserglnpofrglnalaleuphegu 41
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 61 AAGAGCGGCTACTCTGTGGGGCGAGCTCATCGGCCCAATGGCTCTGACAGACGC 120
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 42 lylttrtargleuleucysglyalathrleullealaprdatgtrpleuethrila 61
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGAGGAGCAACCTCAGAAAGAGAG 180
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 62 Hlscysleulysprohargtrylevalhlstleuglgnhlshlnleuglnlysglu 81
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 181 GGCTGTGAGCAGACCCGAGAGCCAGCTAGTCTTCCCAACCCGGCTTCAACAACAGC 240
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 82 GlycysgluglnthrargthralthrghluserPheprohlsproglYphesmsnsr 101
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 241 CTCGCCAACAAGACACCGCATGATCATCTGCTGAGATGGATCGGCACTCTCC 300

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DB 102 loupProasnlysaSPHlsArGAsnspIlleMellleVallyMeAlaserProValSer 121
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 ATCACTGGGGCTGTGGAGACCCCTCAACCCCTCTCAAGCTGTGCTACTGTGGACAC 360
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 122 lletntrpAlaValArGProleuThrleuSerSerArgCysValThrIaIlyThrSer 141
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 361 TGCCTCATTTCCGGCTGGGGAGCAGCTCACGCCCTAGTTCAGCTGCTGCTGACACTTG 420
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 142 CysleuIlleSerClyTtrpIlySerThrSerSerProGlnleuArgleuProhlsThrleu 161
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 421 CGATGCGCCACATCAATCAATCATTTAGACACAGAAAGTGTGAGACGCCCTACCCGGCAAC 480
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 162 ArgCysAlaAsnIlleThrIlelleGlnHsGlnLysCysGlnAsnAlatyrProGlyAsn 181
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 481 ATCAGAGACCATGTGTGTGCTGCCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 182 lletntrpSPHrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 201
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 541 GACTCCGGGGGCCCTCTGTGTGTATACAGAGTCTTCAAGGCAATATCTCTGGGGCCAG 600
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 202 AspSerGlyGlyProleuValCysAsnGlnSerleuGlnGlylletleSertrpGlyGln 221
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 601 GATCCGTGTGCGATATACCGGAAAGCCCTGCTCTACAGAAAGTGTGCAATATGTGAC 660
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 222 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValasp 241
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 661 TGCATCCAGAGACGATGAGAAACAAT 687
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 242 trpIleGlnGlnThrMetLysAsn 250
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX
XX RESULT 7
XX ID AB95526
XX AB95526 standard; Protein; 250 AA.
XX
XX AC AB95526;
XX
XX 19-JUL-2002 (first entry)
XX
XX DE Human angiogenesis related protein PH01279 SEQ ID NO: 208.
XX
XX KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
XX KW cardiac; cytosolic; antiangiogenic; hypotensive; vulnerary;
XX KW antiarteriosclerotic.
XX
XX OS Homo sapiens.
XX
XX PN WO200208284-A2.
XX
XX PD 31-JAN-2002.
XX
XX PF 09-JUL-2001; 2001WO-US21735.
XX
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220664P.
XX 28-JUL-2000; 2000WO-US20710.
XX 02-AUG-2000; 2000US-222695P.
XX 17-AUG-2000; 2000US-0643657.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 07-SEP-2000; 2000US-230978P.
XX 15-SEP-2000; 2000US-000000P.
XX 18-SEP-2000; 2000US-0664610.
XX 18-SEP-2000; 2000US-0665350.
XX 24-OCT-2000; 2000US-242322P.
XX 08-NOV-2000; 2000US-0709238.
XX 08-NOV-2000; 2000WO-US30873.
XX 10-NOV-2000; 2000WO-US30873.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.

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22-JAN-2001; 2001US-0767609.  
PR 26-FEB-2001; 2001US-076498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US0666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828368.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 28-JUN-2001; 2001WO-US00000.

XX (GETH) GENENTECH INC.  
PA (BAKE) BAKER K P.  
PA (FERR) FERRARA N.  
PA (GERB) GERBER H.  
PA (GERR) GERRITSEN M E.  
PA (GODD) GODDARD A.  
PA (GODO) GODOWSKI P J.  
PA (GURN) GURNEY A L.  
PA (HILL) HILLMAN K J.  
PA (MARS) MARSTERS S A.  
PA (PANJ) PAN J.  
PA (PAON) PAONI N F.  
PA (STEP) STEPHAN J F.  
PA (WATA) WATANABE C K.  
PA (WILL) WILLIAMS P M.  
PA (WOOD) WOOD W I.

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillman KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

DR WPI: 2002-171999/22.  
DR N-PSDB; ABL95664.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PI infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11; Fig 208; 567pp; English.

XX The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hyper trophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 250 AA;

Alignment Scores:  
Pred. No.: 1.4e-94 Length: 250  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.67% Indels: 0  
DB: 23 Gaps: 0

US-09-856-320a-1\_copy\_272\_958 (1-687) x ABB95526 (1-250)

OY 1 ATCATCAAGGGGTTTCGATCGAAGCCCTACATCCAGCGCCGAGGAGCCCTGTGAG 60  
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 22 IITellEyselYpNeglucYsLysProHisSerInProTrpGlnAlaIalaLeuPhgln 41

OY 61 AAGACGGGCTACTCTGTGGGGCGAGCCCTCATCGCCCGCCAGATGGCTCTGACAGCACC 120  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 42 LysThrArgLeuLeuLeuGlyAlaIleThrLeuIleAlaProArgTrpLeuLeuThrAlaIa 61  
OY 121 CACTGCTCAAGCCCGGCTACATGTTGCTACCTGGGGCGAGCAACCTCCAGAGGAGGAG 180  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 62 HisCysLeuLysProArgTrpIleValHisLeuIleGlnHisAsnLeuGlnLysGlnL 81  
OY 181 GGCTGTAGCAGACCCCGAGCAGCCAGCTAGTCTCCCGCCAGCCCGGCTTCAACACAGC 240  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 82 GlyCysGlnGlnThrAlaGlyThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 101  
OY 241 CTCCCAACAAGACACACCGCATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121  
OY 301 ATCACTGGGGCTGTGGCAGCCCTTACCTCTCCCTCAGAGCTGTGTACTGCTGGCAGC 360  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 122 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 141  
OY 361 TGCTCATTTCCGGCTGGGCGAGCAGCTCCAGCCCGCATGATGATGATGATGATGATGATG 420  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161  
OY 421 CGATGCCCAACATCATCATCATTTGACACACAGAGTGTGAGAACGGCTTACCCCGGCAAC 480  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 162 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn 181  
OY 481 ATCAACACACACATCATGCTGTGTGCGCAGCTGTGAGAACGGGCGAGCAGCTGTGAG 540  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 182 IleThrAspThrMetValCysAlaSerValGlnIleGlyLysAspSerCysGlnGly 201  
OY 541 GACTCCGGGGGCGCTGT 600  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 202 AspSerIleGlyProLeuValCysAsnGlnSerLeuGlnIleIleSerTrpGlyGln 221  
OY 601 GATCCGTTGCGATCACCCGAAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 222 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyValAsp 241  
OY 661 TGGATCCAGGAG 687  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 242 TrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 8  
ABB84920  
ID ABB84920 standard; Protein: 250 AA.

XX ABB84920;  
AC 16-MAY-2002 (first entry)  
DT 16-MAY-2002 (first entry)

XX Human PRO1279 protein sequence SEQ ID NO:208.

XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
KW gene therapy; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
wound healing; chromosome mapping; gene mapping.

XX Homo sapiens.  
XX WO20020690-A2.  
XX PD 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US19692.  
XX 23-JUN-2000; 2000US-213637P.

PR 20-JUL-2000: 2000US-219556P.  
 PR 25-JUL-2000: 2000US-220624P.  
 PR 25-JUL-2000: 2000US-220664P.  
 PR 28-JUL-2000: 2000OWO-US20710.  
 PR 02-AUG-2000: 2000US-222695P.  
 PR 17-AUG-2000: 2000US-0643657.  
 PR 23-AUG-2000: 2000OWO-US23522.  
 PR 24-AUG-2000: 2000OWO-US23328.  
 PR 07-SEP-2000: 2000US-230978P.  
 PR 18-SEP-2000: 2000US-0664610.  
 PR 18-SEP-2000: 2000US-0665350.  
 PR 24-OCT-2000: 2000US-242922P.  
 PR 08-NOV-2000: 2000US-0709238.  
 PR 08-NOV-2000: 2000OWO-US30952.  
 PR 10-NOV-2000: 2000OWO-US30873.  
 PR 01-DEC-2000: 2000OWO-US32678.  
 PR 20-DEC-2000: 2000US-0747259.  
 PR 20-DEC-2000: 2000OWO-US34956.  
 PR 22-JAN-2001: 2001US-0767609.  
 PR 28-FEB-2001: 2001US-0796498.  
 PR 28-FEB-2001: 2001WO-US06520.  
 PR 01-MAR-2001: 2001WO-US06666.  
 PR 09-MAR-2001: 2001US-0802706.  
 PR 14-MAR-2001: 2001US-0808689.  
 PR 22-MAR-2001: 2001US-0816744.  
 PR 05-APR-2001: 2001US-0828366.  
 PR 10-MAY-2001: 2001US-0854208.  
 PR 10-MAY-2001: 2001US-0854280.  
 PR 25-MAY-2001: 2001US-0866028.  
 PR 25-MAY-2001: 2001US-0866034.  
 PR 30-MAY-2001: 2001WO-US17092.  
 PR 30-MAY-2001: 2001US-0870574.  
 PR 01-JUN-2001: 2001WO-US17443.  
 PR 01-JUN-2001: 2001WO-US17800.  
 XX (GENE) GENE TECH INC.  
 PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godswail PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WT, Ye W;  
 XX N-PSDB: ABL88175.  
 DR WPI: 2002-090516/12.  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX  
 PS Claim 11, Fig 208: 565pp: English.  
 XX  
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytosstatic,  
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 CC carcinoma) and wound healing. The PRO polynucleotides have applications  
 CC in molecular biology, including use as hybridisation probes, and in  
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 CC probes used in the exemplification of the present invention.  
 XX  
 SO Sequence 250 AA:

DB: 23 Gaps: 0  
 US-09-856-320a-1\_COPY\_272\_958 (1-687) x ABB84920 (1-250)  
 QY 1 ATCATCAAGGGGTGGAGTGCAGAAAGCTCACTCCGAGCCCTGGCAGGACGCTGTTCCAG 60  
 DB 22 IleIleLysGlyPheIleLysLysProHisSerGlnProTrpGlnIleAlaLeuPheGlu 41  
 QY 61 AAGACGGGCTACTGTGTGGGGGAGCGTCAATCGCCCGGATGAGCTCTGCAGCAGCC 120  
 DB 42 LysThrArgLeuLeuLysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaIle 61  
 QY 121 CACTGCTCAAGCCCGCTACATGTCACCTGGGGCAGCACAACCTCCAGAGAGAG 180  
 DB 62 HisCysLeuLysProArgTrpIleValHisLeuGlyHisIleAsnLeuGlnGlu 81  
 QY 181 GGCTGTGAGCAGACCGGAGCAGCACTGAGTCCCTCCCGCGGGCTCAACAGCAGC 240  
 DB 82 GlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnSer 101  
 QY 241 CTCGCCAACAAAGACCCGCAATGACATCATGCTGTGAGAGATGGCATCGCCAGTCTCC 300  
 DB 102 LeuProAsnLysAspHisArgAsnSpleMetLeuValLysMetAlaSerProValSer 121  
 QY 301 ATCACCCTGGGCTGTGGAGCCCTCAACCTCTCTCAACGCTGTGTCACTGGCAGCAGC 360  
 DB 122 IleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 141  
 QY 361 TGCCCTCATTTCCGGCTGGGGGAGCAGCTCCACCCCACTTACGCTGCTCAACCTTG 420  
 DB 142 CysLeuIleSerGlyTrpGlySerThrSerProGlnLeuArgLeuProHisThrLeu 161  
 QY 421 CGATGCGCCACATCATGACCATGAGCAGAGAGTGAGAGAGCCCTACCCCGGCAAC 480  
 DB 162 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn 181  
 QY 481 ATCAGACAGCAGCATGCTGTGTGCCAGCTGAGAGAGGGGGAGAGACTCTGCCAGGT 540  
 DB 182 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 201  
 QY 541 GACTCCGGGGGCGCTGTGTGTGTAACGCTCTTCAAGGATATCTCCCTGGGGCCAG 600  
 DB 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221  
 QY 601 GATCCGTGTGCATCACCCGGAAGCTGTGTCTACACAGAAAGTCTGCNAATATGTGAC 660  
 DB 222 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpValAsp 241  
 QY 661 TGATCCAGAGAGCATGAGAACAT 687  
 DB 242 TrpIleGlnGlnThrMetLysAsnAsn 250  
 RESULT 9  
 ID AAU83684 standard: Protein: 250 AA.  
 XX AAU83684;  
 AC 08-MAY-2002 (first entry)  
 XX  
 DE Human PRO protein, Seq ID No 186.  
 XX  
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
 KW pericyte cell proliferation; chondrocyte cell proliferation;  
 KW tumour necrosis factor alpha.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200208288-A2.  
 XX  
 PD 31-JAN-2002.  
 XX

Alignment Scores:  
 Pred. No.: 1.4e-94  
 Score: 1258.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 98.67%  
 Length: 250  
 Matches: 229  
 Conservative: 0  
 Mismatches: 0  
 Indels: 0

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PF 29-JUN-2001; 2001WO-US21066.
XX 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-074725P.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX (GENE) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
DR N-PSDB; ABK33628.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
XX
PS Claim 11; Figure 166; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumours, especially lung
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation or differentiation of chondrocyte cells, for stimulating
XX the release of tumour necrosis factor-alpha from human blood,
XX for stimulating or inhibiting the proliferation of normal human dermal
XX fibroblast cells. The PRO polypeptide may also be used as molecular
XX weight markers and for tissue typing. The PRO nucleic acids have
XX applications in molecular biology, including use as hybridisation probes,
XX and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
XX protein sequences of the invention.
XX
SQ Sequence 250 AA:

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## Alignment Scores:

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Pred. No.: 1,4e-94 Length: 250
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.67% Indels: 0
DB: 23 Gaps: 0

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US-09-856-320a-1\_COPY\_272\_958 (1-687) x AAU83684 (1-250)

```

QY 1 ATATCAAGGGGTTGAGTCAAGACCTCACTCCAGCCCTGGAGGAGGAGCCCTGTTGAG 60
    |||||||
DB 22 IletlelysglypneglucylsyrhoHisserGlnProtrpGlnAlaIalaLeuPheGlu 41
    |||||||
QY 61 AAGACGGGCTACTCTGTGGGCGAGCGCTATCGCCCGCCAGATGGCTCTGACAGGAGCC 120
    |||||||

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DB 42 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 61
    |||||||
QY 121 CACTGCGCTCAAGCCCGCTATCATGTTACCTGGGGAGAGACAACTCCGAAGGAGGAG 180
    |||||||
DB 62 HisCysLeuLysProArgTrpIleValHisLeuIleGlnHisAsnLeuGlnLysGlnGlu 81
    |||||||
QY 181 GCGTGTGAGCAGACCCCGAGCCAGCCATGAGTCTCTCCCGCCAGCCGCTTCAACACAGC 240
    |||||||
DB 82 GLYcysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlnPheAsnAsnSer 101
    |||||||
QY 241 CTCCCGCAACAAGACCAACCGCATGACATCATGCTGTGTAAGATGGCATGGCCAGCTTC 300
    |||||||
DB 102 LeuProAsnLysAspHisAspHisAspHisAspHisAspHisAspHisAspHisAspHis 121
    |||||||
QY 301 ATCACAGGGGCTGGGAGCCCTCAGCCCTCCGCTCCAGCGTGTGCTGCTGCTGCTGCTG 360
    |||||||
DB 122 IletThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 141
    |||||||
QY 361 TGCCCTCATTTCCGGCTGGGAGCAGCAGCCCTCCAGCCCGCTGAGCTGCTGCTGCTGCTG 420
    |||||||
DB 142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161
    |||||||
QY 421 CGATGCGCCCAACATCATCATCATTTGAGCACCAGAGTGTGAGAAAGCCCTACCCCGGAC 480
    |||||||
DB 162 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyProGlnLys 181
    |||||||
QY 481 ATCACAGACACCATGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
    |||||||
DB 182 IletThrAspThrMetValCysAlaSerValGlnGlnLysGlnLysAspSerCysGlnGly 201
    |||||||
QY 541 GACTCCGGGGGCGCTGTGTGTGTGTACCACTCTCTTCAAGGATATCTCTGGGGCCAG 600
    |||||||
DB 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGln 221
    |||||||
QY 601 GATCCGCTGCGATCACCCGAAAGCCCTGCTGTACACGAAAGTCTGCAATATGTGGAG 660
    |||||||
DB 222 AspProCysAlaIleThrArgLysProGlyValThrLysValCysLysTyValAsp 241
    |||||||
QY 661 TGGATCCAGGAGAGCATGATGAACAAT 687
    |||||||
DB 242 TrpLeuGlnLysThrMetLysAsnAsn 250
    |||||||
RESULT 10
ABU66822 standard; Protein: 250 AA.
ID ABU66822;
XX
XX ABU66822;
AC 23-MAY-2003 (first entry)
XX
XX Human PRO polypeptide #253.
DE
XX
XX Human: PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder;
KW cytosolic.
XX
XX Homo sapiens.
OS
XX
XX US2003036180-A1.
PN
XX
XX 20-FEB-2003.
PD
XX
XX 09-MAY-2002; 2002US-0143114.
PF
XX
XX 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.

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PR 14-SEP-1998; 98WO-US19177.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 29-OCT-1998; 98WO-US22991.  
 PR 29-OCT-1998; 98WO-US22992.  
 PR 20-NOV-1998; 98WO-US24855.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 08-JAN-1999; 99WO-US00106.  
 PR 05-MAR-1999; 99WO-US05028.  
 PR 10-MAR-1999; 99WO-US05190.  
 PR 20-APR-1999; 99WO-US08615.  
 PR 14-MAY-1999; 99WO-US10733.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 05-OCT-1999; 99WO-US21547.  
 PR 29-NOV-1999; 99WO-US23089.  
 PR 30-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 02-DEC-1999; 99WO-US28534.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 22-DEC-1999; 99WO-US30720.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05746.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07533.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 22-JUN-2001; 2001WO-US20116.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-FEB-2001; 2001US-0796498.

PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 18-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 05-JUN-2001; 2001US-0874503.  
 PR 14-JUN-2001; 2001US-0882636.  
 PR 19-JUN-2001; 2001US-0886342.  
 PR 21-JUN-2001; 2001US-0887879.  
 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.  
 PR XX  
 PR PA (GENENTECH INC.)  
 PR XX  
 PR PI Baker KP, Beresini M, DePorge L, Desnoyers L, Filvaroff E, Gao W;  
 PR PI Gerritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S;  
 PR PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 PR XX WPI; 2003-332040/31.  
 PR DR N-PSDB; ACA03855.  
 PR XX  
 PR PT New secreted and transmembrane PRO nucleic acids, useful for gene  
 PR PT therapy, in chromosome and gene mapping, as chromosome markers, in  
 PR PT tissue typing, and in chromosome identification  
 PR XX  
 PR PS Claim 12; Fig 506; 660pp; English.

CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The  
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for  
 CC linking bioactive molecules to cells expressing PRO polypeptides,  
 CC for modulating biological activities of cells expressing PRO  
 CC polypeptides, and for identifying agonists or antagonists.  
 CC The PRO polypeptides are useful for stimulating the release of  
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating  
 CC the proliferation or differentiation of chondrocytes, and detecting the  
 CC presence of tumours. The polynucleotide sequences encoding PRO  
 CC polypeptides are useful as hybridisation probes, in chromosome and  
 CC gene mapping, in the generation of antisense RNA and DNA, in the  
 CC preparation of PRO polypeptides, for generating transgenic animals or  
 CC knockout animals, for the genetic analysis of individuals with genetic  
 CC disorders, and in gene therapy. AB06570-AB066844 represent the human  
 CC PRO polypeptides of the invention.  
 CC Note: The sequence data for this patent was obtained in electronic  
 CC format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipdsidentity.html.  
 CC XX

Sequence 250 AA:

Alignment Scores:  
 Pred. No.: 1,4e-94 Length: 250  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.67% Indels: 0  
 DB: 24 Gaps: 0

US-09-856-320A-1\_COPY\_272\_958 (1-687) x AB066822 (1-250)

OY 1 ATCATCAGAGGATTTCGAGTGCAGGCTCCAGCCCTGAGAGCCCTGTTCGAG 60  
 DB 22 Tlletlelysglypnehlucylslystrhltserglnprrtppglnalalaaleupheleu 41  
 OY 61 AAGACGCGGCTACTCTGTGTGGGCGACGCTCATCGCCCCAGATGAGCTTCGTACAGCAGCC 120

Db 42 LysThrIleuLeuLysGlyAlaThrIleLeuIleAlaProArgTrpLeuThrAlaIa 61  
QY 121 CACTGCTCAAGCCCGCTACATAGTTACCTGGGGAGCAGCAACCTCCAGAGAGAG 180  
Db 62 HisCysLeuLysProArgTrpIleValHisLeuLysIleHisAsnLeuGlnGlu 81  
QY 181 GCGTGTAGCAGACCCGAGCAGCCAGTACGTCTCCCGCCCGGCTTCAACAGC 240  
Db 82 GlySerGluGlnThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 101  
QY 241 CTCCCAAGAGAGCAGCCAGATGATGATGCTGGGAGATGGATGGATGGATGG 300  
Db 102 LeuProAsnLysAspHisAlaGlnAspIleMetLeuValLysMetAlaSerProValSer 121  
QY 301 ATCACTGGGCTGTGAGACCCCTGACCTCTCTCAAGCTGTCTCACTGTGAGCAGC 360  
Db 122 IleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgValThrAlaGlyThrSer 141  
QY 361 TGCTCATTTCCGGCTGGGGAGCAGCTCCAGCCCAAGTTACGCTGGCTCAACCTTG 420  
Db 142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161  
QY 421 CGATGCGGCAACATCACCATCATTTAGAGACAGAGAGTGTGAGAGGCTACCCGGGAGC 480  
Db 162 ArgCysAlaAsnIleThrIleLeuGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn 181  
QY 481 ATCAAGAGACACATGATGTGTGAGCAGCTGAGAGAGAGAGAGAGAGAGAGAGAG 540  
Db 182 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 201  
QY 541 GACGCCGGGGCCCTCGGTGTGTACACAGTCTTTCAAGCATTAATCTCTGGGCGCAG 600  
Db 202 AsperGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221  
QY 601 GATCGCTGTGAGTACCCGAGAGCTGTGCTGTACAGAGAGTCAATATATGTGGAG 660  
Db 222 AsproCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpValAsp 241  
QY 661 TGGATCCAGGAGAGATGAGAGACAT 687  
Db 242 TrpIleGlnIleuThrMetLysAsnAsn 250  
RESULT 11  
ABU67098  
ID ABU67098 standard; Protein: 250 AA.  
XX  
AC ABU67098;  
XX  
DF 27-MAY-2003 (first entry)  
XX  
DE Human secreted/transmembrane, PRO, protein SEQ ID 506.  
XX  
KW Human; secreted protein; transmembrane protein; PRO;  
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
KW infertility; birth defects; premature aging; AIDS; biosensor;  
KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
KW bioreactor; tumour.  
XX  
OS Homo sapiens.  
XX  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PF 03-MAY-2002; 2002US-0137865.  
XX  
PR 31-MAR-1997; 97WO-US05230.  
PR 12-JUN-1998; 98WO-US12456.  
PR 14-JUL-1998; 98WO-US14552.  
PR 28-AUG-1998; 98WO-US17888.  
PR 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19093.

PR 14-SEP-1998; 98WO-US19094.  
PR 14-SEP-1998; 98WO-US19177.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 29-OCT-1998; 98WO-US22991.  
PR 29-OCT-1998; 98WO-US22992.  
PR 20-NOV-1998; 98WO-US24855.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 98WO-US25106.  
PR 08-MAR-1999; 98WO-US25028.  
PR 10-MAR-1999; 98WO-US25190.  
PR 20-APR-1999; 98WO-US208615.  
PR 14-MAY-1999; 98WO-US10733.  
PR 02-JUN-1999; 98WO-US12252.  
PR 01-SEP-1999; 98WO-US20111.  
PR 08-SEP-1999; 98WO-US20594.  
PR 13-SEP-1999; 98WO-US20944.  
PR 15-SEP-1999; 98WO-US21090.  
PR 15-SEP-1999; 98WO-US21547.  
PR 05-OCT-1999; 98WO-US23089.  
PR 29-NOV-1999; 98WO-US28214.  
PR 30-NOV-1999; 98WO-US28313.  
PR 30-NOV-1999; 98WO-US28409.  
PR 01-DEC-1999; 98WO-US28301.  
PR 01-DEC-1999; 98WO-US28634.  
PR 02-DEC-1999; 98WO-US28551.  
PR 02-DEC-1999; 98WO-US28564.  
PR 02-DEC-1999; 98WO-US28565.  
PR 16-DEC-1999; 98WO-US30095.  
PR 20-DEC-1999; 98WO-US30911.  
PR 20-DEC-1999; 98WO-US30999.  
PR 22-DEC-1999; 98WO-US30720.  
PR 30-DEC-1999; 98WO-US31243.  
PR 30-DEC-1999; 98WO-US31274.  
PR 05-JAN-2000; 98WO-US300219.  
PR 06-JAN-2000; 98WO-US300277.  
PR 06-JAN-2000; 98WO-US30376.  
PR 11-FEB-2000; 98WO-US30365.  
PR 18-FEB-2000; 98WO-US04341.  
PR 18-FEB-2000; 98WO-US04342.  
PR 22-FEB-2000; 98WO-US04414.  
PR 24-FEB-2000; 98WO-US04914.  
PR 24-FEB-2000; 98WO-US05004.  
PR 01-MAR-2000; 98WO-US05601.  
PR 02-MAR-2000; 98WO-US05746.  
PR 02-MAR-2000; 98WO-US05841.  
PR 10-MAR-2000; 98WO-US06319.  
PR 15-MAR-2000; 98WO-US06884.  
PR 20-MAR-2000; 98WO-US07377.  
PR 21-MAR-2000; 98WO-US07532.  
PR 30-MAR-2000; 98WO-US08439.  
PR 17-MAY-2000; 98WO-US13705.  
PR 22-MAY-2000; 98WO-US14042.  
PR 30-MAY-2000; 98WO-US14941.  
PR 02-JUN-2000; 98WO-US15264.  
PR 28-JUL-2000; 98WO-US220710.  
PR 11-AUG-2000; 98WO-US22031.  
PR 23-AUG-2000; 98WO-US23522.  
PR 24-AUG-2000; 98WO-US23328.  
PR 08-NOV-2000; 98WO-US30952.  
PR 10-NOV-2000; 98WO-US30873.  
PR 01-DEC-2000; 98WO-US32678.  
PR 20-DEC-2000; 98WO-US34956.  
PR 28-FEB-2001; 98WO-US06520.  
PR 01-MAR-2001; 98WO-US06566.  
PR 25-MAY-2001; 98WO-US17092.  
PR 01-JUN-2001; 98WO-US17800.  
PR 22-JUN-2001; 98WO-US19692.  
PR 22-JUN-2001; 98WO-US20116.  
PR 29-JUN-2001; 98WO-US21066.  
PR 09-JUL-2001; 98WO-US21735.  
PR 20-DEC-2000; 98WO-US21735.  
PR 20-DEC-2000; 98WO-US21735.

PR 28-FEB-2001; 2001US-0796498.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 18-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 05-JUN-2001; 2001US-0874503.  
 PR 14-JUN-2001; 2001US-0882636.  
 PR 19-JUN-2001; 2001US-0885342.  
 PR 21-JUN-2001; 2001US-0887879.  
 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR N-PSDB: ACN04276.  
 PI WPI: 2003-331925/31.  
 PT New secreted and transmembrane nucleic acids and polypeptides,  
 PT designated as PRO, useful for treating inflammation, organ failure,  
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature  
 PT aging, AIDS, or cancer -  
 XX  
 PS Claim 12; Fig 506; 659pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising, or which is  
 CC at least 80% identical to, or the full-length coding sequence of, any of  
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide  
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid  
 CC further comprises the full-length coding sequence of the DNA deposited  
 CC under American Type Culture Collection (ATCC) accession number in a list  
 CC given in the specification. Also included are vectors and host  
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO  
 CC antibodies, PRO extracellular domains and mature sequences, methods  
 CC of detecting PRO proteins, methods for stimulating the release of  
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,  
 CC (and the proliferation of differentiation of chondrocyte cells, the  
 CC proliferation of, or gene expression in pericyte cells, the release or  
 CC proteoglycans from cartilage, proliferation of inner ear utricular  
 CC supporting cells, the proliferation of T-lymphocyte cells, the release  
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the  
 CC proliferation of endothelial cells), a method for modulating the uptake  
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,  
 CC a method for inhibiting the binding of A-peptide to factor VIIA,  
 CC or the differentiation of adipocyte cells, a method for detecting the  
 CC presence of a tumour in a mammal and an oligonucleotide probe derived  
 CC from any of the nucleotide sequences cited above. The nucleic acids and  
 CC polypeptides are useful for treating inflammatory diseases, organ  
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,  
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or  
 CC diabetic complications. The nucleic acids are useful as hybridisation  
 CC probes, in chromosome and gene mapping, and in generating antisense RNA  
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors. Both are useful in tissue typing.  
 CC The present sequence represents a PRO protein of the invention.  
 XX  
 SQ Sequence 250 AA:  
 Alignment Scores:  
 Pred. No.: 1,4e-94 Length: 250  
 Score: 1258.00 Matches: 229

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.67% Indels: 0  
 DB: 24 Gaps: 0  
 US-09-856-320A-1\_COPY\_272\_958 (1-687) x ABU67098 (1-250)  
 QY 1 ATCATCAAGGCGTGTGAGTGAAGCCCTCACTCCAGCCCTGACAGGACCGTGTGAG 60  
 Db |||||||  
 QY 22 IIEIIEIYSGLYPHEIIEIYSGLYSPROHISSEIIEIIEIIEIIEIIEIIEIIEIIEIIEI 41  
 Db |||||||  
 QY 61 AAGAGCGGCTACTGTGTGGGCGAGCTCATGCGCCCGAGATGCTCTGACAGAGCC 120  
 Db |||||||  
 QY 42 LYSTHRTARGLEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEI 61  
 Db |||||||  
 QY 121 CAGTGGCTCAAGCCCGGTACATAGTCAACCGGGGACACACACCTCCAGAGAGGAG 180  
 Db |||||||  
 QY 62 HISCYSLEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEI 81  
 Db |||||||  
 QY 181 GCGTGTGACAGACCCGAGACCCCACTGACCTCCCGCCGCTTCAACAGACAGC 240  
 Db |||||||  
 QY 82 GLYCYSGLIUGINTHTARGHRTALHRTGUSERPHEPROHISPROGLYPHEIIEIIEIIEI 101  
 Db |||||||  
 QY 241 CTCCCCACAAAGACCCGCAATGACATCATGTGTGAGATGGCATGCCAGTCTCC 300  
 Db |||||||  
 QY 102 LEUPROASNLYASPHISARGASNAPRIEMETLEIIEIIEIIEIIEIIEIIEIIEIIEIIEI 121  
 Db |||||||  
 QY 301 ATCACCCTGGGCTGTGCGAGCCCTCACCCCTCTCACTGTGTGACCTGTGACAGC 360  
 Db |||||||  
 QY 122 IIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEI 141  
 Db |||||||  
 QY 361 TGCCTCATTTCCGGCTGGGCGAGACGTCACCCCGCATGTCGCTGCTGACAGCTTG 420  
 Db |||||||  
 QY 142 CYSLIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEI 161  
 Db |||||||  
 QY 421 CGATGCGCCACATCATCATCATGACACCGAAGTGTGAGACCGCTTACCCCGGCAAC 480  
 Db |||||||  
 QY 162 ARGYSALIASNIETHTRIETIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEI 181  
 Db |||||||  
 QY 481 ATCAGACACCATGCTGTGTGCGAGCCGCGAGAGAGGCGCAAGAGCTCTGCCAGGT 540  
 Db |||||||  
 QY 182 IIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEI 201  
 Db |||||||  
 QY 541 GACTCGGGGGGCGCTGTGTGTATACAGTCTCTTCAAGCATATCTCTGGGGCCAG 600  
 Db |||||||  
 QY 202 ASPSERGLYGLYPROLEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEI 221  
 Db |||||||  
 QY 601 GATCGGTGTGATCATCCGGAAGCTGTGTACACGAAAGTGTGCAATATGTGAGC 660  
 Db |||||||  
 QY 222 ASPPROCYSAIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEI 241  
 Db |||||||  
 QY 661 TGGATCCAGGAGAGCATGAGAACAT 687  
 Db |||||||  
 QY 242 TPIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEIIEI 250  
 Db |||||||  
 RESULT 12  
 ABU59903  
 ID ABU59903 standard; Protein: 250 AA.  
 XX  
 AC ABU59903;  
 XX  
 DT 13-MAY-2003 (first entry)  
 XX  
 DE Novel secreted and transmembrane protein PRO1279.  
 XX  
 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disorder;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;

KW	dementia; hepatitis; Crohn's disease; chondrocyte proliferation;
KM	chondrocyte redifferentiation; sports injury; arthritis.
XX	
OS	Homo sapiens.
XX	
PN	US2003017563-A1.
XX	
PD	
XX	
XX	23-JAN-2003.
PF	
PE	07-MAY-2002; 2002US-0140808.
XX	
XX	31-MAR-1997; 97WO-US05230.
PR	12-JUN-1998; 98WO-US12456.
PR	14-JUL-1998; 98WO-US14552.
PR	28-AUG-1998; 98WO-US17888.
PR	10-SEP-1998; 98WO-US18824.
PR	14-SEP-1998; 98WO-US19093.
PR	14-SEP-1998; 98WO-US19094.
PR	14-SEP-1998; 98WO-US19177.
PR	16-SEP-1998; 98WO-US19330.
PR	17-SEP-1998; 98WO-US19437.
PR	07-OCT-1998; 98WO-US21141.
PR	29-OCT-1998; 98WO-US22992.
PR	29-OCT-1998; 98WO-US22992.
PR	20-NOV-1998; 98WO-US24855.
PR	01-DEC-1998; 98WO-US25108.
PR	05-JAN-1999; 99WO-US00106.
PR	08-MAR-1999; 99WO-US05028.
PR	10-MAR-1999; 99WO-US05190.
PR	20-APR-1999; 99WO-US06815.
PR	14-MAY-1999; 99WO-US10733.
PR	02-JUN-1999; 99WO-US12252.
PR	01-SEP-1999; 99WO-US20111.
PR	08-SEP-1999; 99WO-US20594.
PR	13-SEP-1999; 99WO-US20944.
PR	15-SEP-1999; 99WO-US21090.
PR	15-SEP-1999; 99WO-US21547.
PR	05-OCT-1999; 99WO-US23089.
PR	29-NOV-1999; 99WO-US28214.
PR	30-NOV-1999; 99WO-US28313.
PR	30-NOV-1999; 99WO-US28409.
PR	01-DEC-1999; 99WO-US28301.
PR	01-DEC-1999; 99WO-US28634.
PR	02-DEC-1999; 99WO-US28551.
PR	02-DEC-1999; 99WO-US28654.
PR	16-DEC-1999; 99WO-US30095.
PR	20-DEC-1999; 99WO-US30911.
PR	20-DEC-1999; 99WO-US30999.
PR	22-DEC-1999; 99WO-US30720.
PR	30-DEC-1999; 99WO-US31243.
PR	30-DEC-1999; 99WO-US31274.
PR	05-JAN-2000; 2000WO-US00219.
PR	06-JAN-2000; 2000WO-US00277.
PR	06-JAN-2000; 2000WO-US00736.
PR	11-FEB-2000; 2000WO-US03565.
PR	18-FEB-2000; 2000WO-US04341.
PR	22-FEB-2000; 2000WO-US04342.
PR	24-FEB-2000; 2000WO-US04414.
PR	24-FEB-2000; 2000WO-US04514.
PR	01-MAR-2000; 2000WO-US05004.
PR	02-MAR-2000; 2000WO-US05601.
PR	02-MAR-2000; 2000WO-US05746.
PR	10-MAR-2000; 2000WO-US05641.
PR	15-MAR-2000; 2000WO-US06884.
PR	20-MAR-2000; 2000WO-US07337.
PR	21-MAR-2000; 2000WO-US07532.
PR	30-MAR-2000; 2000WO-US08439.
PR	17-MAY-2000; 2000WO-US13705.
PR	22-MAY-2000; 2000WO-US14042.
PR	30-MAY-2000; 2000WO-US14941.
PR	02-JUN-2000; 2000WO-US15264.

28-JUL-2000; 2000MO-US20710.  
PR 11-AUG-2000; 2000MO-US22031.  
PR 23-AUG-2000; 2000MO-US23522.  
PR 24-AUG-2000; 2000MO-US23328.  
PR 08-NOV-2000; 2000MO-US30952.  
PR 10-NOV-2000; 2000MO-US30873.  
PR 01-DEC-2000; 2000MO-US32678.  
PR 20-DEC-2000; 2000MO-US34956.  
PR 28-FEB-2001; 2001MO-US06520.  
PR 01-MAR-2001; 2001MO-US06656.  
PR 25-MAY-2001; 2001MO-US17092.  
PR 01-JUN-2001; 2001MO-US17800.  
PR 20-JUN-2001; 2001MO-US19692.  
PR 22-JUN-2001; 2001MO-US20116.  
PR 29-JUN-2001; 2001MO-US21066.  
PR 09-JUL-2001; 2001MO-US21735.  
PR 20-DEC-2000; 2000MO-US074259.  
PR 28-FEB-2001; 2001MO-US076498.  
PR 09-MAR-2001; 2001MO-US072706.  
PR 14-MAR-2001; 2001MO-US086859.  
PR 22-MAR-2001; 2001MO-US0816744.  
PR 05-APR-2001; 2001MO-US0828366.  
PR 10-MAY-2001; 2001MO-US0854280.  
PR 18-MAY-2001; 2001MO-US0854280.  
PR 25-MAY-2001; 2001MO-US0860216.  
PR 25-MAY-2001; 2001MO-US0866028.  
PR 01-JUN-2001; 2001MO-US0872035.  
PR 05-JUN-2001; 2001MO-US0874503.  
PR 14-JUN-2001; 2001MO-US0882636.  
PR 19-JUN-2001; 2001MO-US0886342.  
PR 21-JUN-2001; 2001MO-US0887879.  
PR 18-JUL-2001; 2001MO-US0908827.  
PR 06-AUG-2001; 2001MO-US0924419.  
PR 09-AUG-2001; 2001MO-US0927796.  
PR 16-AUG-2001; 2001MO-US0931836.  
PR 19-DEC-2001; 2001MO-US0028072.  
  
(GETH ) GENENTECH INC.  
  
BAKER KP, Bersini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
PI Geritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S;  
PI Smith V, Stewart Th, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX WPI: 2003-148238/14.  
DR N-PSDB: ABX893933.  
  
Claim 12; Fig 506; 659pp: English.  
  
The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126, PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancers tumors. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumor growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO1312 enhance survival of retinal neurons cells (PRO1312 is also enhances survival/proliferation of



rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosa, AMD, PRO819, PRO813 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpeticiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein.

Sequence 250 AA:

Alignment Scores:  
 Pred. No.: 1,4e-94 Length: 250  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.67% Indels: 0  
 DB: 24 Gaps: 0

US-09-856-320A-1\_COPY\_272\_958 (1-687) x ABUS59903 (1-250)

1 ATCATCAAGGGGTGGAGTGCAGAGCTTCCAGCCCTGGCAGGAGCCCTGTTCAG 60  
 22 ILEILEYSGLYPHEGLUCYSYSPRONHISSEGINPROTGELALALALEUPHEGL 41  
 61 AAGACGGCGCTACTGTGGGCGAGCGTCATCGCCCGAGATGGCTCTGACAGAGCC 120  
 42 LYSTHARGLEULEUCSGLYALATHRIEULIEALAPROALGTIRLEULATHRIAL 61  
 121 CACTGCTCAGACCCCGCTACTAGTCACTGGGCGAGACACACCTCCAGAGAGAG 180  
 62 HISCYSLEULYSPROALGTITYLEVALHISLEUGLHNASLEULINLSGLUGLI 81  
 181 GGCTGTGAGCAGACCCGCGAGCAGCTGAGTCTCCCGCCCGGCTCAACAAGAGC 240  
 82 GLYCSGLUGLINTHARGTHALATHRGUSERPHEPRONHISPROGLYPHENSANBSER 101  
 241 CTCGCCAACAAAGACACCCGCAATGACATCATGTGTGAGAGATGGCATCGCCAGTCC 300  
 102 LEUPROANLYSAPRHISARGSNASPRILEMETLEVALLYMETALASERPROVALSER 121  
 301 ATCAGCTGGGCTGCGAGCCCTCAGCCCTCTCAGCTGTGTACATGCTGGCAGCAGC 360  
 122 ILETHRTPALAVALARGPROLEUTHRIEUSERSERATGYSVALTHRALAGLYTHRSE 141  
 361 TGCCCTATTCCGGCTGGGCGAGCAGTCCAGCCCGGCTGAGCTGCTCACACCTTG 420  
 142 CYSLEULIESERGLYTRPGLYSERTHRSESRPROGLINLEUARGLEUPROHISTHRI 161  
 421 CGATGCGCAACATCATCATCATGTGAGCAGCAGAGTGTGAGAGAGCGCTACCCGCGAAC 480  
 162 ARGYSALANILLETHTRIEULINHSGLINLSCYSGLIANASALATYRPROGLYSEN 181  
 481 ATCAGACAGACCATGCTGTGCGAGCTGCGAGAGAGGGGCGAGAGACTCTGCCAGG 540  
 182 ILETHRTAPTHMETVALCYSALASERVALINGLUGLYLYASPERCYSGINGLY 201  
 541 GACTCGGGGGGCGCTGTGTGTGTAACAGTCTCTTCAAGGATATATCTCGGGGCGAG 600  
 202 ASPSERGLYGLYPROLEUVALCYSANGLINSERLINGLYLILESERTIRPGLYGIN 221  
 601 GATCGGTGCGATCAGCCGAGAGCGTGTCTACAGAGAGTGTGCAATATATGAGAG 660  
 222 ASPROCYSALALILETHRTARGLYSPROGLYVALITYRTHLYSVALCYLALYSTYRVALASP 241  
 661 TGGATCCAGGAGCAGATGAAGAACAAT 687  
 242 TRPILEGINGLUTHRMETLYSASNASN 250

RESULT 13  
 ABUS6739

ID ABUS6739 standard; Protein; 250 AA.  
 XX  
 AC ABUS6739;  
 XX  
 DT 02-APR-2003 (first entry)  
 XX  
 XX Lung cancer-associated polypeptide #332.  
 XX  
 DE Lung cancer-associated polypeptide; cytosolic; emphysema;  
 XX antiinflammatory; antiasthmatic; non-small cell lung cancer;  
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
 XX  
 XX Unidentified.  
 OS  
 XX WO200286443-A2.  
 PN  
 XX 31-OCT-2002.  
 PD  
 XX 18-APR-2002; 2002WO-US12476.  
 PF  
 XX 18-APR-2001; 2001US-284770P.  
 PR 10-MAY-2001; 2001US-290492P.  
 PR 09-NOV-2001; 2001US-339245P.  
 PR 13-NOV-2001; 2001US-350666P.  
 PR 29-NOV-2001; 2001US-334370P.  
 PR 12-APR-2002; 2002US-372246P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 PI  
 XX A212 N, Murray R;  
 PI  
 XX WPI: 2003-093161/08.  
 DR N-PSDB; ABX76468.  
 DR  
 XX  
 PT Detecting a lung cancer-associated transcript in a cell from a patient  
 PT for treating lung cancer, by contacting a biological sample from the  
 PT patient with a polynucleotide that exhibits increased or decreased  
 PT expression in lung cancer -  
 XX  
 PS Claim 27; Page 443-444; 453pp; English.  
 XX  
 CC The invention relates to a method for detecting a lung cancer-associated  
 CC transcript in a cell from a patient, comprising contacting a biological  
 CC sample from the patient with a polynucleotide that selectively hybridises  
 CC to a sequence that is at least 80 % identical to a gene that exhibits  
 CC increased or decreased expression in lung cancer samples. Lung  
 CC cancer-associated polynucleotides and polypeptides are used for  
 CC identifying a compound that modulates a lung cancer-associated  
 CC polypeptide, for inhibiting proliferation of a lung cancer-associated  
 CC cell to treat lung cancer in a patient and for treating a mammal having  
 CC lung cancer by administering a modulatory compound identified. The  
 CC methods are useful for treating lung cancer, such as small cell lung  
 CC cancer, non-small cell lung cancer or other benign or precancerous  
 CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive  
 CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial  
 CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides  
 CC and polypeptides are useful for diagnostic purposes and as targets for  
 CC screening for therapeutic compounds that modulate lung cancer, such as  
 CC antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated  
 CC polypeptides of the invention.  
 XX

SO Sequence 250 AA:  
 Alignment Scores:  
 Pred. No.: 1,4e-94 Length: 250  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.67% Indels: 0  
 DB: 24 Gaps: 0

US-09-856-320a-1\_COPY\_272\_958 (1-687) x ABUS6739 (1-250)

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 Db 22 IletlleysglpHeiglucysLysProHissersinProtrpglnAlaIaleuPheglu 41  
 QY 61 AAGACGGGGCTACTCTGTGGGGCCAGCTATGCCCGCCAGATGGCTCTGACAGCACC 120  
 Db 42 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 61  
 QY 121 CACTGCTCAAGCCCGCTACATGATGTCACCTGGGGAGCAGCACTCCAGAGAGAG 180  
 Db 62 HisCysLeuLysProArgTrpIleValHisLeuGlyInHisAsnLeuGlnLysGln 81  
 QY 181 GCGTGTAGCAGACCCGCGAGACCCAGCTAGCTCTTCCCGCCAGCCGCTTCAACAGC 240  
 Db 82 GlyLysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 101  
 QY 241 CTCCCAACAAAGCCAGCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 Db 102 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 121  
 QY 301 ATCACTGGGCTGGCAGCCCTCAGCTCTCCTCAGCTGTGTGACCTGGGAGCAGC 360  
 Db 122 IleThrTrpAlaValAlaGProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 141  
 QY 361 TGCCCTCATTTCCGGCTGGGGAGCAGCAGCTCCAGCCCGAGTTACGCTGGCTCAGACCTTG 420  
 Db 142 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 161  
 QY 421 CGATGCGCCCAACATCACCATTGATGACACCCAGAAAGTGTGAGAACGGCTACCCCGGCAAC 480  
 Db 162 ArgCysAlaAsnIleThrIleLeuGlnHisGlnLysCysGlnAsnAlaTrpProGlyAsn 181  
 QY 481 ATCAAGACACCATGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
 Db 182 IleThrAspThrMetValCysAlaSerValGlnLysLysAspSerCysGlnGly 201  
 QY 541 GACTCCGGGGCCCTGT 600  
 Db 202 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 221  
 QY 601 GATCCGCTGGGATGACCCGAAAGCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660  
 Db 222 AspProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysTrpValAsp 241  
 QY 661 TGGATCCAGGAGACGATGAAGAACAT 687  
 Db 242 TrpIleGlnIleThrMetLysAsnAsn 250

RESULT 14  
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 ID AAY42439 standard; Protein; 282 AA.  
 XX  
 AC AAY42439;  
 XX  
 DT 08-DEC-1999 (first entry)  
 XX  
 DE CASB12 amino acid sequence.  
 XX  
 KW neuropsin; cancer; assay; inhibitor; serine protease; immunogenic;  
 KW autoimmune disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO9949055-A1.  
 XX  
 PD 30-SEP-1999.  
 XX  
 PF 17-MAR-1999; 99WO-EP01894.  
 XX  
 PR 20-MAR-1998; 98GB-0006095.  
 XX

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Bruck CEM, Cassart J, Coche T, Vinals-Bassols C;  
 XX  
 DR WPI: 1999-580450/49.  
 DR N-PSDB: AA222638.  
 XX  
 FT New human serine protease CASB12, for treatment, prevention and  
 PT diagnosis of cancer and autoimmune diseases  
 XX  
 PS Claim 3; Page 48; 58pp; English.  
 XX  
 CC This is the amino acid sequence of the CASB12 protein. The nucleotide  
 CC sequence of AA222638 shows homology with neuropsin and the encoded  
 CC protein AAY42439 is structurally related to other proteins of the  
 CC serine protease family, having homology and/or structural similarity  
 CC with neuropsin. It is expected that as well as similar structure, these  
 CC proteins will also share similar biological functions and properties.  
 CC The CASB12 polypeptides and polynucleotides can be used to develop  
 CC methods for identifying agonists and antagonists/inhibitors of these  
 CC molecules, and thereby treating conditions associated with CASB12  
 CC polypeptide imbalance. The invention also provides for diagnostic assays  
 CC for detecting diseases associated with inappropriate CASB12 polypeptide  
 CC activity or levels.  
 CC Since CASB12 is either specifically expressed or highly over-expressed  
 CC in tumors compared to normal cells, the polypeptides and polynucleotides  
 CC of the invention are believed to be important immunogens for specific  
 CC prophylactic or therapeutic immunization against tumors. The  
 CC polypeptides and polynucleotides can therefore be targeted by antigen  
 CC specific immune reactions (which result in the destruction of the tumor  
 CC cell) or they can be used to diagnose the occurrence of tumor cells  
 XX  
 S0 Sequence 282 AA;  
 S0

Alignment Scores:  
 Pred. No.: 1,43e-94 Length: 282  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 98.67% Indels: 0  
 DB: Gaps: 0

US-09-856-320a-1\_COPY\_272\_958 (1-687) x AAY42439 (1-282)

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 QY 61 AAGACGGGGCTACTCTGTGGGGCCAGCTATGCCCGCCAGATGGCTCTGACAGCACC 120  
 Db 74 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAla 93  
 QY 121 CACTGCTCAAGCCCGCTACATGATGTCACCTGGGGAGCAGCACTCCAGAGAGAG 180  
 Db 94 HisCysLeuLysProArgTrpIleValHisLeuGlyInHisAsnLeuGlnLysGln 113  
 QY 181 GCGTGTAGCAGACCCGCGAGACCCAGCTAGCTCTTCCCGCCAGCCGCTTCAACAGC 240  
 Db 114 GlyLysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 133  
 QY 241 CTCCCAACAAAGCCAGCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
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 Db 174 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 193  
 QY 421 CGATGCGCCCAACATCACCATTGATGACACCCAGAAAGTGTGAGAACGGCTACCCCGGCAAC 480

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|||||
Db 194 ArgCysAlaAsnIleThrIleIleGluHisGlnIlyScysGlnAsnIleAtyProGlyAsn 213
QY 481 ATCAGACAGACCATGGTGTGTGTCACAGCTGCAGAGAGGGGCAAGACTCTCCAGGGT 540
Db 214 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyAspSerCysGlnGly 233
QY 541 GACTCCGGGGCCCTCTGTGTGTAAACAGTCTTCAAGGCAATTATCTCTGGGGCCAG 600
Db 234 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 253
QY 601 GATCCGTGTGCATACCCGGAAGCCTGTGTCTACAGCAAAAGTCTGCAAAATGTGGAC 660
Db 254 AspProCysAlaIleThrArgIlySerProGlyValIlyThrIlyValCysIlyStyIlyValAsp 273
QY 661 TGGATCCAGAGACGATGAAGAACAT 687
Db 274 TrpIleGlnGluThrMetIlyAsnAsn 282

RESULT 15
AAB11712
ID AAB11712 standard; Protein; 282 AA.
AC AAB11712;
XX
XX
XX 23-OCT-2000 (first entry)
DE Human serine protease BSSP6 (hbSSP6) SEQ ID NO:2.
XX
XX BSSP6; serine protease; human; hbSSP6; mouse; mbSSP6; brain;
XX diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
XX epilepsy; cancer; inflammation; infertility; pancreatitis;
XX prostatic hypertrophy.
XX
XX Homo sapiens.
XX
XX WO200031257-A1.
XX
XX 02-JUN-2000.
XX
XX 19-NOV-1999; 99WO-JP06476.
XX
XX 20-NOV-1998; 98JP-0347802.
XX
XX (FUSO ) FUSO PHARM IND LTD.
XX
XX Uemura H, Okui A, Komihama K, Yamaguchi N, Mitsui S;
XX
XX MPI: 2000-400067/34.
XX
XX N-PSDB: AAA61763.
XX
XX Serine protease BSSP6, useful in detecting homologs, mutants and
XX polymorphic variants as markers for diagnosis of Alzheimer's disease,
XX epilepsy, cancer, inflammation, infertility and prostate hypertrophy,
XX using blood or other tissues.
XX
XX Claim 1; Page 69-70; 94pp; Japanese.
XX
XX The invention relates to novel serine proteases designated BSSP6
XX (AAB11712-111714), and to nucleic acids encoding them (AAA61763-61765).
XX The invention also relates to vectors and transformants comprising BSSP6
XX nucleic acids; transgenic animals in which the expression level of BSSP6
XX can be varied; and an mbSSP6 knockout mouse. The invention additionally
XX encompasses anti-BSSP6 antibodies and methods of production of such
XX antibodies, methods of BSSP6 detection using the antibodies, and the
XX use of BSSP6 proteins or fragments as diagnostic markers for certain
XX medical conditions. Nucleotides encoding BSSP6 were initially
XX isolated in a human brain cDNA library using degenerate PCR primers
XX (AAA61795-61796) based on conserved regions of serine proteases. The
XX BSSP6 serine proteases and nucleotides encoding them are useful in
XX detecting homologues, mutants and polymorphic variants in biological
XX samples (e.g., blood, urine, brain, prostate gland, placenta, testis
XX and spleen) as diagnostic markers for conditions such as Alzheimer's

```

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CC disease, epilepsy, cancer, inflammation, infertility and prostatic
CC hypertrophy. Sequences AAB11712 and AAB11714 represent human BSSP6
CC variants (hbSSP6), and sequence AAB11713 represents murine BSSP6
CC (mbSSP6).
XX
SQ Sequence 282 AA;
Alignment Scores:
Pred. No.: 1,43e-94 Length: 282
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Db 54 IleIleIlyGlyPheGlnCysIlySerProHisSerGlnProTrpGlnIleAlaIlePheGln 73
QY 61 AAGACGGGCTACTGTGTGGGGGAGCGTCATGCGCCCGAGATGGCTCCGAGAGAGCC 120
Db 74 LysThrArgLeuLeuGlyGlyAlaThrIleIleAlaProArgTrpLeuThrAlaAla 93
QY 121 CACTGCCTCAAGCCCGCTACATATGTTCACTTGGGGCAGACACAACTCCAGAGAGAG 180
Db 94 HisCysLeuIlySerProArgTrpIleValHisIleGlyGlnHisAsnIleGlnIlyGln 113
QY 181 GGTGTGAGACAGACCCGAGACAGCTAGTCTTCCCGCCCGGCTTCAACAACAGC 240
Db 114 GlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 133
QY 241 CTCGCCCAAGAACAGCACCGCAATGACATCATCTGTGAAGATGGCATGGCAGTCTCC 300
Db 134 LeuProHisIlyAspHisIlyAsnAspIleIleLeuValIlySerProValSer 153
QY 301 ATCACCTGGGCTGTGCGACCCCTCACCTCTCTCAAGCTGTGTCTCACTGTGGCAGCAG 360
Db 154 IleThrTrpAlaValArgProLeuThrIleSerSerArgCysValThrAlaGlyThrSer 173
QY 361 TGCCTCATTTCCGGCTGGGGCAGCAGCTCAGCCCGCAAGTACGCTGCCACACTTG 420
Db 174 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 193
QY 421 CGATGGCGCAACATCACCATTCATGAGCCAGAGTGAAGAGCGCTAACCCGGGCAC 480
Db 194 ArgCysAlaAsnIleThrIleIleGlnHisGlnIlyScysGlnAsnIleAtyProGlyAsn 213
QY 481 ATCAGACAGACCATGGTGTGTGTCACAGCTGCAGAGAGGGGCAAGACTCTCCAGGGT 540
Db 214 IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyAspSerCysGlnGly 233
QY 541 GACTCCGGGGCCCTCTGTGTGTAAACAGTCTTCAAGGCAATTATCTCTGGGGCCAG 600
Db 234 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 253
QY 601 GATCCGTGTGCATACCCGGAAGCCTGTGTCTACAGCAAAAGTCTGCAAAATGTGGAC 660
Db 254 AspProCysAlaIleThrArgIlySerProGlyValIlyThrIlyValCysIlyStyIlyValAsp 273
QY 661 TGGATCCAGAGACGATGAAGAACAT 687
Db 274 TrpIleGlnGluThrMetIlyAsnAsn 282

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GenCore version 5.1.6  
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Run on: October 15, 2003, 20:16:26 ; Search time 12.2679 Seconds  
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Title: US-09-856-320A-1\_COPY\_272\_958

Perfect score: 1275

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Maximum Match 100%

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6: /cgn2\_6/ptodata/2/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	1219.5	95.5	289	4	US-09-386-642-14
5	1182	92.7	228	4	US-09-205-258-1150
6	1182	92.7	246	4	US-09-205-258-1149
7	884	53.6	260	3	US-09-025-059-3
8	881	53.4	260	3	US-09-070-526-2
9	673	52.8	260	3	US-09-008-271A-7
10	671.5	52.7	288	4	US-09-386-642-13
11	644.5	50.5	293	4	US-09-996-243-309
12	597.5	46.9	268	2	US-08-824-874-1

13	597.5	46.9	268	3	US-09-210-084-1	Sequence 1, Appl1
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15	591.5	46.4	263	2	US-08-790-137-4	Sequence 4, Appl1
16	591.5	46.4	263	2	US-08-824-874-5	Sequence 5, Appl1
17	591.5	46.4	263	3	US-08-807-151-5	Sequence 5, Appl1
18	591.5	46.4	263	3	US-09-210-084-5	Sequence 5, Appl1
19	591.5	46.4	263	4	US-09-478-957-5	Sequence 5, Appl1
20	591.5	46.4	263	4	US-09-764-762-5	Sequence 5, Appl1
21	587	46.0	246	2	US-08-978-404B-44	Sequence 4, Appl1
22	578	45.3	232	2	US-08-768-859A-15	Sequence 4, Appl1
23	577.5	45.3	237	3	US-08-768-859A-16	Sequence 16, Appl1
24	577.5	45.3	237	3	US-08-767-820A-16	Sequence 16, Appl1
25	577.5	45.3	237	3	US-08-622-046B-12	Sequence 12, Appl1
26	577.5	45.3	237	3	US-08-944-483-37	Sequence 37, Appl1
27	577.5	45.3	237	3	US-09-100-264-1	Sequence 1, Appl1
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#### ALIGNMENTS

RESULT 1  
US-09-205-258-427  
Sequence 427, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
CURRENT FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
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EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
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EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
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EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 427  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-427

Alignment Scores:  
Pred. No.: 2.82e-105 Length: 250  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.67% Indels: 0  
DB: 4 Gaps: 0

US-09-856-320a-1\_copy\_272\_958 (1-687) x US-09-205-258-427 (1-250)  
1 ATCATCAAGGGGCTCGAGTGCACCTCACCAGCCCTGCGAGGAGCCCTGTTCGAG 60

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Db 22 IleIleIySgIyPheGluCySAlpProHisSerInPrtGlnAlaAlaLeuPheGlu 41  
Oy 61 AAGAGCGGCTACTCTGTGGGGCGAGCGTCATCCGCCAGATGGCTCTGACAGCAGCC 120  
Db 42 LysThrArgLeuLeuCySgIyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 61  
Oy 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCGAGCAACCTCCAGAGAGAG 180  
Db 62 HisCySleuIySProArgTrpIleValHisIleuGlyInHisAsnIleuGlyInGlu 81  
Oy 181 GCGTGTGAGCAGACCGGAGCAGCAGTACAGTCTTCCCGCCCGGCTTAACAAACAGC 240  
Db 82 GlyCySgIuGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 101  
Oy 241 CTCCCAACAAGACACACCGCATGACATCTGTGCTGGAAGATGGCATGCCAGTCC 300  
Db 102 LeuProAsnIySAspHisArgAsnAspIleMetLeuValIySMeAlaIaSerProValSer 121  
Oy 301 ATCAGCTGGGCTGTGCGACCCCTCAGCCCTCTCAGCGTGTCTACTGTGCGACGAGC 360  
Db 122 IleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCySValThrAlaGlyThrSer 141  
Oy 361 TGCCTCATTTCCGGCTGGGGCGAGCAGTCCAGCCCGCAGTACGCTCTCAACCTTG 420  
Db 142 CySleuIleSerGlyTrpGlySerThrSerProGlnIleuArgLeuProHisThrLeu 161  
Oy 421 CGATCGCGCAATCACCATCATTCATGACAGCAGCAAGTGTGAGAACGCTACCGCGGAGC 480  
Db 162 ArgCySAlaAsnIleThrIleIleGluHisIleInIyScySgluManAlaIyProGlyAsn 181  
Oy 481 ATCAGACAGACCATGTGTGTGTGCGACGCTGAGAGAGGGGGCGAGACCTCTGCCAGGT 540  
Db 182 IleThrAspThrMetValCySAlaSerValGlnIuGlyIySAspSerCySgInGly 201  
Oy 541 GACTCGGGGGCGCTGTGCTGTATACAGTCTTCAAGCATTAATCTGTGGGGCGAG 600  
Db 202 AspSerGlyGlyProLeuValCySAsnGlnSerLeuGlnIyIleIleSerTrpGlyGln 221  
Oy 601 GATCCGTGTGGATCACCCGAAAGCTGTGTCTACAGAAAGTCTGCAATATGTGGAG 660  
Db 222 AspProCySAlaIleThrArgIySProGlyValIyThrIySValCySlySlyValAsp 241  
Oy 661 TGGATCCAGGAGAGATGAGAACAT 687  
Db 242 TrpIleGlnIuThrMetIySAsnAsn 250

RESULT 2  
US-09-025-059-1  
Sequence 1, Application US/09025059  
Patent No. 6075136  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,059  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0481 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGCTT10  
CLONE: 2723646  
US-09-025-059-1

Alignment Scores:  
Pred. No.: 2,89e-105 Length: 282  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.67% Indels: 0  
DB: 3 Gaps: 0

US-09-856-320A-1\_COPY\_272\_958 (1-687) x US-09-025-059-1 (1-282)

QY 1 ATCATCAAGGGGTTGAGTGCAGAGCCCTCCAGCCCTGGAGGAGCCCTGTTGAG 60  
DB 54 ILEILEYSGLYPHEGLUCYLSYSPROHISSEKINPOTRPGIALAIALEUPHEGLU 73  
QY 61 AAGAGCGGCTACTGTGTGGGGGAGCGCATCGCCCGCCAGATGGCTCTGACAGAGCC 120  
DB 74 LYSTHARGLEULEUCYSGLVALATHRLEUILEAIPROARGTRPHEULEUTHRALAIA 93  
QY 121 CACTGCTCAGAGCCCGCTACATAGTTCACCTGGGAGCAGACACCTCCAGAGAGAG 180  
DB 94 HISCYSLLEULYSPROARGTRYLEVALHISLEUGLYGINHISASNLEUGLINSGLIGLU 113  
QY 181 GCGCTGAGCAGACCCGAGCAGCCAGCTGAGTCTCCCGCCAGCCGCGCTTCAACAACAGC 240  
DB 114 GLYCYSGLIGLINTHRARGTHRALATHRGLUSERPHEPROHISPROGLYPHEASNSNSER 133  
QY 241 CTCGCCCAACAAGACGACCGGCAATGACATCATGCTGGTGAAGATGGCATGCCAGTCTCC 300  
DB 134 LEUPROASNLYSASPHISATRGASNAPRIEMELLEVALLYMETALASERPROVALSER 153  
QY 301 ATCACTGGGCTGTGAGACCCCTCACCCTCTCCAGCTGTGTGACATGCTGACAGCAGC 360  
DB 154 ILEHTRTPALAVALAARGPROLEUTHRIEUSERSERARGCYVALITHRALAELYHNSER 173  
QY 361 TGCCTCATTTCCGGCTGGGGGAGCAGCTCAGCCCGCCAGTACGCGCTGACACACTTG 420  
DB 174 CYSTLEUILESERGLYTRPGLYSERTHRSESRERPROGLINLEUARGLEUPROHISHTHRIEU 193  
QY 421 CGATGCGGCAACATACCATCATCATGTAGACACGAGGTGAGAAAGCCCTACCCCGGCAAC 480  
DB 194 ATGYSALAAASNIETHRIELLEGLINHISGLINLYSCYSGLINASNAIATYRPROGLYASN 213  
QY 481 ATCAGCAGACACCATGCTGTGTGCGCAGCTGACAGAAAGGGGAGAGACTCTGCCAGGCT 540  
DB 214 ILEHTRASPETHMEVALCYSLASERVALGINLUGLYGLYLSASPSEKYSGLINGLY 233  
QY 541 GACTCCGGGGGCGCTCTGAGTCTGTAACAGATCTCTTCAAGGCAATATCTCTGGGGCCAG 600  
DB 234 ASPSERGLYGLYPROLEUVALCYLSASNGLINSERLEUGLINTYILLEILSEKTRPGLYGIN 253  
QY 601 GATCGGTGTGGCATCAGCCGGAAGGCTGTGTCCTACAGAAAGTCTGCAAAATATGTGGAC 660

DB 254 ASPROCYSALALETHRARGLYSPROGLYVALTYTHRYVALCYLSYSTYVALASP 273  
QY 661 TGGATCCAGAGACGATGAAGACAAT 687  
DB 274 TTPILEGLINGLINTHRMETLYSASNA 282

RESULT 3  
US-08-944-483-24  
Sequence 24, Application US/08944483  
Patent No. 6232456  
GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KASS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROUDE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 248 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6232456e  
US-08-944-483-24

Alignment Scores:  
Pred. No.: 1.73e-102 Length: 248  
Score: 1227.00 Matches: 227  
Percent Similarity: 99.13% Conservative: 0  
Best Local Similarity: 99.13% Mismatches: 0  
Query Match: 96.24% Indels: 2  
DB: 3 Gaps: 2

US-09-856-320A-1\_COPY\_272\_958 (1-687) x US-08-944-483-24 (1-248)

QY 1 ATCATCAAGGGGTTGAGTGCAGAGCCCTCCAGCCCTGGAGGAGCCCTGTTGAG 60  
DB 22 ILEILEYSGLYPHEGLUCYS---PROHISSEKINPOTRPGIALAIALEUPHE--- 39



QY 61 AAGAGGGGCTACTCTGTGGGCGAGCGTCAATCCCGCCAGATGGCTTCAGACAGACC 120  
DB 40 LysThrArgLeuLeuGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAla 59  
QY 121 CACTGCGCTCAAGCCCGCTACATAGTTCACCTGGGGAGCAGCAACCTCCAGAGAGAGAG 180  
DB 60 HisCysLeuLysProArgTrpTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGln 79  
QY 181 GCGTGTAGAGAGAGCCCGAGAGCCAGCTAGTCTCCCGCCAGCCCGCTTCAGAGAGAG 240  
DB 80 GlyArgGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 99  
QY 241 CTCCCAACAAGAGCCAGCATGATGATCATGCTGGTGAAGAGAGAGAGAGAGAGAG 300  
DB 100 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 119  
QY 301 ATCAACCTGGGCTGGAGCCCGCTCAAGCTCCCTCAAGCTGTGCATCTGCTGGAGAGAG 360  
DB 120 IleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 139  
QY 361 TGCCCTCATTTCCGGCTGGGCGAGCAGCTCCAGCCCGAGTTCAGCTCCCTCAAGAGAG 420  
DB 140 CysLeuLeuSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 159  
QY 421 CGATGGCCCAACATCACCATCATGAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
DB 160 ArgCysAlaAsnIleThrIleLeuGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 179  
QY 481 ATCAACAACAACAGTGTGTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
DB 180 IleThrAspThrMetValCysAlaSerValGlnIleGlyLysAspSerCysGlnGly 199  
QY 541 GACTCCGGGGCCCTGT 600  
DB 200 AsperGlyGlyProLeuValCysAsnGlnSerLeuGlnIleIleSerTrpGlyGln 219  
QY 601 GATCCGTGTGCGATCAGCCCGAAGCCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660  
DB 220 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 239  
QY 661 TGGATCCAGAGAGAGATGAGAGAGAGAT 687  
DB 240 TrpIleGlnGlnThrMetLysAsnAsn 248

RESULT 4  
US-09-386-642-14  
; Sequence 14, Application US/09386642  
; Patent No. 6420157  
; GENERAL INFORMATION:  
; APPLICANT: Darrow, Andrew  
; APPLICANT: Qi, Jensen  
; APPLICANT: Andrade-Gordon, Patricia  
; TITLE OF INVENTION: Zymogen Activation System  
; FILE REFERENCE: ORT-1028  
; CURRENT APPLICATION NUMBER: US/09/386,642  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 289  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
; OTHER INFORMATION: with homo sapien serine protease catalytic domain  
US-09-386-642-14

Alignment Scores:  
Pred. No.: 8,42e-102 Length: 289  
Score: 1219.50 Matches: 223  
Percent Similarity: 98.26% Conservative: 3  
Best Local Similarity: 96.96% Mismatches: 3

Query Match: 95.65% Indels: 1  
DB: 4 Gaps: 1  
US-09-856-320a-1\_copy\_272\_958 (1-687) x US-09-386-642-14 (1-289)

QY 1 ATCAACAAG 57  
DB 52 IleValGlyGlyTyrAsnCysLeuGlnLysHisSerGlnProTrpGlnAlaAlaLeuPhe 71  
QY 58 GAG 117  
DB 72 GlnLysThrArgLeuLeuGlyAlaThrLeuLeuAlaProArgTrpLeuLeuThrAla 91  
QY 118 GCCCATGCTCAAGCCCGCTACATAGTTCACCTGGGGAGCAGCAACCTCCAGAGAGAG 177  
DB 92 AlaHisCysLeuLysProArgTrpTyrIleValHisLeuGlyGlnHisAsnLeuGlnLys 111  
QY 178 GAGGCTGTGAG 237  
DB 112 GlnLysCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 131  
QY 238 AGCTCCCAACAAG 297  
DB 132 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 151  
QY 298 TCCATCACTGGGCTGGAGCCCGCTCAAGCTCCCTCAAGCTGTGTGTGTGTGTGTGTGT 357  
DB 152 SerIleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 171  
QY 358 AGCTCCCTCATTTCCGGCTGGGCGAGCAGCTCCAGCCCGAGTTCAGCTGTGTGTGTGT 417  
DB 172 SerLysLeuLeuSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 191  
QY 418 TTGGAGAGCCCAACATCACCATCATGAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 477  
DB 192 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGly 211  
QY 478 AACATCAACAACAGATGT 537  
DB 212 AsnIleThrAspThrMetValCysAlaSerValGlnIleGlyLysAspSerCysGln 231  
QY 538 GGTGATCCGGGGCCCTGT 597  
DB 232 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnIleIleSerTrpGly 251  
QY 598 CAGGATCCGTGTGAGATCAGCCCGAAGCCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 657  
DB 252 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 271  
QY 658 GACTGATCCAGAGAGAGATGAGAGAGAT 687  
DB 272 AspTrpIleGlnGlnThrMetLysAsnAsn 281

RESULT 5  
US-09-205-258-1150  
; Sequence 1150, Application US/09205258  
; Patent No. 6525174  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/09/205,258  
; EARLIER FILING DATE: 1998-12-04  
; EARLIER APPLICATION NUMBER: PCT/US98/11422  
; EARLIER FILING DATE: 1998-06-04  
; EARLIER APPLICATION NUMBER: 60/048,885  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,375  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,881  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,880  
; EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,896  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/049,020  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,876  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,895  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,884  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,894  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,971  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,964  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,882  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,899  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,893  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,900  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,901  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,892  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,915  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/049,019  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,970  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,972  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,916  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/049,373  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,875  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/049,374  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,917  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,949  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,974  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,883  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,897  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,898  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,962  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,963  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,877  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/048,878  
 EARLIER FILING DATE: 1997-06-06  
 EARLIER APPLICATION NUMBER: 60/070,923  
 EARLIER FILING DATE: 1997-12-18  
 EARLIER APPLICATION NUMBER: 60/092,921  
 EARLIER FILING DATE: 1998-07-15  
 EARLIER APPLICATION NUMBER: 60/094,657  
 EARLIER FILING DATE: 1998-07-30  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 1150

LENGTH: 228  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-205-258-1150

Alignment Scores:  
 Pred. No.: 1,89e-98  
 Score: 1182.00  
 Percent Similarity: 98.67%  
 Best Local Similarity: 98.67%  
 Query Match: 92.71%  
 DB: 4  
 Gaps: 0

US-09-856-320a-1\_copy\_272\_958 (1-687) x US-09-205-258-1150 (1-228)

QY 1 ATCATCAAGGGGTTGAGTGCAGACCTCCATCCAGCCCTGGAGGAGCCCTGTTGAG 60  
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 DB 4 TTTTTLTGLTTPHETLUCYSLSLHNSSTGTPPTPTPTLTAALALEUPHEGLU 23  
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QY 61 AAGACGGGCTACTCTGTGGGGGAGCCGTCATCGCCAGATGCTCTGACGACGCC 120  
 |||||||  
 DB 24 LYSTHrArgLeuLeucCysglYalathrIleuIleAlaProAlgrtrLeuLeuThrAlaAla 43  
 |||||||

QY 121 CACTGCTCAAGCCCGCTACATAGTTACCTGGGCGACGACACACTCCAGAAAGAGAG 180  
 |||||||  
 DB 44 HISCYSLEULYSProArGTYrIleValIhISLeuGIgIhISAsnLeuGIhISgIuGIu 63  
 |||||||

QY 181 GGCTGTGACAGACCCGAGACGACGACTGAGTCTCCACCCCGGCTTCACACACAGC 240  
 |||||||  
 DB 64 GLYCYSGLTGLThrAlaThrAlaThrAlaThrGluSerPheProhISProAlaPheAsnASer 83  
 |||||||

QY 241 CTCGCCCAACAAAGACCCGACCAATGACATCATGCTGTAAGATGCGATCGCAGTCTCC 300  
 |||||||  
 DB 84 LeuProAsnLysAspIleAspIleAsnAspIleMetLeuValLysMetAlaSerProValSer 103  
 |||||||

QY 301 ATCACTGGGCTGTGCGACCCCTCACCTCTCTCCACGCTGTGTCTACTCTGGCACCAC 360  
 |||||||  
 DB 104 ILeThrTrpAlaValArProLeuThrLeuSerSerArGYSaValThrAlaGIhThrSer 123  
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QY 361 TGCCCTCATTTCCGGCTGGGGGAGACAGCTCCAGCCCGGCTGAGCTGCTGACACTTG 420  
 |||||||  
 DB 124 Cys-SerPheProAlaGIAlaAlaArgrProAspProSerTYrAlaCysLeuThrProCY 143  
 |||||||

QY 421 CGATGCGCCACATCATCATTCATGAGCAGCAAGATGTGAGAAACCTTACCCGGGCAAC 480  
 |||||||  
 DB 143 sAspAlaProThrSerProSerLeuSerThrArGYSerValArGThrProThrProAlaTh 163  
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QY 481 ATCAGACAGACCATGTGTGTGCGACGCTGCAGAGGAGGCGCAAGGACTCTGCCAGGT 540  
 |||||||  
 DB 163 rSerGIhThrProTrpCysValProAlaCysArGIYSaValArGThrProAlaArGya 183  
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QY 541 GACTCGGGGGGCGCTGTGCTGTATACAGTCTCTCAAGGCAATTATCTCGGGGGCCAG 600  
 |||||||  
 DB 183 IThrProGIAlaAlaLeuTrpSerValThrSerLeuPheLysAlaLeuSerProGIAlaAr 203  
 |||||||

QY 601 GATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACACCAAGTGTGCAATATGTGAC 660  
 |||||||  
 DB 203 gIleArGValArGSerProGILSerLeuValSerThrArGYSerAlaAsnMettrpH 223  
 |||||||

QY 661 TGGATCCAGAGACCA 676  
 |||||||

DB 223 rGIYSerArGArGArG 228  
 |||||||

RESULT 6  
 US-09-205-258-1149  
 Sequence 1149, Application US/09205258  
 Patent No. 6525174  
 GENERAL INFORMATION:  
 APPLICANT: Young et al.  
 TITLE OF INVENTION: 207 Human Secreted Proteins  
 FILE REFERENCE: P2007P1  
 CURRENT APPLICATION NUMBER: US/09/205,258  
 CURRENT FILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878

EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1149  
LENGTH: 246  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-1149  
Alignment Scores:  
Pred. No.: 1,92e-98 Length: 246  
Score: 1182.00 Matches: 223  
Percent Similarity: 98.67% Conservative: 0  
Best Local Similarity: 98.67% Mismatches: 2  
Query Match: 92.71% Indels: 1  
DB: 4 Gaps: 0  
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QY 1 ATCATCAAGGGGTTGAGTGCAGAGCCCTGAGCCCTGGAGGAGCCCTGTTGAG 60  
DB 22 IlettleysgllypnehlucysgllyleuhtisserglnprrtgrlnalalaLeupheglu 41  
QY 61 AAGAGGGGGTACTCTGTGGGGGAGGCTGTACGGCCCGGAGTGGCTTGGAGCGAGCC 120  
DB 42 LysthrtrgyleuLeucysgllyalathrleuilelalelProamrgtrpleuhtthAlala 61  
QY 121 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGAGAGCACAACCTTCAGAGAGAG 180  
DB 62 Hiscysleuysproamrgtyrilevalhtisleucllygnhtnsanleuclnlysglgu 81  
QY 181 GGGTGTAGCAGACCCGGAGCAGCCAGTGAAGTCTTCCCCACCCGGCTTACACAGC 240  
DB 82 Glycysgluglntrrargthralathrcluserpheptomhsproglypheasnsnser 101  
QY 241 CTCCCAAGAACGACCCGATGACATGATGCTGGTGAAGATGGATGCCAGTCTCC 300  
DB 102 LeuproasnlysaBPhlsargasnaspIleleucllyskelalaserProvalSer 121  
QY 301 ATCACTGGGCTGTGCACCCCTGCACCTCTCTCAAGCTGTCTCACTGTGCAGCAGC 360  
DB 122 IletthrtrplalavalargproleuthrleuhserserargysvalthrAlaglythSer 141  
QY 361 TGCCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCAATTAGCCTGCTCACACCTG 420  
DB 142 Cys-SerpheprolaaglyalalaargproaspProserlyrAlacysleuhtProcy 161  
QY 421 CGATGGCGCAACATCATCATGAGCAGCAGAGTGTGAGAGCGCTACCCGGGAGC 480  
DB 161 sasAlaProthrserProserleuhtthargSerValargthtrProthrProalath 181  
QY 481 ATCAAGACACCATGTGTGTGCCAGGTGCAGGAGAGGGGGCAAGAGCTCTGCAGAGT 540  
DB 181 rserglnthrProtrpyValProalacysarglygllyAlargthtrProalargva 201  
QY 541 GACTCGGGGGCCCTGTGGTCTGTACCAAGTCTTTCAAGGCAATTATCTCTGGGGCAG 600  
DB 201 lThrProglyAlaleuhtpSerValthrSerleuPhelyslaleuhtSerProglyAlaar 221  
QY 601 GATCGGTGGGATCACCCGAAAGCTGTGTGTACAGGAAGAGCTCAATATATGTGAG 660  
DB 221 gllleargValargserProgluserleuValserThrarglyserAlaasnketrrpn 241  
QY 661 TGGATCCAGAGACGA 676  
DB 241 rglYserArgArgarg 246



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; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-070-526-2

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Alignment Scores:	
Pred. No.:	2,19e-53
Score:	681.00
Percent Similarity:	70.54%
Best Local Similarity:	51.79%
Query Match:	53.41%
DB:	3
Length:	266
Matches:	116
Conservative:	42
Mismatches:	64
Indels:	2
Gaps:	2

US-09-856-320A-1\_COPY\_272\_958 (1-687) x US-09-070-526-2 (1-260)

OY	ATCATCAAGGGGATTCAGATCAAGCACTCACTCCAGACCCCTGGACAGACCCCTGGTTCAG	60
Db	.....          .....      .....      .....      .....      .....	33
Db	ValLeuGlyIylHisIleCysGlnProHisSerGlnProTyrGlnAlaIleAurepHein	52
OY	61 AAGACGGGCTACTGTGTGGGGGAGAGCTCATGGCCCCAGATGGCTCTCCAGACAGCC	120
Db	.....      .....      .....      .....      .....      .....	53
Db	GlyLeuGlnIleuLeuGlyGlnIleValIleGlyIleAsnTyrValIleuThrAlaIle	72
OY	121 CAGTCGGCTCAAGCCCGGATACATAGTTCACCTCTGGGGGAGAGCACTCCAGAGAGAG	180
Db	.....                .....      .....      .....	73
Db	HisGlyIysIysProIuStyIThrValAlaGlnGlyAurepHisSerIleGlnIlnIysAsp	92
OY	181 GGGTGTGAGCAGACCCGGACAGGCACTGAGCTCTCTCCAGCCCGGCTCCAGACAG	240
Db	.....      .....      .....      .....      .....	93
Db	GlyProGlnGlnIleuTyrProValIleGlnSerIleProHisIleProCysTyrAurepSer	110
OY	241 CTCGCCAACAAGACCCGAGATGATCATGATCTGTGGTAAAGATGGCATCCGACATCC	300
Db	.....      .....      .....      .....      .....      .....	113
OY	301 ATCAGCTGGGCTGTGGACCCCTCAACCCCTCACTCTCCAGCTGTGTCACTGTGGACAGC	360
Db	...      .....      .....      .....      .....      .....	132
Db	LeuGlySerLeuValIysProIleSerIleThrAlaAurepHisCysThrGlnProGlyIlnIys	150
OY	361 TGGCTATTTCCGGGCGGGGGGAGCAACAGCTCCAGCCCGGACATTCAGGCTGCTCACACTTG	420
Db	.....      .....      .....      .....      .....      .....	152
Db	CysThrValSerIleTyrIleTyrValIlnSerProAlaGlnAurepHeProAspThrIleu	170
OY	421 CGATGGCCCAATTCATCATATTGAGCAGCAAGATGTGAGAGAGCCTTACCCGGCAGAC	480
Db	...      .....      .....      .....      .....      .....	172
Db	AsnGlyAlaIleValIysIlePheProGlnIlnIysCysGlnAurepAlaTyrProGlyln	190
OY	481 ATCAGACAGACCACTGTGTGTGTGCGACAGCTGACAGAGAGGGGAGAGACTCTCCAGGGT	540
Db	.....      .....      .....      .....      .....      .....	192
Db	IleThrAspIleuValIleValCysAlaIleIysSerIysGlyAla - - AspThrCysGlnGly	210
OY	541 GACTCCGGGGGCGCTGTGGTCTGTATACAGAGTCTTCAGGCAATATGCTCGGGGCGAG	600
Db	.....      .....      .....      .....      .....      .....	211
Db	AspSerGlyIleProIleuValCysAspGlyAlaIleGlnGlyIleThrSerTyrIleSer	230
OY	601 GATCCGTGTGCGATCACCCGAAAGCCGTGTCTACAGAAAGTCTGCAAAATATGTGAC	660
Db	...      .....      .....      .....      .....      .....	231
Db	AspProCysGlnIylTyrSerAspIysProGlyValIylThrAsnIleCysAlaGlyIleAurep	250
OY	661 TGGATCCAGAG 672	
Db	.....      .....      .....      .....      .....	251
Db	TyrIleIleIysIys 254	

RESULT 9  
US-09-008-271A-7  
; Sequence 7, Application US/09008271A  
; Patent No. 6203979  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; Hillman, Jennifer L

```

? yue, Henry
? Guegler, Karl J.
? Corley, Neil C.
? Tang, Tom Y.
? Shan, Puvi
? TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
? NUMBER OF SEQUENCES: 24
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Incyte Pharmaceuticals, Inc.
? STREET: 317A Porter Dr.
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/008,271A
? FILING DATE: 16-Jan-1998
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: <Unknown>
? FILING DATE: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Mohan-Peterson, Sheela
? REGISTRATION NUMBER: 41,201
? REFERENCE/DOCKET NUMBER: PF-0458 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-855-0535
? TELEFAX: 650-845-4166
? INFORMATION FOR SEQ ID NO: 7 :
?     SEQUENCE CHARACTERISTICS:
?         LENGTH: 260 amino acids
?         STRANDEDNESS: single
?         TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: COLNOT27
? CLONE: L198496
? ? SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
US-09-008-271A-7

Alignment Scores:
Pred. No.:      1.15e-52          Length:    260
Score:           673.00            Matches:   115
Percent Similarity: 70.09%        Conservative: 42
Best local similarity: 51.34%       Mismatches: 65
Query Match:      52.78%          Indels:    2
DB:               3                gaps:      2

US-09-856-320A-L_COPy_272.958 (1-687) x US-09-008-271A-7 (1-260)

OY      1 ATCATCAAGGCGTTCATGACGTGAAGCCCTCACCAGCCSTGGACAGGACGCCCTTGAG 60
      ::::: ||| |::::::::::||| |::::::::::||| |::::::::::||| |::::::::::|||
Db      33 ValLeucUglYlHisLUcysGLInProHIsSerGIInPOTPrGlNaIAlSeSerGIIn 52
      ::::::::::::::::::::||| |::::::::::||| |::::::::::||| |::::::::::|||
OY      61 AAGAAGCGGCCTACTGTGTGGGCGAGCGCTCATCGCCCCAGATGGCTCTTAGAGAGACC 120
      ::::::::::::::::::::||| |::::::::::||| |::::::::::||| |::::::::::|||
Db      53 GlYglNolnleucUcysglglYValIUvalIUglYaIntTrVallEtThrlalaE 72
      ::::::::::::::::::::||| |::::::::::||| |::::::::::||| |::::::::::|||
OY      121 CATGGCTCAAAGCCCAGTTACATTAGTTAACTCTGGGGGACACMACTTCACAGAGAGAG 180
      ||||||| |::::::::::||| |::::::::::||| |::::::::::||| |::::::::::|||
Db      73 HisCySLyuSLyrSProluStylThrValArgleugILyaRhlsserLieuGlnAslyLaSR 92
      ||||||| |::::::::::||| |::::::::::||| |::::::::::||| |::::::::::|||
OY      181 GGCTGGAGACAGAACCCGAGACAGCACTAGTCCTCCSCCAACCCSGGCTTCACAAGAGC 240
      ||| |||||| |::::::::::||| |::::::::::||| |::::::::::||| |::::::::::|||
Db      93 GLrPGroGUngInGUllErProVaLYalGINserLLIErOnHlsProcSYtAnSSer 112
      ||| |||||| |::::::::::||| |::::::::::||| |::::::::::||| |::::::::::|||
OY      241 CTCGCCAACAAAAGCACCGCATGACATGATGCTGTGAAGATGGCATGCCAGTCTCC 300
      :::||||| |::::::::::||| |::::::::::||| |::::::::::||| |::::::::::|||
Db      113 ---ASPvALglUArPlrsISnhLSAPeuWcttleULeuGLINleudARqSGlNALseSR 131

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QY 301 ATCACTGGGCTGTGGAGACCCCTACCCCTCTCTACGCTGTGTACCTGTGGACAC 360
    ::::::::::::::::::::
Db 132 LeuGlySerIysValIysProIleSerIleuAlaAspHisCysThrGlnProGlyIlnLys 151
QY 361 TGGCCATTTCCGGGGGGGAGACAGCAGCTCCAGCCCAATTACGCTGTGGACACCTTG 420
    ||| ::::::::::::::::::::
Db 152 CysThrValSerIlyTrpGlyThrValThrSerProAlaGluAsnIleuAspHisLeu 171
QY 421 CGATGGCCCAATCAACCATTCATTTGAGACACAGAAAGTGTGAGAACGCTTACCCGGCAAC 480
    ||||| ::::::::::::::::::::
Db 172 AsnCysAlaGluValIysIlePheProGlnIlySycGluAspAlaIlyrProGlyIln 191
QY 481 ATCAACAGACACCATGTGTGTGTGTCACAGCTGTCAGAGAGGGGGCAAGACTCTGCCAGG 540
    ||||| ::::::::::::::::::::
Db 192 IleThrAspGlyMetValCysAlaGlySerSerIysGlyAla---AspThrCysGlnGly 210
QY 541 GACTCGGGGGGCTGTGTGTGTGTGTAAACAGCTCTCAAGGATTCATTCCTGGGGCCAG 600
    ||||| ::::::::::::::::::::
Db 211 AspSerGlyGlyProIleuValCysAspGlyAlaLeuGlnGlyIleThrSerTrpGlySer 230
QY 601 GATCCGTGTGCATCAACCCGAAAGCTGTGTCTACAGCAAGATGTGCAAAATATGTGAC 660
    ||||| ::::::::::::::::::::
Db 231 AspProCysGlyArgSerAspIysProGlyValIlyrThrAsnIleCysArgIlyrIleuAsp 250
QY 661 TGGATCCAGGAG 672
    ||||| ::::::::::::::::::::
Db 251 TrpIleLysLys 254
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## RESULT 10

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US-09-386-642-13
; Sequence 13, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Ol, Jensen
; APPLICANT: Andrade-Cordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-13
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## Alignment Scores:

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Pred. No.: 1,6e-52 Length: 288
Score: 671.50 Matches: 116
Percent Similarity: 70.228 Conservative: 42
Best Local Similarity: 51.56% Mismatches: 64
Query Match: 52.67% Indels: 3
DB: 4 Gaps: 3
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US-09-856-320a-1\_COPY\_272\_958 (1-687) \* US-09-386-642-13 (1-288)

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QY 1 ATCATCAAGGGGTGAGTGC---AAGCTCACTCCCAAGCCCTGGACAGACCCCTGTTTC 57
    ||| ::::::::::::::::::::
Db 52 IleValIglyIlyrAsnCysAlaGluProHisSerGlnProTrpGlnAlaIleuPhe 71
QY 58 GAGAAGACGCGCTACTGTGTGGGCGACGCTCATCGCCCGCCAGATGGCTCTGCACAGCA 117
    ::::::::::::::::::::
Db 72 GlnGlyIlnGlnIleuLeuCysGlyValIleuValIglyIlyrAsnTrpAlaIleuThrAla 91
QY 118 GCCCACTGCTCAACCCCGCTACATAGTCACTACCTGGGGGACCAACCTCCAGAGAG 177
    ||||| ::::::::::::::::::::
Db 92 AlaHisCysLysIlyrProLysTrpIlyrThrValArgLeuGlyAspHisSerIleuGlnAsnLys 111
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QY 178 GAGGCTGTGACAGACCCGAGACGCAAGCCACTGAGTCCCTCCCAACCCCGCTTCAACAC 237
    ::::::::::::::::::::
Db 112 AspGlyProGlnGlnIleuIleProValValGlnSerIleProHisProCysIlyrIlnSer 131
QY 238 AGCCCTCCCAACAAAGACACCGCAATGACATCATAGCTGTGTGTAAGATGGCAATCCGAC 297
    ||| ::::::::::::::::::::
Db 132 Ser---AspValGluAspHisAsnHisAspIleuMetIleuGlnIleuArgAspGlnAla 150
QY 298 TCCATCACTGGGCTGTGTGTGTGTGTGACACCCCTCTCTCTACGCTGTGTACCTGTGGAC 357
    ||||| ::::::::::::::::::::
Db 151 SerIleuGlySerIlyrValIlyrProIleSerIleuAlaAspHisCysThrGlnProGlyIln 170
QY 358 AGCTGCTCATTTCCGGCTGTGGGCGACAGCTGTCAGAGCCCAATTACGCTGTGCACAC 417
    ||| ::::::::::::::::::::
Db 171 LysCysThrValSerIlyrTrpGlyThrValThrSerProArgGluAsnIleuAspHis 190
QY 418 TTGCAGATGGCCCAATCAACCATTCATTTGAGACACAGAAAGTGTGAGAGACCTTACCCGG 477
    ||| ::::::::::::::::::::
Db 191 LeuAsnCysAlaGluValIlyrIlePheProGlnIlyrLysCysGluAspAlaIlyrProGly 210
QY 478 AACATCAACAGACACCATGTGTGTGTGTGTGACAGCTGTCAGAGAGGGGGCAAGACTCTGCCAG 537
    ||||| ::::::::::::::::::::
Db 211 GlnIleThrAspGlyMetValCysAlaGlySerSerIysGlyAla---AspThrCysGln 229
QY 538 GGTGACTCCGGGGGCTGTGTGTGTGTGTAAACAGCTCTTCAAGGATTCATTCCTGGGGC 597
    ||||| ::::::::::::::::::::
Db 230 GlyAspSerGlyIlyrProIleuValCysAspGlyAlaLeuGlnGlyIleThrSerTrpGly 249
QY 598 CAGGATCCGTGTGCATCAACCCGAAAGCTGTGTCTACAGCAAGATGTGCAAAATATGTG 657
    ||||| ::::::::::::::::::::
Db 250 SerAspProCysGlyArgSerAspIysProGlyValIlyrThrAsnIleCysArgIlyrIleu 269
QY 658 GACTGGATCCAGGAG 672
    ||||| ::::::::::::::::::::
Db 270 AspTrpIleLysLys 274
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## RESULT 11

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US-09-996-243-309
; Sequence 309, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C13
; CURRENT APPLICATION NUMBER: US/09/996,243
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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1	PRIOR APPLICATION NUMBER: 60/062250
2	PRIOR FILING DATE: 1997-10-17
3	PRIOR APPLICATION NUMBER: 60/065186
4	PRIOR FILING DATE: 1997-11-12
5	PRIOR APPLICATION NUMBER: 60/065311
6	PRIOR FILING DATE: 1997-11-13
7	PRIOR APPLICATION NUMBER: 60/066770
8	PRIOR FILING DATE: 1997-11-24
9	PRIOR APPLICATION NUMBER: 60/075945
10	PRIOR FILING DATE: 1998-02-25
11	PRIOR APPLICATION NUMBER: 60/078910
12	PRIOR FILING DATE: 1998-03-20
13	PRIOR APPLICATION NUMBER: 60/083322
14	PRIOR FILING DATE: 1998-04-28
15	PRIOR APPLICATION NUMBER: 60/084600
16	PRIOR FILING DATE: 1998-05-07
17	PRIOR APPLICATION NUMBER: 60/087106
18	PRIOR FILING DATE: 1998-05-28
19	PRIOR APPLICATION NUMBER: 60/087607
20	PRIOR FILING DATE: 1998-06-02
21	PRIOR APPLICATION NUMBER: 60/087609
22	PRIOR FILING DATE: 1998-06-02
23	PRIOR APPLICATION NUMBER: 60/087759
24	PRIOR FILING DATE: 1998-06-02
25	PRIOR APPLICATION NUMBER: 60/087827
26	PRIOR FILING DATE: 1998-06-03
27	PRIOR APPLICATION NUMBER: 60/088021
28	PRIOR FILING DATE: 1998-06-04
29	PRIOR APPLICATION NUMBER: 60/088025
30	PRIOR FILING DATE: 1998-06-04
31	PRIOR APPLICATION NUMBER: 60/088026
32	PRIOR FILING DATE: 1998-06-04
33	PRIOR APPLICATION NUMBER: 60/088028
34	PRIOR FILING DATE: 1998-06-04
35	PRIOR APPLICATION NUMBER: 60/088029
36	PRIOR FILING DATE: 1998-06-04
37	PRIOR APPLICATION NUMBER: 60/088030
38	PRIOR FILING DATE: 1998-06-04
39	PRIOR APPLICATION NUMBER: 60/088033
40	PRIOR FILING DATE: 1998-06-04
41	PRIOR APPLICATION NUMBER: 60/088326
42	PRIOR FILING DATE: 1998-06-04
43	PRIOR APPLICATION NUMBER: 60/088367
44	PRIOR FILING DATE: 1998-06-05
45	PRIOR APPLICATION NUMBER: 60/088202
46	PRIOR FILING DATE: 1998-06-05
47	PRIOR APPLICATION NUMBER: 60/088212
48	PRIOR FILING DATE: 1998-06-05
49	PRIOR APPLICATION NUMBER: 60/088217
50	PRIOR FILING DATE: 1998-06-05
51	PRIOR APPLICATION NUMBER: 60/088655
52	PRIOR FILING DATE: 1998-06-09
53	PRIOR APPLICATION NUMBER: 60/088734
54	PRIOR FILING DATE: 1998-06-10
55	PRIOR APPLICATION NUMBER: 60/088738
56	PRIOR FILING DATE: 1998-06-10
57	PRIOR APPLICATION NUMBER: 60/088742
58	PRIOR FILING DATE: 1998-06-10
59	PRIOR APPLICATION NUMBER: 60/088810
60	PRIOR FILING DATE: 1998-06-10
61	PRIOR APPLICATION NUMBER: 60/088824
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63	PRIOR APPLICATION NUMBER: 60/088826
64	PRIOR FILING DATE: 1998-06-10
65	PRIOR APPLICATION NUMBER: 60/088858
66	PRIOR FILING DATE: 1998-06-11
67	PRIOR APPLICATION NUMBER: 60/088861
68	PRIOR FILING DATE: 1998-06-11
69	PRIOR APPLICATION NUMBER: 60/088876
70	PRIOR FILING DATE: 1998-06-11
71	PRIOR APPLICATION NUMBER: 60/089105
72	PRIOR FILING DATE: 1998-06-12
73	PRIOR APPLICATION NUMBER: 60/089440

1	PRIOR FILING DATE: 1998-06-16	
2	PRIOR APPLICATION NUMBER: 60/089512	
3	PRIOR FILING DATE: 1998-06-16	
4	PRIOR APPLICATION NUMBER: 60/089514	
5	PRIOR FILING DATE: 1998-06-16	
6	PRIOR APPLICATION NUMBER: 60/089532	
7	PRIOR FILING DATE: 1998-06-17	
8	PRIOR APPLICATION NUMBER: 60/089538	
9	PRIOR FILING DATE: 1998-06-17	
10	PRIOR APPLICATION NUMBER: 60/089558	
11	PRIOR FILING DATE: 1998-06-17	
12	PRIOR APPLICATION NUMBER: 60/089599	
13	PRIOR FILING DATE: 1998-06-17	
14	PRIOR APPLICATION NUMBER: 60/089600	
15	PRIOR FILING DATE: 1998-06-17	
16	PRIOR APPLICATION NUMBER: 60/089653	
17	PRIOR FILING DATE: 1998-06-17	
18	PRIOR APPLICATION NUMBER: 60/089801	
19	PRIOR FILING DATE: 1998-06-18	
20	PRIOR APPLICATION NUMBER: 60/089907	
21	PRIOR FILING DATE: 1998-06-18	
22	PRIOR APPLICATION NUMBER: 60/089908	
23	PRIOR FILING DATE: 1998-06-18	
24	PRIOR APPLICATION NUMBER: 60/089947	
25	PRIOR FILING DATE: 1998-06-19	
26	PRIOR APPLICATION NUMBER: 60/089948	
27	PRIOR FILING DATE: 1998-06-19	
28	PRIOR APPLICATION NUMBER: 60/089952	
29	PRIOR FILING DATE: 1998-06-19	
30	PRIOR APPLICATION NUMBER: 60/090246	
31	PRIOR FILING DATE: 1998-06-22	
32	PRIOR APPLICATION NUMBER: 60/090252	
33	PRIOR FILING DATE: 1998-06-22	
34	PRIOR APPLICATION NUMBER: 60/090254	
35	PRIOR FILING DATE: 1998-06-22	
36	PRIOR APPLICATION NUMBER: 60/090349	
37	PRIOR FILING DATE: 1998-06-23	
38	PRIOR APPLICATION NUMBER: 60/090355	
39	PRIOR FILING DATE: 1998-06-23	
40	PRIOR APPLICATION NUMBER: 60/090429	
41	PRIOR FILING DATE: 1998-06-24	
42	PRIOR APPLICATION NUMBER: 60/090431	
43	PRIOR FILING DATE: 1998-06-24	
44	PRIOR APPLICATION NUMBER: 60/090435	
45	PRIOR FILING DATE: 1998-06-24	
46	PRIOR APPLICATION NUMBER: 60/090444	
47	PRIOR FILING DATE: 1998-06-24	
48	PRIOR APPLICATION NUMBER: 60/090445	
49	PRIOR FILING DATE: 1998-06-24	
50	PRIOR APPLICATION NUMBER: 60/090472	
51	PRIOR FILING DATE: 1998-06-24	
52	PRIOR APPLICATION NUMBER: 60/090555	
53	PRIOR FILING DATE: 1998-06-24	
54	PRIOR APPLICATION NUMBER: 60/090540	
55	PRIOR FILING DATE: 1998-06-24	
56	PRIOR APPLICATION NUMBER: 60/090542	
57	PRIOR FILING DATE: 1998-06-24	
58	PRIOR APPLICATION NUMBER: 60/090557	
59	PRIOR FILING DATE: 1998-06-24	
60	PRIOR APPLICATION NUMBER: 60/090676	
61	PRIOR FILING DATE: 1998-06-25	
62	PRIOR APPLICATION NUMBER: 60/090678	
63	PRIOR FILING DATE: 1998-06-25	
64	PRIOR APPLICATION NUMBER: 60/090650	
65	PRIOR FILING DATE: 1998-06-25	
66	PRIOR APPLICATION NUMBER: 60/090657	
67	PRIOR FILING DATE: 1998-06-25	
68	PRIOR APPLICATION NUMBER: 60/090696	
69	PRIOR FILING DATE: 1998-06-25	
70	PRIOR APPLICATION NUMBER: 60/090655	
71	PRIOR FILING DATE: 1998-06-25	
72	PRIOR APPLICATION NUMBER: 60/090696	
73	PRIOR FILING DATE: 1998-06-25	
74	PRIOR APPLICATION NUMBER: 60/090662	
75	PRIOR FILING DATE: 1998-06-25	



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; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Alignment Scores:
Pred. No.: 4,3e-50      Length: 293
Score: 644.50          Matches: 117
Percent Similarity: 67.97% Conservative: 40
Best Local Similarity: 50.65% Mismatches: 67
Query Match: 50.55%      Indels: 7
DB: 4                  Gaps: 4

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US-09-856-320a-1\_COPY\_272\_958 (1-687) x US-09-966-243-309 (1-293)

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OY 1 ATCATCAAGGGGTTCGAGTGCAGGCTCCAGCCCTGCGAGGAGCC--CTGTTC 57
    ||||| ||| :||| ||||| ||||| ||||| ||||| ||||| |||||
DB 67 ILEILEASGLYSERPSASPMEHISHTHGLINPROTGILALALALEULEU 86
    :||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 58 GAGAGAGCGGGCTCTGTCGGGCGAGGCTCATCGCCCGGAGATGGTCTGACAGA 117
    :||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 87 ARGPROASGLINLEUTYSGLYALVALLEUVALHISPROGLINPREULEUTHRALA 106
    :||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 118 GCCCACTGCTTCACAGCCCGGCTACATAGTTCACTGGGCGAGCAGACCTCCAGAAG-- 174
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
DB 107 ALAHISCYSLARGLYLVALRHEARGVALARGLEUGLNHSITYSERLEUSERPROVAL 126
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
OY 175 GAGGAGGGCTGTGACAGACAGCCGAGACGCGCTGAGTCCCGCCCGGCTTCAAC 234
    ||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 127 TYRGLUSERGLYGLINMERHENGINGLYVALYSSERILEPROHISPROGLIYURSER 146
    ||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 235 AACAGCCCTCCCAAGAACGACCGCAATGACATGATGCTGGAAGTGGCATCGGCA 294
    :||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 147 -----HISPROGLIYHISERASINASPRLEUMETLEULEYLSLEUASNARG 162
    :||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 295 GTCTCCATACCTGGGCTGTGCGAGCCCTGACCCCTGCTGCTGCTGCTGCTGAGC 354
    :||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 169 ILEARGPROTHRLYASPRVALARGPROILEASNVALSERHISCYSEPROSERALAGLY 182
    :||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 355 ACCAGCTGCTCATTTCCGGCTGGGCGAGACGCTGACGCGCCGAGTTACGCTGCTGAC 414
    ||| ||||| :||| ||||| ||||| ||||| ||||| ||||| |||||
DB 183 THRYSYSLERVALSERGLYTRPGLYTHRLYSERPROGLINVALHISHPEROLYS 202
    ||| ||||| :||| ||||| ||||| ||||| ||||| ||||| |||||
OY 415 ACCTGGGATGGGCGCAATGACATGAGCAACGAGTGGAGAACGCGCTTACCC 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 203 VALLEUGLNCYSLEASNILESERVALLEUSERGLNLSARGCYGLASPRALATYRPRO 222
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 475 GGCAACATCACAGACCATGCTGTGCGAGCTGCGAGGAGGCGCAAGACTCTGAC 534
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 223 ARGGLNILEASPRTHLMETHECHESALAGLY--ASPRYALAGLYARGSPERCYSL 241
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 535 CAGGGTACCTCGGGGGCGCTGTGCTGTGAACAGCTCTTCAAGCAAGCTTATCTGCG 594
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 242 GINGLYASPSERGLYGLYPROVALYALCYASNSGLYSERLEUGLINGLYLEUVALSERTR 261
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 595 GGCCAGGATCGGTGGCGATCACCGGCAAGCGCTGCTGCTACAGCAAGTGTGCAATAT 654
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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DB 262 GLYASPTYRPROCYSALARGPROASNARGPROGLYVALTYRTHASMLEUCYSLSYPHE 281
OY 655 GTGAGCTGATCCAGAGAGATGAGAACAAAT 687
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 282 THRYSYSLERGLNGLNTHRLILEGLINLEUVALASN 292

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# RESULT 12

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US-08-824-874-1
; Sequence 1, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lai, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KERANOTO2
; CLONE: 820694
; US-08-824-874-1

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Alignment Scores:
Pred. No.: 7,11e-46      Length: 268
Score: 597.50          Matches: 110
Percent Similarity: 66.52% Conservative: 39
Best Local Similarity: 49.11% Mismatches: 68
Query Match: 46.86%      Indels: 7
DB: 2                  Gaps: 4

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US-09-856-320a-1\_COPY\_272\_958 (1-687) x US-08-824-874-1 (1-268)

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OY 19 TSCAAGCTCATCTCCAGCCCTGGCAGGAGCCGTGTGAGAGAGCGGCTACTGTG 78
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 50 CYSYTHPRO--SERARGGLYGLINLALALALEULEUVALARGPROASNGLINLEUTYRCS 68
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 79 GGGGCGAGCGTCATCGCCCGCCAGATGGCTCTGACAGCAGCCGCTCAAGCCCGCG 138
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 69 GLYALVALLEUVALHISPROGLINTRPLEULEUTHRLALAHISCYALRGLYSVAL 88
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 139 TACATAGTCCACCTGGGCGAGCAGCAACCTCCGAGAG--GAGGAGGCTGTGAGCAGACC 195
    :||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 89 PHEARGVALARGLEUGLNHSITYSERLEUSERPROVALTYRGLUSERGLYGLINMET 108
    :||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY 196 CGGACGACCACTGAGTCTTCCCGCCAGCCGCTTCAACAACACCTCCCGCAACAAAGAC 255
D 109 PheGlnGlyValLysSerIleProH1sProGlyTyrSer-----HisProGly 124
QY 256 CACCGCAATGACATCATCTGTGAGAGTGGCATCGGACGATCCATACACCTGGGGCTGTG 315
D 125 HisSerAsnAspLeuMetLeuIleLysLeuAsnArgArgIleArgProThrLysAspVal 144
QY 316 CGACCCCTGACACCTCTCTCTGACGCTGTGACAGCTGGACACACCTGCTCATTTCCGCG 375
D 145 ArgProIleAsnValSerSerHisCysProSerIleGlyThrLysCysLeuValSerGly 164
QY 376 TGGGGCAGCAGCTGCTCCACGATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 435
D 165 TrpIleThrThrLysSerProGlnValHisPheProLysValLeuGlnCysLeuAsnIle 184
QY 436 ACCATCATGAGCAGCAAGTGTGAGACGCTACCCCGGACACATCAGACACCATG 495
D 185 SerValLeuSerGlnLysArgCysGlnAspAlaTyrProArgGlnIleAspAspThrMet 204
QY 496 GTGTGTCCAGCAGCTGACAGAAAGGGGCAAGACTCTGCGAGGGTGAATCCGGGGCCCT 555
D 205 PheCysAlaGly--AspLysAlaGlyArgAspSerCysGlnGlyAspSerGlyGlyPro 223
QY 556 CTGGTCTGTACACGATCTCTTCAAGGCAATATCTCTGCGGGCCAGGATCCGTGTGCATC 615
D 224 ValValCysAsnGlnLysSerLeuGlnGlyLeuValSerTrpLysAspTyrProCysAlaArg 243
QY 616 ACCCGAAAGCCTGTGTCTACACGAAAGTGTGCAAAATATGTGACATGATCCAGAGACG 675
D 244 ProAsnArgProGlnValLysThrAsnLeuCysLysPheThrLysTrpIleGlnIuThr 263
QY 676 ATGAGAACAT 687
D 264 IleGlnAlaAsn 267

RESULT 13
US-09-210-084-1
; Sequence 1, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,084
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KERN0702
; CLONE: 820694
US-09-210-084-1
Alignment Scores:
Pred. No.: 7 11e-46
Score: 597.50 Length: 268
Percent Similarity: 66.52% Matches: 110
Best Local Similarity: 49.11% Conservative: 39
Query Match: 46.86% Mismatches: 68
DB: 3 Gaps: 7
US-09-856-320a-1_COPY_272_958 (1-687) x US-09-210-084-1 (1-268)
QY 19 TGCAGGCTCAGTCCCGCCAGCCCTGTGCGAAGACGCGGCTACTGTGT 78
D 50 CysThrPro--SerArgGlnAlaIleLeuLeuArgProAsnGlnLeuTyrCys 68
QY 79 GGGCGACGCTCATCGCCCGCCAGATGCTCTGACAGCAGCCGATGCTCAAGCCCGCC 138
D 69 GlnValValLeuValHisProGlnTrpLeuThrAlaIleCysArgTyrLysVal 88
QY 139 TACATAGTTCACGCGGGGAGCAGCAACCTCCAGAG--GAGGAGGCTGTGAGCAGAC 195
D 89 PheArgValArgLeuGlnLysTyrSerLeuSerProValTyrGlnSerGlyGlnMet 108
QY 196 CGGACGACCACTGAGTCTTCCCGCCAGCCGCTTCAACAACACCTCCCGCAACAAAGAC 255
D 109 PheGlnGlyValLysSerIleProH1sProGlyTyrSer-----HisProGly 124
QY 256 CACCGCAATGACATCATCTGTGAGAGTGGCATCGGACGATCCATACACCTGGGGCTGTG 315
D 125 HisSerAsnAspLeuMetLeuIleLysLeuAsnArgArgIleArgProThrLysAspVal 144
QY 316 CGACCCCTGACACCTCTCTCTGACGCTGTGACAGCTGGACACACCTGCTCATTTCCGCG 375
D 145 ArgProIleAsnValSerSerHisCysProSerIleGlyThrLysCysLeuValSerGly 164
QY 376 TGGGGCAGCAGCTGCTCCACGATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 435
D 165 TrpIleThrThrLysSerProGlnValHisPheProLysValLeuGlnCysLeuAsnIle 184
QY 436 ACCATCATGAGCAGCAAGTGTGAGACGCTACCCCGGACACATCAGACACCATG 495
D 185 SerValLeuSerGlnLysArgCysGlnAspAlaTyrProArgGlnIleAspAspThrMet 204
QY 496 GTGTGTCCAGCAGCTGACAGAAAGGGGCAAGACTCTGCGAGGGTGAATCCGGGGCCCT 555
D 205 PheCysAlaGly--AspLysAlaGlyArgAspSerCysGlnGlyAspSerGlyGlyPro 223
QY 556 CTGGTCTGTACACGATCTCTTCAAGGCAATATCTCTGCGGGCCAGGATCCGTGTGCATC 615
D 224 ValValCysAsnGlnLysSerLeuGlnGlyLeuValSerTrpLysAspTyrProCysAlaArg 243
QY 616 ACCCGAAAGCCTGTGTCTACACGAAAGTGTGCAAAATATGTGACATGATCCAGAGACG 675
D 244 ProAsnArgProGlnValLysThrAsnLeuCysLysPheThrLysTrpIleGlnIuThr 263
QY 676 ATGAGAACAT 687
D 264 IleGlnAlaAsn 267

RESULT 14
US-09-764-762-1
; Sequence 1, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:

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## Alignment Scores:

Pred. No.:	2,45e-45	Length:	263
Score:	591.50	Matches:	106
Percent Similarity:	63.03%	Conservative:	44
Best Local Similarity:	44.54%	Mismatches:	79
Query Match:	46.39%	Indels:	9
DB:	2	Gaps:	2

US-09-856-320a-1\_COPY\_272\_958 (1-687) x US-08-790-137-4 (1-263)

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OY 1 ATCATCAAGGGGTCGAGTCGACGCTCCAGCCCTGGACGAGCCCTGTTCGAG 60
    ||||| ||||| |||::: ||||| ||||| ||||| ||||| ||||| |||||
Db 25 IleIleGIyGlyPheAsnCysGluLysAsnSerGlnProTrpHisValAlaValTyrArg 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 AAGACGGGCTACTCTGTGGGCGACGCTCATGCGCCCGCCAGATGGCTCTGACAGCACC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 45 PheAlaTrgTyrGlnCysGlyValLeuLeuAsnPalAsnTrpValLeuThrAlaAla 64
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 CACTGCCCTCAAGCCCCGCTACATAGTTCACCTGGGGCGACACAACTCCAGAGAGAGAG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65 HisCysTyrAsnAspLysTyrGlnValTrpLeuGlyLysAsnAsnArgPheGluAspGlu 84
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 181 GGCCTGTGACAGACCCCGACAGCCACGTGACCTTCCCGCCACCCCGGCTTCACACACAGC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 85 ProSerAlaGlnHisGlnLeuIleSerLysAlaIleProHisProGlyPheAsnMetSer 104
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 241 CTCCCAACAACAAAGACAC-----CGCAATGACATCATGCTG 276
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 105 LeuLeuAsnLysAspHisThrProHisProGluAspAspTyrSerAsnAspLeuMetLeu 124
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OY 277 GTGAAGATGCGATGCGCAGTCTCATCTACCTGGGCTGGCGACCCCTCACCTCTCTCA 336
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 125 ValArgLeuLysLysProAlaGluIleThrAspValValLysProIleAspLeuProThr 144
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 337 CGCTGTGTCACCTGCGACACCGCTCATTTCCGGCTGGGGCGACGACGTCC--AGC 393
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 145 GluGluProThrValGlySerArgCysLeuAlaSerGlyTrpGlySerThrThrProThr 164
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OY 394 CCCAGTTACGCGCTGCTGACACCTTGCGATGCGCAACATCACCATCATTTGAGCACCG 453
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 165 GluGluPheGluTyrSerHisAspLeuGlnCysValTyrLeuGluLeuLeuSerAsnGlu 184
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 454 AAGTGTGAGAACGGCTACCCCGGCAACATCACAGACACATGCTGTGCTGCCAGCGTGCAG 513
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 185 ValCysAlaLysAlaHisThrGluLysValThrAspThrMetLeuCysAlaGlyGluMet 204
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 514 GAAGGGGGCAAGACCTCGTCCAGGTGACTCCGGGGGCCCTGTGCTGTAAACAGTCT 573
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 205 AspGlyGlyLysAspTrpHisCysValGlyAspSerGlyGlyProLeuIleCysAspGlyVal 224
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 574 CTTCAGGCAATTATCTCTGTGGGCGACAGATCCGTGCGATCACCCGAAAGCCTGTGTCT 633
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 225 LeuGlnGlyIleThrSerTrpGlyProThrProCysAlaLeuProAsnValProGlyIle 244
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 634 TACACGAAAGTCTCAATATGTGACTGATCCAGAGACAGATGAAGACAAT 687
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 245 TyrThrLysLeuIleGluTyrArgSerTrpIleLysAspValMetAlaAsnAsn 262
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Search completed: October 15, 2003, 20:29:02  
Job time : 16.2679 secs

GenCore version 5.1.6  
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OM nucleole - protein search, using frame\_plus\_n2p model

Run on: October 15, 2003, 19:44:50 ; Search time 89.3292 Seconds  
(without alignments)  
7516.609 Million cells updates/sec

Title: US-09-856-320A-1  
Perfect score: 2370  
Sequence: 1 ctcgcttcctccacacctgg.....aaaaaaaaaaaaaaaa 1301

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1661050

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_n2p.model -DEV=xlp  
-O/cgn2.1/USPTO.spool.p/US09856320/runat.15102003.105639.8524/app.query.fasta.1.2318  
-DB=SPTRMBL.23 -GFWT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPTC=0 -LOPEXT=0  
-INITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCFALIG=200 -THR.SCORE=pcit -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09856320@cgn.1.1.159@runat.15102003.105639.8524 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEOBVERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTRMBL.23:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.rodent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	1332.5	56.2	275 4 Q81XD7	Q81XD7 homo sapien

2	1187	50.1	276 11 Q9QYN3	Q9QYN3 mus musculus
3	1129	47.6	249 11 Q9QYN4	Q9QYN4 mus musculus
4	692	29.2	260 4 Q81W69	Q81W69 homo sapien
5	685.5	28.9	255 4 Q96R00	Q96R00 homo sapien
6	683.5	28.8	254 11 Q8CGR4	Q8CGR4 mus musculus
7	678	28.6	276 11 Q8CGR6	Q8CGR6 mus musculus
8	665	28.1	251 11 Q9DB08	Q9DB08 mus musculus
9	632.5	26.7	293 11 Q9D140	Q9D140 mus musculus
10	626	26.4	250 11 Q8CGR5	Q8CGR5 mus musculus
11	602	25.4	261 11 Q9JW70	Q9JW70 mus musculus
12	600.5	25.3	246 11 Q9Z1B9	Q9Z1B9 mus musculus
13	599.5	25.3	234 11 Q9CIV7	Q9CIV7 mus musculus
14	598.5	25.3	246 11 Q9R077	Q9R077 mus musculus
15	597.5	25.2	239 11 Q63275	Q63275 mus musculus
16	597	25.2	246 11 Q9QUR9	Q9QUR9 mus musculus
17	592.5	25.0	261 6 Q9N1Q1	Q9N1Q1 saginus oe
18	591.5	25.0	261 6 Q29474	Q29474 canis faml
19	587.5	24.8	235 11 Q63274	Q63274 rattus norv
20	582	24.6	249 11 Q91VE3	Q91VE3 mus musculus
21	576	24.3	263 11 Q9JW71	Q9JW71 mus musculus
22	575	24.3	244 13 Q8QGW3	Q8QGW3 anguilla ja
23	572.5	24.2	261 11 Q8C232	Q8C232 mus musculus
24	572	24.1	251 11 Q54854	Q54854 rattus norv
25	570.5	24.1	263 11 Q9JW69	Q9JW69 mus musculus
26	570.5	24.1	269 4 Q81U55	Q81U55 homo sapien
27	568.5	24.0	253 11 Q91Y82	Q91Y82 mus musculus
28	568	24.0	246 11 Q88301	Q88301 mus musculus
29	567.5	23.9	247 11 Q9CPN7	Q9CPN7 mus musculus
30	567	23.9	240 13 Q98TH0	Q98TH0 engraulis j
31	566	23.9	245 13 Q42160	Q42160 petromyzon
32	564.5	23.8	237 13 Q91515	Q91515 fuigu rubrip
33	563	23.8	247 13 Q42158	Q42158 petromyzon
34	562	23.7	247 13 Q42608	Q42608 petromyzon
35	561	23.7	247 11 Q9CPN9	Q9CPN9 mus musculus
36	560.5	23.6	253 4 Q8V5N9	Q8V5N9 mus musculus
37	560	23.6	244 13 Q42159	Q42159 homo sapien
38	559	23.6	242 13 Q92099	Q92099 petromyzon
39	558	23.5	254 6 Q9XSN6	Q9XSN6 sus scrofa
40	556	23.5	238 13 Q9W706	Q9W706 paratichthy
41	555.5	23.4	222 13 Q8AV11	Q8AV11 oncorhynch
42	555.5	23.4	242 13 Q8AV13	Q8AV13 brachydanto
43	553	23.3	261 11 Q88309	Q88309 mus musculus
44	552	23.3	242 13 Q9W707	Q9W707 paratichthy
45	551	23.2	247 13 Q9W705	Q9W705 paratichthy

## ALIGNMENTS

### RESULT 1

ID	Q81XD7	PRELIMINARY;	PRT;	275 AA.
AC	Q81XD7;			
DT	01-MAR-2003 (TREMBlrel. 23, Created)			
DT	01-MAR-2003 (TREMBlrel. 23, Last sequence update)			
DT	01-MAR-2003 (TREMBlrel. 23, Last annotation update)			
DE	Variant form hippostasin/KUK11.			
GN	KUK11.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Nakamura T., Mitsui S., Miki T., Yamaguchi N.;			
RT	"Molecular cloning and expression of a variant form of			
RT	hippostasin/KUK11 in prostate."			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB078780; BAC54105.1; "			
SO	SEQUENCE 275 AA; 30165 MW; 257A42B28F40E2C4 CRC64;			

Alignment Scores:

Pred. No.: 2.33e-99

Length:

275

Score: 1332.50  
 Percent Similarity: 90.91%  
 Best Local Similarity: 90.91%  
 Query Match: 56.22%  
 Matches: 250  
 Conservative: 0  
 Mismatches: 0  
 Indels: 25  
 Gaps: 1

US-09-856-320a-1 (1-1301) x Q81XD7 (1-275)

```

QY 209 ATGAGGATTCGACGTTAAATCCTGCTGCTGCAACAGGCGTTGAGGGGAGAGACC 268
    1 MetArgIleuLeuGlnIleuIleuLeuAlaLeuAlaThrGlyLeuValGlyGluThr 20
QY 269 AGCATCATCAAGGGGTTGATGCAAGCCTTACTCCAGCCCTGGCAGGAGCCCTGTC 328
    21 ArgIleIleuGlyPheGluCysLysProHisSerGlnProTyrGlnAlaAlaLeuPhe 40
QY 329 GAGAGAGCGCGCTCTGTGGGCGCAGCTCATGCGCCAGATGGCTCTGACAGCA 388
    41 GluLysThrArgLeuLeuCysGlyAlaThrIleuLeuAlaProArgTyrPheLeuThrAla 60
QY 389 GCCCACTGCTCAAGCCC----- 406
    61 AlaHisCysLeuLysProTyrValSerLeuThrSerProThrHisValSerProAspLeu 80
QY 407 -----CGTAACTAGTTCACCTGGGCGCAGC 433
    81 SerSerSerAsnTyrCysLeuSerHisLeuSerArgTyrIleValHisLeuGlyHis 100
QY 434 AACCTCCAGAGAGAGGCGCTGTAGCAGACCCGCGACAGCCAGCTGATCCTTCCCCAC 493
    101 AsnLeuGlnLysGluGluGlyCysGluGlnThrArgThrAlaThrGlnLysPheProHis 120
QY 494 CCGCGCTTCAACAACAGCCTCCCAACAAGACACCGCAATGACATCATGCTGTCGAG 553
    121 ProGluPheAsnAsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLys 140
QY 554 ATGGCATCGCAGCTCCATACCTGGGCTGTGGAGCCCTCAGCCCTCTCTCCAGCTGT 613
    141 MetAlaSerProValSerIleThrThrPalaValArgProLeuThrLeuSerSerArgCys 160
QY 614 GTCACCTGCTGGCAGCAGCTGCTCATATTCGGGCTGGGCGCAGCAGCTCAGCCCGACTTA 673
    161 ValThrIleGlyThrSerCysLeuIleSerGlyTyrPheLysThrHisSerProGlnLeu 180
QY 674 CGCCTGCTCAGACCTTGGCAGTCGCCCAACATCACCATTCATGACACACAGAGCTGTAG 733
    181 ArgLeuProHisThrLeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlu 200
QY 734 AACGCTTACCGCGCAATCAGACAGACAGCATGCTGTGGCAGCGAGGAGGGGGC 793
    201 AsnAlaTyrProGlyAsnIleThrHisPheMetValCysAlaSerValGlnGluGly 220
QY 794 AAGGACTCTGCCAGGGTGAATCCGGGGCCCTCTGCTGTGTAAACAGTCTTCAAGGC 853
    221 LysAspSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnInsLeuGlnGly 240
QY 854 ATATTCCTCGGGGCGCAGATCCCTGTGCCATCACCCGAAAGCCTGGTGTCTACAGCAA 913
    241 IleIleSerTyrGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLys 260
QY 914 GTCTCAATATGTGACTGGATCCAGAGACAGATGAAGAACAAT 958
    261 ValCysLysTyrValAspTyrPheGlnGlnThrMetLysAsnAsn 275
  
```

RESULT 2

Q9QYN3 PRELIMINARY; PRT; 276 AA.

AC Q9QYN3; 01-MAY-2000 (Tremblurel. 13, Created)  
 DT 01-MAY-2000 (Tremblurel. 13, Last sequence update)  
 DT 01-MAR-2003 (Tremblurel. 23, Last annotation update)  
 DE Hipostasin prostate type.  
 GN PRSS20.

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Yamaguchi N., Mitsui S.;
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA MEDLINE-20525460; PubMed-11072088;
RA Mitsui S., Okui A., Komiyama K., Uemura H., Yamaguchi N.;
RT "cDNA cloning and tissue-specific splicing variants of mouse
RT hipostasin/TLSP (PRSS20).";
RL Blochm. Biophys. Acta 1494:206-210(2000).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB016227; BAA36955.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.257; -.
DR MGD; MGI:1929977; Prss20.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser. protease_Try.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPsin.
DR SMART; SM00020; TRYp-Spc; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS0134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 276 AA; 30753 MW; 90BDC03ABAB17BD6 CRC64;
  
```

Alignment Scores:

Pred. No.: 1,37e-87 Length: 276  
 Score: 1187.00 Matches: 217  
 Percent Similarity: 86.88% Conservative: 28  
 Best Local Similarity: 76.95% Mismatches: 31  
 Query Match: 50.08% Indels: 6  
 DB: Gaps: 2

US-09-856-320a-1 (1-1301) x Q9QYN3 (1-276)

```

QY 113 ATGCAAGGTTGAGCTGCTGCGGAGCTGGAAGTCATCGGGCAGAGTCTTCACAGCACC 172
    1 MetArgArgLeuLys-----SerAspTyrLysLeuSer-----ThrGluThr 14
QY 173 AAGGAACTGGGGCGCGCTCTCTCCCTCCAGGCGATGAGGATTCGAGTTAATCTGTG 232
    15 ArgGluProGlyAlaArgProAlaLeuLeuGlnAlaArgMetIleLeuArgLeuIleAla 34
QY 233 CTTCCTGTGCAACAGGCTTGTAGGGGAGAGACACAGATCATCAAGGGCTTGCAGTGC 292
    35 LeuAlaLeuValThrGlnHisValGlyGlyThrArgIleIleLysGlyTyrGlnCys 54
QY 293 AAGCTACTTCCAGCCCTTGGCAGGAGCCCTGTGTGAGAAAGACGGCTACTGTGGG 352
    55 ArgProHisSerGlnProTyrGlnValAlaLeuPheGlnLysThrArgLeuLeuCysGly 74
QY 353 GCGAGCTCATGCGCCCAATGAGTGGCTCTTACAGACAGCCAGTGCCTCAGAGCCCGCTAC 412
    75 AlaThrIleuLeuAlaProLysTyrPheLeuThrAlaAlaHisCysAlaGlySproHisTyr 94
QY 413 ATAGTCACTGGGGCGCAGCAACCTTCAGAGAGAGAGGCTGTGAGCAGAGCCGAGCA 472
    95 ValIleLeuLeuGlyGlnHisAsnLeuGlnLysThrAspLysGluGlnArgGlnMet 114
QY 473 GCGACTGAGTCTTCCCGCAGCCCGGCTTCAACACAGCTCCCGCAACAAAGCAGCCGC 532
    115 AlaThrGlnSerPheProHisProAspPheAsnAsnSerLeuProAsnLysAspHisArg 134
QY 533 AATGACATCATGCTGGGGAAGATGGCATGCCAGTCTCCATCAGTGGGCTGTGGAGCC 592
    111
  
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Db      135 AsnAspIleMetIleuValIysMetSerSerProValPhePheThrArgAlaValGlnPro 154
QY      593 CTGACCCCTCTCTACACGCTGTGTCTACTGCTGGCAGCAGCTGCTCAATTCGGCTGGGGC 652
Db      155 LeuThrLeuSerProIleCysValAlaIaIaGlyThrSerCysLeuIleSerGlyTrpGly 174
QY      653 AGCAGCTGCAGCCCGCAGTACGCGCTGCTGCACCTGACCTGCGATGGCCCAACATACACATC 712
Db      175 ThrThrSerSerProIleLeuThrLeuProIleHisSerLeuArgCysAlaSerIle 194
QY      713 ATTGACGACACGAGAGTGTGAGAAAGCTACCCCGGACATCATCAGACATGAGTGT 772
Db      195 IleGlnHisIleGlyGlnCysGlnIlySalATyrProGlyAlaHisIleThrSphrMetLeuCys 214
QY      773 GCGACGCTGACGAGAGGGGCGCAAGAGCTCTGCGACGAGTACTCGGGGGCCCTGTGTC 832
Db      215 AlaSerValArgGlySerGlnIlyLysAspSerCysGlnIlyAspSerGlyIlyProLeuVal 234
QY      833 TGTAAACGATCTCTTCAAGGATATATCTCTGGGGCGAGATCCGCTGCGATACCCCA 892
Db      235 CysAsnGlySerLeuGlnIlyIleIleSerTrpGlyGlnAspProCysAlaValThrArg 254
QY      893 AAGCCTGTGTCTACACGAAAGTCTGCAATATATGTGAGTGGATGTCAGAGAGCATGAG 952
Db      255 LysProGlyValIlyThrIlyValCysLysTyrPheAsnTrpIleHisGlnValMetArg 274
QY      953 AACCAAT 958
Db      275 AsnAsn 276

```

## RESULT 3

Q09YN4 PRELIMINARY; PRT; 249 AA.

```

ID      090YN4;
AC      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      HIPOSTRASIN (2310015108RIK protein).
GN      PRS520 OR 2310015108RIK.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      Yamaguchi N., Mitsui S.;
RT      Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RL      [2]
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      Mitsui S., Yamaguchi N.;
RT      "CDNA cloning of a novel brain serine protease, Hipostasin.";
RL      Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE= Tongue;
RC      MEDLINE=21085660; PubMed=11217851;
RA      Kawai T., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata S.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Glass C., King B., Kochia H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Sacchi L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsi G.,
RA      Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA      Mordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

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RA      Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA      Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA      Hayashizaki Y.,
RT      "Functional annotation of a full-length mouse cDNA collection.";
RL      Nature 409:685-690(2001).
DR      EMBL: AB016226; BAA88825.1; -
DR      EMBL: AK009720; BAB26461.1; -
DR      EMBL: AK009360; BAB26241.1; -
DR      HSSP: P00763; IDPO.
DR      MEROPS: S01.257; -.
DR      MGD: MGI:1929977; Prss20.
DR      InterPro: IPR001254; Ser. protease_Try.
DR      Pfam: PF00089; Trypsin; I.
DR      SMART: SM00020; Tryp_Spc; I.
DR      PROSITE: PS00240; TRYPSIN_DOM; 1.
DR      PROSITE: PS00134; TRYPSIN_HIS; 1.
DR      PROSITE: PS00135; TRYPSIN_SER; 1.
KW      Hydrolase; Protease; Serine protease.
SQ      SEQUENCE 249 AA; 27604 MW; F9FF9CB457D727D5 CRC64;

```

## Alignment Scores:

Pred. No.:	6,65e-83	Length:	249
Score:	1129.00	Matches:	201
Percent Similarity:	90.738	Conservative:	24
Best Local Similarity:	81.058	Mismatches:	23
Query Match:	47.648	Indels:	0
DB:	11	Gaps:	0

US-09-856-320a-1 (1-1301) x Q09YN4 (1-249)

```

QY      215 ATTCTGCACTTAATCTGCTGTGCTGCGACACAGGGCTTGTAAGGGGAGAGACCATGATC 274
Db      215 LeuArgLeuIleAlaLeuAlaLeuValThrGlnHisValGlyIleThrArgIle 21
QY      275 ATCAAGGGGTGTGAGTGTGAGAGGCTGCTGCGACAGGCTGCGACAGGAGGCTGTGAGAG 334
Db      22 IleLysGlyTyrGlnCysArgProHisSerGlnProTrpIleValAlaLeuPheGlnLys 41
QY      335 AGCGGGCTACTGTGTGGGGGAGAGCTGATGCGGCGGCGAGTGGCTGTGACAGAGCGGAC 394
Db      42 ThrArgLeuIleCysGlyAlaThrIleLeuIleAlaProLysTyrLeuThrLeuThrAlaHis 61
QY      395 TGGCTGACCGGCGGCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 454
Db      62 CysArgLysProHisTyrValIleLeuLeuGlnHisAsnLeuGlnLysThrAspGly 81
QY      455 TGTGAGCAGACCGGCGAGAGAGCTGATGCTGCGGCGGCGGCGGCTGCAAGAGCGGCTC 514
Db      82 CysGlnGlnArgArgMetAlaThrGlnSerPheTronHisProAspPheAsnSerLeu 101
QY      515 CCCAACAAAGACCCAGCGGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 574
Db      102 ProAsnLysArgHisArgAsnAspIleMetLeuValIlyMetSerSerProValPhePhe 121
QY      575 ACCTGGGCTGTGAGACCCCTGACCTGTGCTGACGCTGTGATGATGATGATGATGATGATGAT 634
Db      122 ThrArgAlaValAlaIleProLeuThrLeuSerProHisCysValAlaIaIaGlyThrSerCys 141
QY      635 CTGATTTCCGGTGGGGGAGAGAGCTGACCGGCGGCGGCTGATGATGATGATGATGATGATGAT 694
Db      142 LeuIleSerGlyTyrPheIlyThrSerSerProGlnLeuArgLeuProHisSerLeuArg 161
QY      695 TCGCGCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 754
Db      162 CysAlaAsnValSerIleIleGlnHisLysGlnCysGlnLysAlaIlyTrpGlyAsnIle 181
QY      755 ACAGACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 814
Db      182 ThrAspThrMetLeuCysAlaSerValAlaArgLysGlnIlyLysAspSerCysGlnLysP 201
QY      815 TCGGGGGGCGGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 874
Db      202 SerGlyIlyProLeuValCysAsnGlySerLeuGlnIlyIleIleSerTrpIlyLysP 221

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OY 875 CCGTGCATACACCCAGAACCTGGTGTCTACACGAAGTCTGCAATATGTGACTGG 934
|||||
Db 222 ProctylalvalTtrArgLysProGlyValTyrThrLysValCysLysTyrPheAsnTtr 241
935 ATCCAGAGACAGATGAGAACAAAT 958
|||
Db 242 IleHisGluValMetArgAsnAsn 249

RESULT 4
Q81W69 PRELIMINARY; PRT; 260 AA.
AC O81W69:
DT 01-MAR-2003 (TRMBLrel. 23, Created)
DT 01-MAR-2003 (TRMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC040887; AAI40887.1; -.
KW Hypothetical protein.
SQ SEQUENCE 260 AA; 28090 MW; EF5934EB96295660 CRC64;

Alignment Scores:
Pred. No.: 1.51e-47 Length: 260
Score: 692.00 Matches: 125
Percent Similarity: 66.93% Conservative: 45
Best Local Similarity: 49.21% Mismatches: 80
Query Match: 29.20% Indels: 4
Gaps: 3

US-09-856-320a-1 (1-1301) x Q81W69 (1-260)
OY 188 CGGTCTCTCCCTCCAGCCATGAGATTCTGCAATTAACTGCTT-----GCTCTG 241
|||||
Db 3 ArgProArgProArgAlaAlaLysLThrTrrMetPheLeuLeuLeuGlyGlyAlaTtr 22
242 GCACACAGGCTTGTAGGGGAGACAGCCAGATCATCAAGGGTTCGAGTCAAGCCCTCAC 301
|||||
Db 23 AlaGlyHisSerArgAlaGlnArgLysValLeuGlyLysHisGlyCysGlnProHis 42
302 TCCACGCCCTGGAGCGAGCCCTGTCGACAGACGCGGCTACTGTGGGCGACCTC 361
|||||
Db 43 SerGlnProTrrPrlAlaAlaLeuPheGlnGlyGlnLeuLeuLeuGlyGlyValLeu 62
362 ATCGCCCCAGATGCTCTGACAGACGCGCTGCTCAAGCCCGCTGACATGATTGAC 421
|||||
Db 63 ValGlyGlnTrrValLeuThrAlaAlaHisCysLysLysProLysTyrThrValArg 82
422 CTGGGGGACACACACTCCAGAAAGAGAGAGGCTGTGACGACGCCGAGACGACATGAG 481
|||||
Db 83 LeuGlyAspHisSerLeuGlnAsnLysAspGlyProGlnGlnGlnIleProValAlaGln 102
482 TCCCTCCCGCACCACCGGCTTCACACACAGCTCCCAACAACAACCCGCAATGACATC 541
|||||
Db 103 SerTrrPrlPrlProCysArgTrrAsnSer---AspValGlnAspHisAsnHisAspLeu 121
542 ATGCTGTGTAAGATGGCATGGCCAGTCTCATCATCACTGGGCTGGGACCCCTCACCCCTC 601
|||||
Db 122 MetLeuLeuGlnIleuLysArgPrlAlaSerLeuGlySerLysValLysProLleSerLeu 141
602 TCCCTCAGCTGTGTCTACTGTGGCAGCAGCAGCTCATTTCCGCTGGGGCAGACAGCTCC 661
|||||
Db 142 AlaAspHisCysThrGlnProGlnLysCysThrValSerLysTrrPrlGlyThrValThr 161
662 AGCCCCCAGTTCAGCCCTGCTCAGCCCTGACACTTGGCGCCCAACAATCAGCATATTGAGAC 721
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Db 162 SerProArgGluAsnPheProAspThrLeuAsnGlyAlaGluValLysIlePheProGln 181
OY 722 CAGAAAGTGTGAAGGCTTACCCGGGCAACATACACACACACAGGCTGTGCCAGGCTG 781
|||||
Db 182 LysLysCysGlnAspAlaLysProGlyGlnIleThrAspAlaMetValCysAlaGlySer 201
OY 782 CAGGAAGCGGCAAGACTCTCTGACAGGAGACTCCGGGGCCCTCTGCTGTATACAG 841
|||||
Db 202 SerLysGlyAla---AspThrCysGlnGlyAspSerGlyGlyProLeuValCysAspGly 220
OY 842 TCTCTTCAAGGCATTATCTCTGGGCGCAGAGATCCGTGCGATCACCCCAAGCCGTGT 901
|||||
Db 221 AlaLeuGlnGlyIleThrSerTrrPrlGlySerAspProCysGlyArgSerAspLysProGly 240
OY 902 GCTTCACAGAAAGCTGCAATATGTCAGATCGATCCAGAG 943
|||||
Db 241 ValTyrThrAsnIleCysArgTyrLeuAspTrrLleLysLys 254

RESULT 5
Q96R00 PRELIMINARY; PRT; 255 AA.
AC Q96R00:
DT 01-DEC-2001 (TRMBLrel. 19, Created)
DT 01-DEC-2001 (TRMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
DE Prostinogen.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21226193; PubMed=11327827;
RA Takayama T.K., Carter C.A., Deng T.;
RT "Activation of prostate-specific antigen precursor (pro-PSA) by
RT prostin, a novel human prostatic serine protease identified by
RT degenerate PCR."
RL Biochemistry 40:1679-1687(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF303046; AAK62813.1; -.
DR HSP: P00761; 1ANI.
DR MEROPS; S01.081; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 255 AA; 27986 MW; 00D5B79E14B9468F CRC64;

Alignment Scores:
Pred. No.: 5.05e-47 Length: 255
Score: 685.50 Matches: 129
Percent Similarity: 65.00% Conservative: 40
Best Local Similarity: 49.62% Mismatches: 76
Query Match: 28.92% Indels: 15
Gaps: 4

US-09-856-320a-1 (1-1301) x Q96R00 (1-255)
OY 209 ATGAGGATTGTGAGATTAACTCCGTGCTTGTGCAACAGGCTTGTAGGGGAGAGACC 268
|||||
Db 1 MetTrrPheLeuLeuThrLeuSerPheLeuAlaSerThrAlaGlnAspGlyAsp--- 19
269 AGCATCATCAAGGGGTTTCAGATGCAAGCTCACTCCAGCCCGGAGAGCAGCCGTGTC 328
|||||
Db 20 LysLeuLeuGlnLysArgLysGlyAlaProHisSerGlnProTrrPrlAlaAlaLeuTyr 39
329 GAGAAACGGGCTACTCTGTGGGCGACAGCTCATGCGCCCAAGATGCTCTGACAGCA 388
|||||
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Db      40 GIUARGGLYArgPheasnCysGLYAlaSerLeuIleSerProHistiRyValLeuSerAla 59
QY      389 GCCACATGCTGCTCAAGCCCGGTACATAGTTCACCTGGGGGACACAACTCCAGAGAG 448
        |||||
Db      60 AlaHIScysGlnSerArgPheMetAlaArgLeuGLYHISAsnLeuArgLysAla 79
QY      449 GAGGGCTGTGACACAGCCGGACAGCCATGAGTCTTCCGCCACCCGGCTTCACAAC 508
        :|||:|
Db      80 AspGlyProGLuGLuLeuArgThrHisSerArgValIleProHISProArgTyrGlu 98
QY      509 ACCCTCCCAACAAAGACCCGCAATGATCATGCTGAGTGAAGTGCATCCGACAGTC 568
        99 -----AlaArgSerHisArgAsnAspIleMetLeuLeuArgLeuValGlnProAla 115
QY      569 TCCATCACCTGGGCTGTGGACCCCTCACCTCTCCATCCGCTGTGTCTCATCTGGACCC 628
        :|||:|
Db      116 ArgLeuAsnProGLuValArgProAlaValLeuProHISProArgCysProHISProGLu 135
QY      629 AGCTGCCATATTCGGGCTGGGGGACAGCAGCTCC-----AGC 664
        :|||:|
Db      136 AlaCysValAlaSerGLYTrpGLYLeuValSerHISAsnGLuProGLYThrAlaGlySer 155
QY      665 CCC-----CAGTTACGCTGCTCCACACCTTGCGATGGCCCAACATCCATCATTTAG 718
        |||||
Db      156 ProArgSerGlnValSerLeuProAspThrLeuHIScysAlaAsnIleGLYIleIleSer 175
QY      719 CACCAAGAGTGTAGACAGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCACAC 778
        |||||
Db      176 AspThrSerCysAlaSerGLYTrpProGLYArgLeuThrAsnThrMetValCysAlaGly 195
QY      779 GTGCAGAGAGGGGCGACAGACTCTGCCAGGGTGAATCTCGGGGGCCCTTGCTGTAC 838
        :|||:|
Db      196 AlaGLuGLYArgGLYAlaGLuSerCysGLuGLYAspSerGLYGLYProLeuValCysGLY 215
QY      839 CAGTCTCTCAAGCATATTCCTCTGGGGCCAGAGTCCGTGTCGATCCCGGAAAGCT 898
        |||||
Db      216 GLYIleLeuGlnGLYIleValSerTrpGLYAspValProCysAspAsnThrThrIysPro 235
QY      899 GGTGTCTACAGCAAAAGTGTGCAAAATATGTGATCGATCCAGAGACGATGAACAAT 958
        |||||
Db      236 GLYValIYTrpThrGLYValCysHISTrpLeuGLUTrpIleArgGLUThrMetLysArgAsn 255

RESULT 6
Q8CGR4 PRELIMINARY; PRT; 254 AA.
AC      08CGR4;
DT      01-MAR-2003 (TREMBLrel. 23, Created)
DT      01-MAR-2003 (TREMBLrel. 23, last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE      ProstIn.
GN      KLR15.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      MEDLINE=22325484; PubMed=12437987;
RA      Olsson A.Y., Lundwall A.;
RT      "Organization and evolution of the glandular kallikrein locus in Mus
RT      musculus."
RL      Biochem. Biophys. Res. Commun. 299:305-311(2002).
SQ      SEQUENCE FROM N.A.
DR      EMBL; AY154434; AAN78422.1; -; AAB9E38BEBD01861 CRC64;
SE      SEQUENCE 254 AA; 28042 MW; AAB9E38BEBD01861 CRC64;

Alignment Scores:
Pred. No.: 7.33e-47 Length: 254
Score: 683.50 Matches: 128
Percent Similarity: 65.10% Conservative: 38

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Best Local Similarity: 50.20% Mismatches: 74
Query Match: 28.84% Indels: 15
DB: 11 Gaps: 4

US-09-856-320A-1 (1-1301) x Q8CGR4 (1-254)

QY      218 CTGCAGTTAATCCCTGCTCTGCTGTCGACAGAGGCTTGTAGGGGAGAGACCAAGATCATC 277
        |||||
Db      3 LeuLeuLeuAlaPheValLeuLeuValSerAlaIleGlnAspGLYAsp---LysValLeu 21
QY      278 AAGGGGTGTGATGTCAGAGCTCCTACCTCCAGCCCTGGCAGGACCCCTGTTCAGAAAGAG 337
        :|||:|
Db      22 GlnGLYGLuGLuCysValProHISerGlnProTrpGLuValAlaLeuPheGluArgGLY 41
QY      338 CGGCTACTGTGTGGGGGAGAGCTCATCGCCCGCCAGATGGCTCTCTGCACAGCCCACTG 397
        |||||
Db      42 ArgPheAsnCysGLYAlaPheLeuLeuIleSerProArgTrpValLeuThrAlaHIScys 61
QY      398 CTCAAGCCCGGCTACATAGTTCACCTGGGGGACAGACACCTCCAGAGAGAGAGGCTGT 457
        |||||
Db      62 GlnThrArgPheMetArgValArgLeuGLYGLuHISAsnLeuArgLysPheAspGLYPro 81
QY      458 GAGCAGACCCGGAGACAGCCACCTAGTCTTCCCGCCAGCGGGTTCACAAACAGCCCTCCC 517
        |||||
Db      82 GlnGlnLeuArgSerValSerArgIleIleProHISProGLYTrpLys----- 97
QY      518 AACAAAGACCCGCAACATGATCATGCTGTGTAAGATGCAATCCGCACTCTTCATCAC 577
        :|||:|
Db      98 AlaArgThrHISArgHISAspIleMetLeuLeuArgLeuPheLysProAlaArgLeuThr 117
QY      578 TGGGCTGTGCAACCCCTCACCTCTCTCACGCTGTGTCAGTGTGTCAGTGTGTCAGTGTGTC 637
        :|||:|
Db      118 AlaTyrValArgProValAlaLeuProArgArgCysProLeuIleGLYGLuAspCysVal 137
QY      638 ATTTCCGGCTGGGGC-----AGCACGTCACAGCCC----- 667
        |||||
Db      138 ValSerGLYTrpGLYLeuLeuSerAspAsnAsnProGLYAlaThrGLYSerGLuLysSer 157
QY      668 CAGTTACGCTCCTCACACCTTGCGATCGCCCAACATCACCATCATTTGAGCACCAAG 727
        :|||:|
Db      158 HISValArgLeuProAspThrLeuHIScysAlaAsnIleSerIleIleSerGlnAlaSer 177
QY      728 TGTGAGACGCTTACCCCGGCAACATCACAGACACCATGCTGTGTCAGCTGCAGAA 787
        |||||
Db      178 CysAsnLysAspTrpProGLYArgValLeuProThrMetValCysAlaGLYAlaGLY 197
QY      788 GGGGGCAAGAGCTCTGCCAGGGTGTACCTCGGGGGGCCCTGTGCTGTACAGCTCTT 847
        |||||
Db      198 GLYGLYThrAspSerCysGLuGLYAspSerGLYGLYProLeuValCysGLYGLYAlaLeu 217
QY      848 CAAGGCATATTCCTCTGGGGCCAGATCCGTGTGCGATCCCGGAAAGCCGTGTGTAC 907
        |||||
Db      218 GlnGLYIleValSerTrpLysPValProCysAspThrThrThrLysProGLYValTyr 237
QY      908 ACGAAAGTGTGCAAAATATGTGACATGATCCAGACAGCATGTGAAG 952
        |||||
Db      238 ThrLysValCysSerTrpLeuGLUTrpIleTrpGLuAsnValArg 252

RESULT 7
Q8CGR6 PRELIMINARY; PRT; 276 AA.
AC      08CGR6;
DT      01-MAR-2003 (TREMBLrel. 23, Created)
DT      01-MAR-2003 (TREMBLrel. 23, last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE      Glandular kallikrein KLR13.
GN      KLR13.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.

```

Accession	Gene	Species	Length (bp)	Score	Percent Similarity	Best Local Similarity	Query Match	DB
RA	MEDLINE=22325484; PubMed=12437987;							
RA	Olsson A.Y., Lundwall A.;							
RT	"organization and evolution of the glandular kallikrein locus in Mus							
RT	musculus.";							
RL	Biochem. Biophys. Res. Commun. 299:305-311(2002).							
RP	(2)							
RP	SEQUENCE FROM N.A.							
RA	Adams M., Mural R.;							
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.							
DR	EMBL; AY152432; AA08420.1; -							
SO	SEQUENCE 276 AA; 30360 MW; 33E189C67492FDCA CRC64;							
DB:								
Alignment Scores:								
Pred. No.:	2,076-46	Length:	276					
Score:	678.00	Matches:	127					
Percent Similarity:	64.15%	Conservative:	43					
Best Local Similarity:	47.92%	Mismatches:	81					
Query Match:	28.61%	Indels:	14					
DB:	11	Gaps:	3					
US-09-856-320A-1 (1-1301) x Q8CGR6 (1-276)								
QY	197 CCCCCTCCAGGCCATGAGGATCTGCGAGTTAACTCGTTGCTTGACCAAGCGGCTGTA	256						
Db	3 ProeuValAlaA-----ThrlleAcysleuThrlleAlaAleuSercluglyIleSer	20						
QY	257 GGGGAGAGACAGGATCATCAAG-----GGG	283						
Db	21 ArgApTYrProlylIleleuAsnGlyThrAsnGlyThrSerGlyPheleuProglyIle	40						
QY	284 TTTCAGTGCAGACCCCTACCTCCAGCCCGGAGCGACGCCCTTGAGAAAGCGCGCTA	343						
Db	41 TyrThrcysleuProHisSerGlnProTrpGlnAlaAlaLeuIleArgGlyArgLeu	60						
QY	344 CTCTGTGGGGGCGACCTCATCGCCGCCAGATGCTCTGTACAGACGCCATGCTCTCAAG	403						
Db	61 leucysgllyGlyValleuValHisprolystrValleuThrlAlaAlaHisCysArglys	80						
QY	404 CCCCCGTCATAGTTCACCTGGGGGAGACACAACCTCCAGAAAGAGAGGGCTGTAGCAG	463						
Db	81 AspelylTYrThrValHisleuGlyLysHisAlaLeuGlyArgValGluAsnGlyleuGln	100						
QY	464 ACCGGAGACGACGATGCTTCCTCCGCCACCCCGGCTTCACACAGCGCTCCCAACAA	523						
Db	101 AlAmetGluValValArgSerIleProHisProGluTYrGlnValThrProThrlHisLeu	120						
QY	524 GACCACGGCAATGACATCATCTGGTGAAGATGGCATGCCAGCTCCATCACTGGGGCT	583						
Db	121 AsnHisAspHisAspIleMetleuGlnleuLeuLysSerProValGlnleuSerHis	140						
QY	584 GTGGGACCCCTCACCCCTCTCTCA---GCGTGTGCACTGCTGGGACACAGCTGCCAT	640						
Db	141 ValTrgThrlleuLysleuSerAlaAspAspCysleuProThrlGlyThrlCysAspArgVal	160						
QY	641 TCCGCGTGGGAGACAGCTCCAGGCCCGGAGTTACCTGCGTCACACCTTGAGATGGCC	700						
Db	161 SercllylrrpGlyThrThrlSerProGlnValAsnTYrProlystrThrlleuGlnsAla	180						
QY	701 AACATCAACCATGATGAGACACAGAGTGTGAGAAAGCGCTACCCGGCAACATCACAGAC	760						
Db	181 AsnIleGluLeuArgSerArgSpGlnGluCysArgGlnValTYrProGlyLysIleThrAla	200						
QY	761 ACCATGGTGTGTGGCAGCGCTGACAGAAAGGGGACAGACTCTGCCAGGGTACTCCGG	820						
Db	201 AsnMetleuCysAlaGlyThrlGlyGlnGlyLysAspSerCysGlnGlyLysPserGly	220						
QY	821 GGCCCTGCGTGTACACCAAGTTCACAGGCAATTAATCTCTGGGGCCAGATCCGT	880						
Db	221 GlyProleuIleCysAsnGlyLysleuTYrGlyIleIleSerTrpGlyAspPheProCys	240						
QY	881 GCGATCAACCCGAGCCGTGTGTACAGAAAGTCTGAATATATGTGACAGGATCCAG	940						
Db	241 GlyGlnProAsnArgProGlyValTYrThrlArgValSerIleTYrleuArgTrpIleGly	260						

QY	94	GAGACGATGAGAAC	955
Db	261	GI101161kxgash	265
RESULT 8			
Q9DB8	09DB8	PRELIMINARY;	PRT; 251 AA.
AC	09DB8:		
DT	01-JUN-2001 (TrEMBLrel. 17, Created)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	1200016C12RIK protein.		
GN	1200016C12RIK.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Lung;		
RX	MEDLINE=21085660; PubMed=111217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi Y., Fukuda S.,		
RA	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,		
RA	Sato T., Okazaki Y., Gotojori T., Bono H., Kasukawa T., Saito R.,		
RA	Kasato K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Glasl C., King B., Kochiya H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,		
RA	Schirral L.M., Scandali F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Guastacchi S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Momberts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,		
RA	Yusufshaw-Sorits A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,		
RA	Hayashizaki Y.;		
RA	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001)		
CC	-1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.		
DR	EMBL; AK004807; BAB23579.1;		
DR	HSSP; P00763; IDPO.		
DR	MEROPS; S01.307;		
DR	MGD; MGI:1921082; 1200016C12RIK.		
DR	InterPro; IPR001314; Chymotrypsin.		
DR	InterPro; IPR001254; Ser_protease_Try.		
DR	Pfam; PF00089; trypsin; 1.		
DR	PRINTS; PR00722; CHYMOTRYPSIN.		
DR	SMART; SM00020; TRYSPC; 1.		
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.		
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.		
DR	Hydrolase; Protease; Serine protease.		
SO	SEQUENCE 251 AA; 28153 MW; F4D667F8C80C4A23 CRC64;		

Alignment Scores:

Pred. No.:	2,3e-45	Length:	251
Score:	665.00	Matches:	126
Percent Similarity:	67.21%	Conservative:	40
Best Local Similarity:	51.018	Mismatches:	81
Query Match:	28.06%	Indels:	0
DB:	11	Gaps:	0

US-09-856-320A-1 (1-1301) x Q9DB8 (1-251)

QY	218	CTCGACCTTAATCTCTGCTCTCTGCGAACAGGCGCTTGAGGGGAGAGACGAGCATCATC	2177
Db	5	LeuThrlieuValIeuPheserIeuIuallgHtscyGlyAlaAspThrIrgAlaIval	24
QY	278	AAGGGGTGCAGTGCAGACGCTTACATCCACGCGCTTGCGAGGACGCGCTTGTGAGAAAGACG	337

Db	25	GLYAlaArgGluCysValAlaArgAsnSer***ProTrpGluAlaIaIyLeuPheTyrLeuThr	44
OY	338	CGGCTACTCTGTGGGGCGGACGCTCATCGCCCCAGATGGCTCTGACAGACGCCCACTGC	397
Db	45	ArgGlnLeuLeuGlyValAlaThrLeuLeuLeuLeuAsnArgProTrpLeuLeuThrAlaAlaHisCys	64
OY	398	CTCAAGCCCCCGCTACATAGTTACCTCCGGGGGAGACACACCTCCAGAAAGGAGAGGGCTGT	457
Db	65	ArgIysProTyrLeuTrpValAlaArgLeuGlyGluHisHisLeuTrpArgTrpGluGlyPro	84
OY	458	GAGCAGACCCCGGACAGCCACTAGTCTCTCCGCCACCCCGGGCTTCAACAACAGCTCCGCC	517
Db	85	GluGlnLeuLeuLeuValThrAspPhePheProHisProGlyPheAsnProLeuLeuSer	1040
OY	518	AACAAGAACCACCCGCAATGACATCATGCTGTGGTGAAGATGGCATGCCAGTCTTCATCAC	577
Db	105	AlaAsnAspHisAsnAspHisPheMetLeuIleArgLeuProArgIysValArgLeuThr	1244
OY	578	TGGGTGTGGCGACCCCTCACCTCTCCACGCTGTGTCACGCTGTGGACACACCTCGCTC	637
Db	125	ProAlaValGlnProLeuAsnLeuThrGluSerArgProProValAlaIyTrpGlnCysLeu	1444
OY	638	ATTTCGCGGTGGGGGACAGCAGTCACAGCCCCAGTTACGCGTCCGCACACCTTGCATCAC	697
Db	145	IlePheGlyTrpGlySerValSerSerIysLeuGlnIyTrpPheMetThrLeuGlnCys	1664
OY	698	GCCAAATCATCACCATCATTTAGACACACAGAAAGTGTAGAACGCCCTTACCCCGGCAATCAC	757
Db	165	AlaAsnIleSerIleLeuAspAsnIysPheCysArgTrpAlaIyTrpProGlyHisIlePhe	1844
OY	758	GACACCATAGTGTGTGTGCCAGCTGCAGAAAGGGGGCAGAGATCTTGTCCAGGGTACTCC	817
Db	185	LysIysIleLeuCysAlaGlyLeuTrpGluGlyArgGlySerCysGlnGlyAspPhe	204
OY	818	GGGGGCGCTGTGTGTGTATACCAAGTCTCTCAAGGCATTTATCTCTGGGGCGAGATCCG	877
Db	205	GlyGlyProLeuValCysGluGlyThrLeuAlaGlyIleValAlaPheGlyGlyPheGluPro	2244
OY	878	TGTGGCATCACCCGAAAGCTGTGTCTTACACGAAAGTCTGCAATATGTGGACTGGATC	937
Db	225	CysSerArgProArgProAlaValIyThrAsnValPheAspIyTrpLeuGluTrpIle	2444
OY	938	CAGGACAGCATGACAGAACAT	958
Db	245	GluSerProMetGluIyAsn	251
RESULT 9			
O9D140			
ID	O9D140	PRELIMINARY;	PRT; 293 AA.
AC	O9D140:		
DT	01-JUN-2001 (TREMBLrel, 17, Created)		
DT	01-JUN-2001 (TREMBLrel, 17, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel, 23, Last annotation update)		
DE	1110030019RIK		
GN	1110030019RIK		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	SPRAIN-C57Bl/6J; TISSUE=Embryo;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shingawa A., Shidata K., Yoshino M., Adachi J., Fukuda S.,		
RA	Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,		
RA	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,		
RA	Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		

Accession	Gene	Protein	Length	Score	Percent Similarity	Best Local Similarity	Query Match	DB
US-09-856-320A-1 (1-1301) x Q9D140 (1-293)								
QY	199	CTCCAGGCGATGAGGATTCGTGACATTAATCTGTTCTGTGGCAACAGGGCTTGAGG	293	632.50	63.748	45.048	26.698	11
Db	38	ProSerC1yHrclInProSerG1yHrAsnArGaPleuSerThrAspSerLySer-G1	57					
OY	259	GAGGAGAGACC-----AGATCATCAAGGAGGTTCCGATGCAAGCCCTCA	300					
Db	57	ygluAspThrArgSerAspSerSerSerArgIleValAsnIlySerAspCysGlnIyAs	77					
OY	301	CTCCAGGCGCGTGGCAGCGACC---CTGTTCCAGAAAGAGCGGCTACTCTGTGGCGGAC	357					
Db	77	pAlaGlnProTprGlnGlyAlaIleuIleuIleuGlyProAsnIlySerIyGlyAlaIyA	97					
OY	358	GCTCATGGCCCCAGATGGCTCTCTGACAGCAGCCCATGTGCTCAAGCCCCGCTACATAGT	417					
Db	97	IleuIleSerProGlnTprLeuIleuThrAlaIleHisCysArgIySerProValPheArgI	117					
OY	418	TCAACGTGGGCGACAAACAATCCACAAAG---GAGAGGGCTGTGAGCAGACCCGAGACG	474					
Db	117	eArgIleuGlyHisIleSerMetSerProValIyGlnIleArgIleuIleuMetPheGlnI	137					
OY	475	CACGTGAGTCCTCCCGCCAGCCGCGGCTTCAACAACAGCCTCCGCAACAAGACACGCCAA	534					
Db	137	yIleIySerIleProHisIleProGlyIySer-----HisProGlyHisSerAs	153					
OY	535	TGACATCATCTGGTGAAGATGGATGGCATGGCCATCTCATCAACTGGGGCTGTGCAGCCCT	594					
Db	153	naPleuMetIleuIleuMetAsnArgIyIleArgAspSerHisSerValIySerProva	173					
OY	595	CACCCCTCTCTCAACGCTGTGTCTACAGTCTGTGGCAGCAGCTGCTCATTTCCGGCTGGGCA	654					
Db	173	IgluIleIleIleCysAspCysAlaThrIgluIlyThrArgCysMetValSerIyIleProGly	193					
OY	655	CACGTGAGCCCGCCAGTTACGCGCTCCACACCTTGCGAGAGCGGCAACATCACCATCAT	714					
Db	193	rThrSerSerSerHisAsnAspPheProIyValIleuGlnCysIleuAsnIleThrValIe	213					





Db 99 Pheasnrglystrhleuan-----asnspillekmetlleuileysleuser 114  
 QY 560 TCGCCATGTCACATCACCCTGGCTGTGCAGACCCCTTCCTCAGCTGTGTACT 619  
 Db 115 SerProvalthrleuanalargvalalathrvalalaleuProserSerCysAlapro 134  
 QY 620 GCTGGACCAAGCGCCCATTTCCGGCTGGGGAGCAGACGTCACACCCCAAGTTACGGCTG 679  
 Db 135 AlaglythrincysleuileserglytyrpglyasnthrleuSerPheglyvalserglu 154  
 QY 680 CCTCACACATGTCGATCGCCACCATCATCATTCATGAGACACAGAACTGTGAGAACGCC 739  
 Db 155 ProaspleueneugincysleuasphalaProleuLeuProglinalaaspcysglualaser 174  
 QY 740 TACCCCGGCAACATCAGACAGACACCATGTGTGTGCCAGCTGAGAGAGGGGAGAGAC 799  
 Db 175 TyrProglylysthrleuarglyasnmetvalcyslaaladlyPheuleuglucglylyasp 194  
 QY 800 TCCTGCCAGGGGTGACTCGGGGGGCCCTGTGTGTACACAGTCTTCAAGCATATATC 859  
 Db 195 SerCysglincylaspserglytyrpglyprovalvalcysasnelygluleuglincylval 214  
 QY 860 TCTGTGGGCGCAGATCCGTGTGCATCACCAGAAAGCTGTGTGTACAGAAAGCTGTC 919  
 Db 215 Sertrpelytyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyr 233  
 QY 920 AAATATGTGACGTGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 958  
 Db 234 AsnTyValaspTrpIleGlnAspThrIleAlaAlaasn 246

## RESULT 13

ID Q9CV76 PRELIMINARY; PRT; 234 AA.  
 AC Q9CV76;

DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE 2310008B01RLK protein (Fragment).  
 GN 2310008B01RLK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.  
 OC NCBI\_Taxid=10090;  
 RN [1]  
 RE SEQUENCE FROM N.A.  
 RC STRAIN-G57B/6J; TISSUE-Tongue;  
 RX MEDLINE-21085660; PubMed-11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito K.,  
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Glisli C., King B., Kochwa H.,  
 RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,  
 RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 CC 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 DR EMBL; AK009217; BAB26143.1; -;  
 DR HSSP; P00763; IDPO.  
 DR MEROPS; S01.020; -;  
 DR MGD; MGI:1916761; 2310008B01RLK.  
 DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR Pfam; PF00089; Trypsin.1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYPSIN\_SPEC.1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM.1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS.1.  
 DR PROSITE; PS00135; TRYPSIN\_SER.1.  
 KW Hydrolase; Protease; Serine protease.  
 FT NON\_TER 1  
 SQ SEQUENCE 234 AA; 25888 MW; 6D81E609EDD39110 CRC64;

## Alignment Scores:

Pred. No.: 4.52e-40 Length: 234  
 Score: 599.50 Matches: 108  
 Percent Similarity: 64.07% Conservative: 40  
 Best Local Similarity: 46.75% Mismatches: 78  
 Query Match: 25.30% Indels: 5  
 DB: 11 Gaps: 4

## US-09-856-320a-1 (1-1301) x Q9CV76 (1-234)

QY 269 AGCATCATCAAGGGGTTGAGTGCAGACCTCCTACCTCCAGCCCTGGCAGGAGCCCTGTTC 328  
 Db 8 LysIleTyrAsnsglyvalglucysvallylAsnserInProtrpglnvalglyleuphe 27  
 QY 329 GAGAGAGCGGGCTACTCTGTGTGGGCGAGCTCATGCGCCCGAGATGCTCTGACAGCA 388  
 Db 28 Hisgllystlyrleuargcysglylvalleuvalasparglystrvalleuthrala 47  
 QY 389 GCCCATGCTCAAGCCCGCTCATATGTCACCTGGGGGAGCAGCAGCAACCTCCAGAGAG 448  
 Db 48 AlaHisCys--ArgasplytyrvalvalargleuvalgluHisSerleuthrlyLeu 66  
 QY 449 GAGGGCTGTGAGCAGACCCCGCAGCCAGCTGATCTCCCGCAGCCCGCTTCACAGAAC 508  
 Db 67 AsprtrprrhrglueuarghlysthrThrPheSerlethrHisProserTyrnglly 86  
 QY 509 AGCCTCCCAACAGACCCAGCATGATCATGTGCTGTAAGATGATGATGATGATGATGAT 568  
 Db 87 AlaTyrglnasn-----HisgluHisAspLeuargleuvalargleuvalargleuval 104  
 QY 569 TCCATCTCGGGGTGTGGGAGCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCC 628  
 Db 105 HisleuthrargalavalargprovalalaleuProserSerCysvalInthrlyAla 124  
 QY 629 AGCTGCTCATTTCCGGCTGGGGAGCAGCTCCAGCCCGCAGTTACGCTGCTCCACACC 688  
 Db 125 MetCysHisValSerglytyrpglyThrThrAsnlysertrrppasppropheProasparg 144  
 QY 689 TTGGAGTGGCCCAACATCACCATCATGTAGCACCAGAGAGTGTGAGAACGCTTACCCGGC 748  
 Db 145 LeuclncysleuasnleuSerThrValSerAsnlythrCysargalavalalpheProgly 164  
 QY 749 AACATCAGACAGACACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 808  
 Db 165 Argvalthrtrgluasnleuvalcysalaagly--glygluvalaglylvalasphalaCysglu 183  
 QY 809 GGTGACTCCGGGGCCCTGTGTGTAACTGTCTTCAAGGACATATATCTCTGGGGC 868  
 Db 184 GlyAspertrlyglProleuvalcysglglylvalleuclnclyleuvalsertrpgly 203  
 QY 869 CAG--GATCGGTGTGCATCACCAGAACCTGGGTGTTCACAGAAAGTCTCAATAT 925  
 Db 204 SerValglyProCysgllynglynglylleProglyValtyrThrlyrsValcyslystyr 223  
 QY 926 GTGGATCGATCCAG 958  
 Db 224 ThrAspTrpIleArgIleValIleArgAsnasn 234

## RESULT 14

ID Q9ROT7 PRELIMINARY; PRT; 246 AA.  
 AC Q9ROT7;



Accession	Gene	Species	Length (bp)	Score	Similarity (%)	Matches	Conservative
01-MAV-2000 (TREMblrel. 13, Created)			5,496-40	246			
01-MAY-2000 (TREMblrel. 13, Last sequence update)			596.50	118			
01-MAR-2003 (TREMblrel. 23, Last annotation update)			62.85%	41			
Pancreatic trypsin (0910001B19R1K protein) (Trypsinogen 8).							
DR	01-MAR-2003 (TREMblrel. 23, Last annotation update)						
DE	Pancreatic trypsin (0910001B19R1K protein) (Trypsinogen 8).						
GN	DR OR 0910001B19R1K OR TRYP.SIN.OGEN.						
OC	Mus musculus (Mouse).						
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
NC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
OX	NCBI_TaxID=10090;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=129SVJ;						
RC	MEDLINE=99436155; PubMed=10506205;						
RX	RA Kawai J., Shinaaga A., Shibata K., Yoshino M., Itoh M., Ishi Y.,						
RA	Arkawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,						
RA	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,						
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,						
RA	Kadota T., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,						
RA	Fleischmann W., Gaasterland T., Glisel C., Kling B., Kochia H.,						
RA	Kuehl P., Lewis S., Matsuo Y., Nikdel I., Pesole G., Quackenbush						
RA	Schirral L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio						
RA	Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,						
RA	Blake J., Botfield D., Bojunga N., Carinci P., de Bonado M.F.,						
RA	Gustinstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi T.,						
RA	Brummett S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,						
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarats P.,						
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,						
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.,						
RA	Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilmberg						
RA	Yushwa-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,						
RA	Hayashizaki Y.;						
RT	"Functional annotation of a full-length mouse cDNA collection.";						
RL	[3]						
RN	Nature 409:685-690(2001).						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=129;						
RX	MEDLINE=21103195; PubMed=11160223;						
RA	Chen F., Rowen L., Hood L., Rothenberg E.V.;						
RT	"Differential transcriptional regulation of individual TCR beta						
RT	segments before gene rearrangement.";						
RL	J. Immunol. 166:1771-1780(2001).						
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.						
DR	EMBL: AB017032; BAA74761.1; -						
DR	EMBL: AK008667; BAB25821.1; -						
DR	EMBL: AK003064; BAB25242.1; -						
DR	EMBL: AEO00664; AAB69056.1; -						
DR	HSSP: P00763; ISLU.						
DR	MEROPS: S01.057; -						
DR	MCD: MGI:1913350; 0910001B19R1K.						
DR	Interpro: IPR001314; Chymotrypsin.						
DR	Interpro: IPR001254; Ser_Protease_Try.						
DR	Pfam: PF00089; trypsin. 1.						
DR	PRINTS: PR00722; CHYMOTRYP.SIN.						
DR	SMART: SM00020; TRYP.SPC. 1.						
DR	PROSITE: PSS0240; TRYP.SIN.DOM. 1.						
DR	PROSITE: PSS0134; TRYP.SIN.HIS. 1.						
DR	PROSITE						

[illegible]



Search completed: October 15, 2003, 20:25:39  
Job time : 96.3292 secs

RA Zintz C.B., Ma J.-X., Chao J., Chao L.:  
RT "Isolation and characterization of a new rat kallikrein CDNA with  
RT predominant expression in the kidney."  
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL: L33840; AAA58782.1; -  
DR HSSP: P00759; 1TON.  
DR InterPro: IPR001254; Ser\_protease\_Try.  
DR Pfam: PF00089; Trypsin\_1.  
DR SMART: SM00020; TRYP\_SPC; 1.  
DR PROSITE: PS50240; TRYP\_SIN\_DOM; 1.  
DR PROSITE: PS00134; TRYP\_SIN\_HIS; 1.  
DR PROSITE: PS00135; TRYP\_SIN\_SER; 1.  
KW Hydrolase; Protease; Serine protease.  
FT NON\_TER 1  
SQ SEQUENCE 239 AA; 26382 MW; 3CBD761AF06AB53 CRC64;  
  
Alignment Scores:  
Pred. No.: 6,58e-40 Length: 239  
Score: 597.50 Matches: 107  
Percent Similarity: 64.85% Conservative: 48  
Best Local Similarity: 44.77% Mismatches: 73  
Query Match: 25.21% Indels: 11  
DB: 11 Caps: 3  
  
US-09-856-320a-1 (1-1301) x Q63275 (1-239)  
  
QY 260 GGAGAGACCCAGATCATCAAGGGGTCGAGTCGACAGCCCTCAGCCCTGGCAGGCA 319  
DB 5 G1yGlnSerArgValValG1yG1yPheLysCysGlnLysAsnSerGlnProTPrGlnVal 24  
QY 320 GCCCTGTTCGAGAGAGCGGGCTACTCTGTGGGGCGAGCGTCATCGCCCCAGATGGCTC 379  
DB 25 AlaValIleAsnGluAsp-----LeuCysG1yG1yValIleuIleAspProSerTPrVal 42  
QY 380 CTGACAGACGCCCACTGCTCTCAAGCCCGCTACATAGTTCACCTGGGCGACAGACACCTC 439  
DB 43 IleThrIalaIleAsnLysTyrSerAspAsnTyrHisValIleuLysGlnAsnAsnIleu 62  
QY 440 CAGAGAGAGAGCGGCTGTGACAGACCCGAGACAGCCAGTCGTCCTCCCGACCCCGGC 499  
DB 63 SerGluAsp-----ValGlnHisArgLeuValSerGlnSerIleArgHisProAsp 79  
QY 500 TTC-----AACACAGCCCTCCCAACAAAGCCACCGCATGACATC 541  
DB 80 TyrIleuProPheIleuMetArgAsnHisThrArgLysProLysAspTyrSerAsnAspLeu 99  
QY 542 ATGCTGTGTAAGATGCGATGCGCATGCTCCATCAGCTGCGGCTGCGACCCCTCAGCCCTC 601  
DB 100 MetIleuLeuHisIleuSerGluProIleAspIleThrAspG1yValIleValIleAspLeu 119  
QY 602 TCCTCAGCGTGTGTCACTGCTGCGACACAGCTGCGCTCAATTCGGCTGGGCGACAGCTCC 661  
DB 120 ProThrLysGluProLysValG1ySerThrCysLeuValSerG1yTPrG1ySerThrAsn 139  
QY 662 AGCCCCAGTTAGCCCTCCTCACACCTTCGATGCGCCCAACATCACCATCATTTGAGCAC 721  
DB 140 ProSerGluTPrGluPheProAspAspLeuGlnCysValAsnIleHisIleuLeuSerAsn 159  
QY 722 CAGAGTGTGAGAGCGCTACCCCGCGACATCAGACACACATGATGTGTGCCAGCGCTG 781  
DB 160 GlnLysCysIleLysAlaTyrLysGlnLysValThrAspLeuMetLeuCysAlaG1yGlu 179  
QY 782 CAGGAAGGGGCGAGAGCTCTCCAGAGGTGACTCCGGGGGCGCTGTGTCTGAACCAAG 841  
DB 180 LeuGlnG1yG1yLysAspThrCysArgG1yAspSerG1yG1yProLeuIleCysAspG1y 199  
QY 842 TCTCTCAAGGCATTTATCTCTGGGGCGAGATCCG1GTGCGATCACCCGAAGCGTGGT 901  
DB 200 ValLeuGlnIleLysThrSerTPrG1ySerValProCysG1yG1yProAsnLysProG1y 219  
QY 902 GTCTACAGAAATCTGCAATATATGTGAGTGGATCGACAGACGATGAGAGACAAT 958  
DB 220 IleTyrThrLysLeuIleLysPheThrSerTPrIleLysGlnValMetLysLysAsn 238

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 11:49:23 ; Search time 3549.61 Seconds  
(without alignments)  
8908.057 Million cell updates/sec

Title: US-09-856-320A-1

Perfect score: 1301  
Sequence: 1 cgcctgtctccacacctgg.....aaaaaaaaaaaaaaaa 1301

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_hnv:\*  
19: em\_gss\_pin:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_pig:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1263.8	97.1	1294	11	BC015551 Homo sapi
2	855.6	65.8	1072	12	BM559782 AGENCOURT
3	825.2	63.4	1074	12	BM559617 AGENCOURT
4	757.4	58.2	761	12	BM982377 UI-CF-EN1

5	725.6	55.8	853	10	BG720793	BG720793 602692015
6	719.4	55.3	841	12	B1818697	B1818697 603037514
7	701.4	53.9	747	13	BX109836	BX109836 B109836
8	668.2	51.4	673	13	B0684799	B0684799 UI-CF-EN1
9	659.6	50.7	678	12	B1763040	B1763040 603047836
10	657.4	50.5	973	10	BE867930	BE867930 601443517
11	638.2	49.1	1295	11	AK009360	AK009360 Mus muscu
12	638.2	49.1	1295	11	AK009720	AK009720 Mus muscu
13	630.8	48.5	708	10	BG697071	BG697071 602660281
14	626.2	48.1	1269	11	AK009659	AK009659 Mus muscu
15	616	47.3	654	13	B0676834	B0676834 UI-CF-D01
16	559.8	43.0	639	10	BG747134	BG747134 602704354
17	548	42.1	644	10	BE219655	BE219655 hv60910.x
18	536.2	41.2	645	9	AW511566	AW511566 x60a02.x
19	525.4	40.4	560	10	BF476474	BF476474 naa25d06.
20	493.6	37.9	517	9	A1217150	A1217150 qf47e06.x
21	491.4	37.8	501	9	A1521607	A1521607 t65e07.x
22	480.4	36.9	483	9	A1183346	A1183346 qd41b10.x
23	469	36.0	469	14	CA437458	CA437458 UI-H-D10-
24	468.4	36.0	539	12	BM837078	BM837078 K-EST0113
25	456.2	35.1	502	9	A1283289	A1283289 qul3f05.x
26	445	34.2	579	12	B1046611	B1046611 MR3-FN020
27	444.6	34.2	479	9	AW000834	AW000834 w46b01.x
28	435	33.4	449	9	AA436049	AA436049 zu01c07.t
29	426	32.7	426	9	AA435952	AA435952 zu01c02.s
30	424.2	32.6	441	9	AA532717	AA532717 nj59c09.s
31	421.4	32.4	425	14	CD107547	CD107547 AGENCOURT
32	410.4	31.5	420	10	BE673570	BE673570 7d39e01.x
33	406.2	31.2	422	9	A1624187	A1624187 ts42a04.x
34	404.2	31.1	417	9	AA403004	AA403004 zu54e10.s
35	401.4	30.9	809	10	BE679282	BE679282 60213475
36	387.8	29.8	526	10	BE898804	BE898804 601681783
37	387.6	29.8	528	4	BX528424	BX528424 R2PD Mus
38	370.6	28.5	484	14	CB270157	CB270157 1009064.H
39	370.2	28.5	696	12	BM020073	BM020073 603648624
40	369.4	28.4	419	9	A1913780	A1913780 w401910.x
41	369	28.4	391	9	AA402971	AA402971 zu53i10.t
42	368.4	28.3	406	14	W60282	W60282 zd29b01.s1
43	362.2	27.8	966	14	BY709314	BY709314 BY709314
44	359.8	27.7	467	9	AA073833	AA073833 m399b09.t
45	359.8	27.7	467	9	A1893370	A1893370 m399b09.y

## ALIGNMENTS

RESULT 1  
LOCUS BC015551 1294 bp mRNA HTC 29-OCT-2001  
DEFINITION Homo sapiens, kallikrein 11, clone IMAGE:3847565, mRNA.  
ACCESSION BC015551  
VERSION BC015551.1 GI:15930236  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1294)  
REFERENCE Strausberg, R.  
AUTHORS Submitted (01-OCT-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgabbs@remail.nih.gov](mailto:cgabbs@remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
 Series: IRK Plate: 20 Row: 1 Column: 12

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 8574438  
 This clone has the following problem: frame shifted.

## FEATURES

## source

Location/Qualifiers

1. 1294  
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 /mol\_type="mRNA"  
 /db\_xref="LocusID:11012"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3847565"  
 /tissue\_type="Colon, adenocarcinoma"  
 /clone\_id="NIH\_MGC\_65"  
 /lab\_host="DH10B"  
 /note="Vector: PCMV-SPORT6"  
 BASE COUNT 317 a 391 c 334 g 252 t  
 ORIGIN

## Query Match

Best Local Similarity 97.18; Score 1263.8; DB 11; Length 1294;  
 Matches 1279; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

4 CCTTGCACACCTGGTCAAGGGAGAGAGGAGAAAGCCAGAGGAGGACTTAAT 63  
 10 CCGTCTCCACACTGGTCAAGGGAGAGAGGAGAAAGCCAGAGGAGGACTTAAT 69  
 64 GAAACAAACAGCTGGAGAGAGAGAGATTCGGCTCGGGTTCGCGAGATGACAGATT 123  
 70 GAAACAAACAGCTGGAGAGAGAGAGATTCGGCTCGGGTTCGCGAGATGACAGATT 129  
 124 GAGTGGCTCGGGAGAGAGAGATTCGGCTCGGGTTCGCGAGATGACAGATT 183  
 130 GAGTGGCTCGGGAGAGAGAGATTCGGCTCGGGTTCGCGAGATGACAGATT 189  
 184 GGGCGGCTCGGGAGAGAGAGATTCGGCTCGGGTTCGCGAGATGACAGATT 243  
 190 GGGCGGCTCGGGAGAGAGAGATTCGGCTCGGGTTCGCGAGATGACAGATT 249  
 244 AACAGGGCTGTGAGGGAGAGAGAGATTCGGCTCGGGTTCGCGAGATGACAGATT 303  
 250 AACAGGGCTGTGAGGGAGAGAGAGATTCGGCTCGGGTTCGCGAGATGACAGATT 309  
 304 CCAAGCCTGGAGAGAGAGAGATTCGGCTCGGGTTCGCGAGATGACAGATT 363  
 310 CCAAGCCTGGAGAGAGAGAGATTCGGCTCGGGTTCGCGAGATGACAGATT 369  
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 370 CCGCCCGAGATGGCTCTGACAGAGAGAGAGATTCGGCTCGGGTTCGCGAGATT 429  
 420 ACCTGGGGAGAGAGAGAGAGAGAGAGATTCGGCTCGGGTTCGCGAGATT 479  
 430 ACCTGGGGAGAGAGAGAGAGAGAGAGATTCGGCTCGGGTTCGCGAGATT 489  
 480 AGTCTTCCCCAGAGAGAGAGAGAGAGAGATTCGGCTCGGGTTCGCGAGATT 539  
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 600 TCATGCTGAGAGATGGAGAGAGAGAGAGAGATTCGGCTCGGGTTCGCGAGATT 659  
 610 TCATGCTGAGAGATGGAGAGAGAGAGAGAGATTCGGCTCGGGTTCGCGAGATT 669  
 660 CCAAGCCTGGAGAGAGAGAGAGAGAGATTCGGCTCGGGTTCGCGAGATT 719

|||||  
 670 CCAGCCCCAGATGAGCTGGCTCAGACCTTGCATGCGCCAGATCACCATTGATGAGC 729  
 720 ACCAGAGTGGAG 779  
 730 ACCAGAGTGGAG 789  
 780 TGCAG 839  
 790 TGCAG 849  
 840 AGTCTTTCAGAGAGATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 899  
 850 AGTCTTTCAGAGAGATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 909  
 900 GTGCTTACAG 959  
 910 GTGCTTACAG 969  
 960 AGACTGAG 1019  
 970 AGACTGAG 1029  
 1020 TTCACTCTGTATTAAG 1079  
 1030 TTCACTCTGTATTAAG 1089  
 1080 TGGACTGAG 1139  
 1090 TGGACTGAG 1149  
 1140 GGAATTAATTCCTGAG 1199  
 1150 GGAATTAATTCCTGAG 1209  
 1200 CTGTTGATATCCAG 1259  
 1210 CTGTTGATATCCAG 1269  
 1260 TTGCTAATGAG 1284  
 1270 TTGCTAATGAG 1294

RESULT 2  
 BM559782 1072 bp mRNA linear EST 20-FEB-2002  
 LOCUS AGENCOURT\_6565460 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5744410  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BM559782  
 VERSION BM559782.1 GI:18803655  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 1072)  
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
 Plate: LRAM12765 row: 1 column: 11  
 High quality sequence stop: 684.  
 Location/Qualifiers  
 1. 1072

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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:5744410"
/tissue_type="medulla"
/lab_host="DH10B"
/clone_lib="NIH_MGC_119"
/Note="Organ: brain; Vector: pCMV-Sport6; Site: 1; NotI;
Site: 2; EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb. Insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
BASE COUNT      238 a      340 c      307 g      185 t      2 others
ORIGIN

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Query Match      65.8%; Score 855.6; DB 12; Length 1072;
Best Local Similarity 97.3%; Pred. No. 5.7e-81;
Matches 891; Conservative 0; Mismatches 21; Indels 4; Gaps 2;

18 TGGTCAGGGAGAGAGGGAGGAAAGCCAGGAGGAGGACCTTAAGTGAAGAAACAAAGC 77
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21 TGGTCAGGGAGAGAGGGAGGAAAGCCAGGAGGAGGACCTTAAGTGAAGAAACAAAGC 80
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78 TGGGAGAGAGAGAGATCTGCGCTCGGGTCCGAGATGACAGAGTGAAGTGGCTGGGG 137
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81 TGGGAGAGAGAGAGATCTGCGCTCGGGTCCGAGATGACAGAGTGAAGTGGCTGGGG 140
|||||
138 ACTGGAAGTATCGGCGAGAGGCTTCACAGCAGCCAGAACCTGGGGCCGCTCTCC 197
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141 ACTGGAAGTATCGGCGAGAGGCTTCACAGCAGCCAGAACCTGGGGCCGCTCTCC 200
|||||
198 CCTCCAGGCGATGAGATTCGAGTAACTCTGCTTGGCAACAGGGCTTGAAG 257
|||||
201 CCTCCAGGCGATGAGATTCGAGTAACTCTGCTTGGCAACAGGGCTTGAAG 260
|||||
258 GGGGAGAGAGAGATCTGCGCTCGGGTCCGAGATGACAGAGTGAAGTGGCTGGGG 317
|||||
261 GGGGAGAGAGAGATCTGCGCTCGGGTCCGAGATGACAGAGTGAAGTGGCTGGGG 320
|||||
318 CAGCCCTGTTGAGAAAGAGCGGGCTACTGTGTGGGCGAGCTATCCGCCAGATGGC 377
|||||
321 CAGCCCTGTTGAGAAAGAGCGGGCTACTGTGTGGGCGAGCTATCCGCCAGATGGC 380
|||||
378 TCCCTACAGAGCCCAAGGCTCAAGCCCGCTACATAGTTCACCTGGGCGAGCAACGC 437
|||||
381 TCCCTACAGAGCCCAAGGCTCAAGCCCGCTACATAGTTCACCTGGGCGAGCAACGC 440
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438 TCCAGAGAGAGAGGCTGTGAGCAGACCCGAGACCCAGCTGAGTCTTCCGCCACCCG 497
|||||
441 TCCAGAGAGAGAGGCTGTGAGCAGACCCGAGACCCAGCTGAGTCTTCCGCCACCCG 500
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498 GCTTAAACAGAGCTTCCCAAAAGAACACACCCAGTGAATGATGCTGTGGAAGTGG 557
|||||
501 GCTTAAACAGAGCTTCCCAAAAGAACACACCCAGTGAATGATGCTGTGGAAGTGG 560
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558 CATGCCAGTCTCCATCACTGAGGCTGTGAGCAGCCCTCAACCTCTCCCTCAGCTGTGCA 617
|||||
561 CATGCCAGTCTCCATCACTGAGGCTGTGAGCAGCCCTCAACCTCTCCCTCAGCTGTGCA 620
|||||
618 CTGCTGGAGACAGAGCTCTCATTTCCGGCTGGGAGAGAGCCAGCCCGAGTTAAGCC 677
|||||
621 CTGCTGGAGACAGAGCTCTCATTTCCGGCTGGGAGAGAGCCAGCCCGAGTTAAGCC 680
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678 TGCCTACAGACTTGGGATGCGCAACATCACCATATTGAGACCAAGAGTGTGAAGC 737
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681 TGCCTACAGACTTGGGATGCGCAACATCACCATATTGAGACCAAGAGTGTGAAGC 740
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738 CCTACCCGGGCAACATCAAGACACCATGTGTGTGCCAGGTGAGAGAGGGGCAAGG 797
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Db 741 CCTACCCCGGACATCAACAGACACCATGCTGTGCCAGCGTCGAGAGAGGGGCAAGC 800
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798 ACTCTGCGAGGATGACTCCGGGGCCCTGCTGCTGTAACAGCTCTTCAAGCATTA 857
|||||
801 ACTCTGCGAGGATGACTCCGGGGCCCTGCTGCTGTAACAGCTCTTCAAGCATTA 860
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858 TCTCTGTGGG-CCAGATTCGCTGTCGATACACCGAAGCCGTGTCTACAC---GAA 913
|||||
861 TCTCTGTGGGCGCCAGATTCGCTGTCGATACACCGAAGCCGTGTGTCTACACCGAAG 920
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914 GCTGCAATATATGAG 929
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921 GCTGCAATATATGAG 936
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RESULT 3
BM559617
LOCUS BM559617
DEFINITION BM559617 1074 bp mRNA linear EST 20-FEB-2002
AGENCOURT.6565456 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5744314
5', mRNA sequence.
ACCESSION BM559617
VERSION BM559617.1 GI:18803348
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1074)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMT)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILMT at:
http://image.llnl.gov
Plate: L14M12765 row: h column: 11
High quality sequence stop: 689.
Location/Qualifiers
1. 1074

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FEATURES
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5744314"
/tissue_type="medulla"
/lab_host="DH10B"
/clone_lib="NIH_MGC_119"
/Note="Organ: brain; Vector: pCMV-Sport6; Site: 1; NotI;
Site: 2; EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb. Insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
BASE COUNT      238 a      339 c      311 g      184 t      2 others
ORIGIN

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Query Match      63.4%; Score 825.2; DB 12; Length 1074;
Best Local Similarity 98.3%; Pred. No. 8.5e-78;
Matches 885; Conservative 0; Mismatches 10; Indels 5; Gaps 5;

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18 TGGTCAGGGAGAGAGGGAGGAAAGCCAGGAGGAGGACCTTAAGTGAAGAAACAAAGC 77
|||||
21 TGGTCAGGGAGAGAGGGAGGAAAG-CAAGGAGAGGACCTTAAGTGAAGAAACAAAGC 79
|||||
78 TGGGAGAGAGAGAGATCTGCGCTCGGGTCCGAGATGACAGAGTGAAGTGGCTGGGG 137
|||||

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Db      80  TGGGAGAGAGAGATCTGCGCTGGGTTCCGCGAGATGACAGAGTTGAGTGCTGGCGG 139
QY      138  ACTGGAAGTATCTGCGGAGAGGTTCTCAACAGCAGCCAGAACTGGGGCCGCTCTCC 197
Db      140  ACTGGAAGTATCTGCGGAGAGGTTCTCAACAGCAGCCAGAACTGGGGCCGCTCTCC 199
QY      198  CCCCTCAGAGCCATAGAGTTCTGCAAGTTAATCTGCTGCTCTGGCAACAGGCTTGTAG 257
Db      200  CCCCTCAGAGCCATAGAGTTCTGCAAGTTAATCTGCTGCTCTGGCAACAGGCTTGTAG 259
QY      258  GGGGAGAGAGCAGATCATCAAGGGGTTGAGTGCAGAGCCCTCAGTCCAGCCCTGGAGG 317
Db      260  GGGGAGAGAGCAGATCATCAAGGGGTTGAGTGCAGAGCCCTCAGTCCAGCCCTGGAGG 319
QY      318  CAGCCCTGTTGAGAGAGAGCGGCTACTGTTGGGGGAGCGCTCATGCGCCCAAGATGCG 377
Db      320  CAGCCCTGTTGAGAGAGAGCGGCTACTGTTGGGGGAGCGCTCATGCGCCCAAGATGCG 379
QY      378  TCCCTGAGAGAGAGCCCATGCTCTCAAGCCCGCTCATAGTTCACTGGGGGAGCAAC 437
Db      380  TCCCTGAGAGAGAGCCCATGCTCTCAAGCCCGCTCATAGTTCACTGGGGGAGCAAC 439
QY      438  TCCAGAGAGAGAGAGGCTGTGAGCAGACCCGAGCAGCCACTGAGTCTCTCCCAACCCG 497
Db      440  TCCAGAGAGAGAGAGGCTGTGAGCAGACCCGAGCAGCCACTGAGTCTCTCCCAACCCG 499
QY      498  GCTTCAACAACAGAGCTCCCAACAAGACCAACCGCAATGACATCATGCTGGTGAAGTG 557
Db      500  GCTTCAACAACAGAGCTCCCAACAAGACCAACCGCAATGACATCATGCTGGTGAAGTG 559
QY      558  CATGCGCAGTCTCATACCTGGGCTGTGGAGACCCCTCAGCTCTCTCTCAGCGTGTGCA 617
Db      560  CATGCGCAGTCTCATACCTGGGCTGTGGAGACCCCTCAGCTCTCTCTCAGCGTGTGCA 619
QY      618  CTGCTGGCAGCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 677
Db      620  CTGCTGGCAGCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 679
QY      678  TGCTCTACACCTCTGCGATGCGCCCAACATCATGAGCAGCAGCAGTGTGAGAAGC 737
Db      680  TGCTCTACACCTCTGCGATGCGCCCAACATCATGAGCAGCAGCAGTGTGAGAAGC 739
QY      738  CCTACCCCGGCAATCATACAGACACCATGCTGTGAGCAGCAGCAGGAGGGGCAAG 797
Db      740  CCTACCCCGGCAATCATACAGACACCATGCTGTGAGCAGCAGCAGGAGGGGCAAG 799
QY      798  ACTCTGCGCAGAGGTTGACTCC-GGGGGCCCTCTGCTGTGTAACAGTCTTCAAGGCA 856
Db      800  ACTCTGCGCAGAGGTTGACTCCGGGGGGGCGCTGCTGTGTAACAGTCTTCAAGGCA 859
QY      857  ATCTCTCT-GGGGCGCAGATCCGT-GTGGCATCACCGGAA-GCCTGCTGTACAGGAA 913
Db      860  ATCTCTCTGGGGGCGAGNATCCGTGTGCGATCACCGGAAAGCCTGCTGTACAGGAA 919

RESULT 4
LOCUS   BM982377/ 761 bp mRNA linear EST 21-FEB-2003
DEFINITION
UI-CF-EN1-acs-o-17-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
ACCESSION
BM982377
VERSION
BM982377.1 GI:19605813
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 761)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477

```

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PUBMED
COMMENT
8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this CDNA
sequence: 17-100, >LINE2 (matched compliment)
Seq primer: M13 FORWARD
POLYA-Tes.

FEATURES
source
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-acs-o-17-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dr)18 tail. The
sequence tag for this library is CTGCTCAGT.
TAG_Lib-UI-CF-EN1
TAG_TISSUE=Human Lung Epithelial Cell lines untreated LPS
6hr to LPS 24h
TAG_SFO="CTGCTCAGT"

BASE COUNT
172 a 170 c 222 g 195 t 2 others
ORIGIN
Query Match 58.2%; Score 757.4; DB 12; Length 761;
Best Local Similarity 99.6%; Pred. No. 1.3e-70;
Matches 758; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      527  CACCGCAATGATCATGCTGTGAGAGAGCATCGGCATCTTCATCAGTGGGCTGTG 586
Db      761  CACCGCAATGATCATGCTGTGAGAGAGCATCGGCATCTTCATCAGTGGGCTGTG 702
QY      587  CGACCCCTACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 646
Db      701  CGACCCCTACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 642
QY      647  TGGGAGAGAGCAGTCCAGCCCGGAGTACGCTGCTCTACACCTTGGAGTGGCCACATC 706
Db      641  TGGGAGAGAGCAGTCCAGCCCGGAGTACGCTGCTCTACACCTTGGAGTGGCCACATC 582
QY      707  ACCATATTGAGCAGCAGAGAGTGTGAGAACGCTTACCCGGCAATCATCAGACCATG 766
Db      581  ACCATATTGAGCAGCAGAGAGTGTGAGAACGCTTACCCGGCAATCATCAGACCATG 522
QY      767  GTGTGTGACAGCGCTGAGAGAGGGGCAAGAGACTCTGCGAGGCTCTCGGGGGCGCT 826

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VERSION      B1818697.1  GI:15930247
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    NIH-MGC http://mgc.nci.nih.gov/
AUTHORS      1 (bases 1 to 841)
TITLE        Unpublished
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabds-remail.nih.gov
              Tissue Procurement: Life Technologies, Inc.
              CDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLML)
              DNA Sequencing by: Incyte Genomics, Inc.
              DNA distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNLML at:
              http://image.lnl.gov
              plate: LLM11445 row: k column: 03
              High quality sequence stop: 784.
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                /clone_1id="NIH_MGC_115"
                /note="Organ: pooled brain, lung, testis; Vector:
                PCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
                source anonymous pool of 6 male brains, age range 23-27; 1
                male lung, age 27; and 1 male testis, age 69. Library is
                oligo-dT primed and directionally cloned (EcoRV site is
                destroyed upon cloning). Average insert size 1.8 kb,
                insert size range 1-3 kb. Library is normalized and
                enriched for full-length clones and was constructed by C.
                Gruber (Invitrogen). Research Genetics tracking code
                021. Note: this is a NIH_MGC Library."
BASE COUNT   180 a      288 c      206 g      167 t
ORIGIN
Query Match      55.3%  Score 719.4;  DB 12;  Length 841;
Best Local Similarity 97.1%  Pred. No. 1.1e-66;
Matches 817;  Conservative 0;  Mismatches 16;  Indels 8;  Gaps 8;

QY      286  CGAGTGCAGGCTCTACTCCAG-CCCTGGAGGAGCCCTGTTGAGAGAAGCGGGCTAC 344
Db      1   CGAGTGCAGGCTCTACTCCAGTCCCTGGAGGAGCCCTGTTGAGAGAAGCGGGCTAC 60

QY      345  TCTGTGGGGGAGCCTATGCGCCCGAGATGGCTCTGACAGACGCCCACTGGCTCAAGC 404
Db      61  TCTGTGGGGGAGCCTATGCGCCCGAGATGGCTCTGACAGACGCCCACTGGCTCAAGC 120

QY      405  CCCGCTCATATGTTACCTGGGGAGGACCAACCTCCAGAAAGAGAGGGGCTGTAGAGA 464
Db      121  CCCGCTCATATGTTACCTGGGGAGGACCAACCTCCAGAAAGAGAGGGGCTGTAGAGA 180

QY      465  CCC-GGACAGCAGCATGAGTCTTCCGCCACCCGGCTTCAACAACAGCCTCCCAACAA 523
Db      181  CCCGAGAGAGCAGCATGAGTCTTCCGCCACCCGGCTTCAACAACAGCCTCCCAACAA 240

QY      524  GACACCGCATATGATGCTGTGGTAAAGATGGCATGGCAAGTCTCC-ATCACCTGGGC 582
Db      241  GACACCGCATATGATGCTGTGGTAAAGATGGCATGGCAAGTCTCCATCACCTGGGC 300

QY      583  TGTGCGAGCCCTCCCTCCCTCCAGAGCTGTGACGTGGGACGACGCTGCCCATTTTC 642
Db      301  TGTGCGAGCCCTCCCTCCCTCCAGAGCTGTGACGTGGGACGACGCTGCCCATTTTC 360

QY      643  CGGCTGGGGAGAGCAGTCCAGAGCCCGATTACGGCTGCTCCACACCTTGGAGATGGCAA 702
Db      361  CGGCTGGGGAGAGCAGTCCAGAGCCCGATTACGGCTGCTCCACACCTTGGAGATGGCAA 420

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QY      703  CATCACCATCATTTGAGACCGAGAGTGTGAGAACGCCCTACCCCGCAACATCACAGACAC 762
Db      421  CATCACCATCATTTGAGACCGAGAGTGTGAGAACGCCCTACCCCGCAACATCACAGACAC 480

QY      763  CATGCTGTGTGCCAGCTGTCAGAGA-AAGGGGCAAGAGACTCTGCGAGGATGACTCCGGGG 821
Db      481  CATGCTGTGTGCCAGCTGTCAGAGAGAGGGGCAAGAGACTCTGCGAGGATGACTCCGGGG 540

QY      822  GCCCTGTGTGTGTAACAGAGTCTCTTCA-GGATATATCTCTGGGGCCAGAGATCCGTGT 880
Db      541  GCCCTGTGTGTGTAACAGAGTCTCTTCAAGATATATCTCTGGGGCCAGAGATCCGTGT 600

QY      881  GCGATTCACCCGAAAGCCTGTGTCTTACAGCAAAAGTGTCAAAATATGTGAGATGATCCAG 940
Db      601  GCGATTCACCCGAAAGCCTGTGTCTTACAGCAAAAGTGTCAAAATATGTGAGATGATCCAG 660

QY      941  GAGACGATGAAAGCAATTTAGACTGAGACCCACCA-CCACAGCCCATACCTTCATTTTC 999
Db      661  GAGACGATGAAAGCAATTTAGACTGAGACCCACCAAGATGATGATGATGATGATGATGAT 720

QY      1000  CACTTGTGTGTTGTCTCTGTCTTCACTCTGTATA-AGAAACCTTAAGCCAGACCTTC 1057
Db      721  CACTTGTGTGTTGTCTCTGTCTTCACTCTGTATAAGATGATGATGATGATGATGATGAT 780

QY      1058  TACGACATCTTTGGGCTCTCTGAGTACAGAGATGCTGTCAATTAATCAACCTG 1117
Db      781  TCGACACCTCTTTGGGCTCTCTGAGTACAGAGATGCTGTCAATTAATCAACCTG 840

QY      1118  G 1118
Db      841  G 841

RESULT 7
BX109836      747 bp  mRNA  linear  EST 07-FEB-2003
BX109836 Soares, fetal, heart, NBH119W Homo sapiens cDNA clone
IMAGE998A02781 ; IMAGE:342025, mRNA sequence.
BX109836
BX109836.1  GI:27877879
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 747)
Ebert, L., Hell, O., Hennig, S., Neubert, P., Patsch, E., Peters, M.,
Radeflo, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IMAGE998A02781.
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/cloncards/cg1-
bin/showlib.pl.cgi?response=libno=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 101
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAAGACGTATGAC.
Location/Qualifiers
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source

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Best Local Similarity 99.68; Pred. No. 2.9e-61;  
Matches 670; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 679 GCTTCACACCTTGGGATGCGGCAACATCACCATCATTTGAGCAGCAAGATGTGAAGCG 738
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LOCUS 603047836F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:518796 5',  
DEFINITION mRNA sequence.  
ACCESSION B1763040  
VERSION B1763040.1 GI:15754618  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 678)  
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://lml1469.lnl.gov>  
plate: lml1469 row: h column: 09  
High quality sequence stop: 647.

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Location/Qualifiers  
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source anonymous pool of 3 clones; Age 26 yo male, 49 yo  
female, 71 yo male colon; 46 yo male kidney, and pool of 2  
stomachs, 62 yo male and 70 yo female. Library is  
oligo-dT primed and directionally cloned (EcoRV site is  
destroyed upon cloning). Average insert size 1.4 kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruber (Invitrogen). Research Genetics tracking code  
023. Note: this is a NIH-MGC Library."

BASE COUNT 152 a 234 c 172 g 120 t  
ORIGIN

Query Match 50.7%; Score 659.6; DB 12; Length 678;  
Best Local Similarity 98.78; Pred. No. 2.3e-60;

Matches 665; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 5 CCTGTTTCGAGAAAGACGCGGTACTGTGTGGGGGAGAGCTTACGCCCCAGATGCTCC 64
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Db 65 TGACAGCAGCCACTGCTCAAGCCCGGCTACATATGTTCACTGGGGGAGACACCTCC 124
QY 441 AGAAGGAGGAGGGGTGTGAGAGAGACCGGAGCGCATGATGCTTCCGACCCGGCT 500
Db 125 AGAAGGAGGAGGGGTGTGAGAGAGACCGGAGCGCATGATGCTTCCGACCCGGCT 184
QY 501 TCAACAACAGCTCCCAACAAGAACCCGCAATGATCATATGCTGTGAAGTGCAT 560
Db 185 TCAACAACAGCTCCCAACAAGAACCCGCAATGATCATATGCTGTGAAGTGCAT 244
QY 561 CGCAGTCTCATATACCTGGGCTGTGAGACCCCTCAACCTCTCTCAAGCTGTCACTG 620
Db 245 CGCAGTCTCATATACCTGGGCTGTGAGACCCCTCAACCTCTCTCAAGCTGTCACTG 304
QY 621 CTGGCAGCAGGTGCTCATTTCCGGCTGGGGGAGCAATGACGCCCCAGTTACGCTGC 680
Db 305 CTGGCAGCAGGTGCTCATTTCCGGCTGGGGGAGCAATGACGCCCCAGTTACGCTGC 364
QY 681 CTGACACCTTGCATGCGGCAACATCAATCATATTTGAGCAAGAGTGTGAGAACGCT 740
Db 365 CTGACACCTTGCATGCGGCAACATCAATCATATTTGAGCAAGAGTGTGAGAACGCT 424
QY 741 ACCCGGGCAACATCAGACACCATGCTGTGTGCGACGCTGCAAGAAAGGGGCAAGACT 800
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LOCUS   BB867930
DEFINITION 60143517F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847565 5',
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ACCESSION BE867930
VERSION   BE867930.1 GI:10316706
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
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          Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 973)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          plate: LLAM9562 row: a column: 06
          High quality sequence stop: 714.
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BASE COUNT 241 a 302 c 288 g 142 t
ORIGIN
Query Match 50.5%; Score 657.4; DB 10; Length 973;
Best Local Similarity 90.7%; Pred. No. 3.1e-60;
Matches 759; Conservative 0; Mismatches 66; Indels 12; Gaps 5;

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Db      61 GCTGGAGAGAGAGAGATCTGCGCTCGGGTCCGAGATGCAAGAGTTGAGGTGCTCGG 120

Oy      136 GGACTGGAAGTCAATCGGCGAGAGTCTCACAGCAGCAGCAAGAACTGGGCGCCGCTCCTC 195
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Db      121 GGACTGGAAGTCAATCGGCGAGAGTCTCACAGCAGCAGCAAGAACTGGGCGCCGCTCCTC 180

Oy      136 CCCCTCCAGAGCCATGAGAGATTCTCAGATTAACTCTGCTGTGCGCAACAGGGCTTGT 255
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        |||||
Db      301 GGCAGGACAGCCCTGTTTCAGAGAGACGGCGCTACTCTGTGGGGAGAGCTCATCGGCCCA 360

Oy      372 GATGGCTCTGACAGAGCCCACTGCTCAAGCC---CCGTTACATTAATTCACTTCACTG 427
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Db      361 GATGGCTCTGACAGAGCCCACTGCTCAAGCCCGCGGCTGCTACATTAATTCACTTCACTG 420

Oy      428 CAGCAGCAACCTCCAGAGAGAGAGGCGCTGTGAGCAGACCCGAGACCCGCTGCTTC 487
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Db      421 CAGCAGCAACCTCCAGAGAGAGAGGCGCTGTGAGCAGACCCGAGACCCGCTGCTTC 480

Oy      488 CCCCAACCCCGGCTTCAACACAGACCTCCCAACAAAGACACCGCAATGACATCATGCTG 547
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Oy      548 GTGAAGATGGCATTCGCCAGTCTTCATACCTGAGGCTGTGCGACCCCTCACTCTCTCA 607
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Db      541 GTGAAGATGGCATTCGCCAGTCTTCATACCTGAGGCTGTGCGA-CCCTCACTCTCTCTCA 599

Oy      608 CGCTGTGCTACGTGTGGACACAGCTGCCATTTCCGGTGGGG--CAGCAGTCCAGGC 665
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Db      600 CGCTGTGCTACGTGTGGACACAGCTGCCATTTCCGGTGGGGCAGACAGTCCAGGC 659

Oy      666 CCCAGTTACGCTGCTGCCTCACACCTTGCAGTGGCCCAACATCACATCATTTAGACACAGA 725
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Oy      726 ACTGTGAGAGAGCGCTTACCCCGCAATCACAGACACCATGTGTG-TGCCAGCTGCAG 784
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Db      720 GTGTGAGAGAGCGCTTACCCCGCAATCACAGACACCATGTGTGTGCCAGCTGCAG 779

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LOCUS   AK009360
DEFINITION AK009360 1295 bp mRNA linear HTC 05-DEC-2002
          Mus musculus adult male tongue cDNA, RIKEN full-length enriched
          library, clone:2310015108 product:protease, serine, 20, full insert
          sequence.
ACCESSION AK009360
VERSION   AK009360.1 GI:12844110
KEYWORDS HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS   Carninci, P. and Hayashizaki, Y.
TITLE     High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
MEDLINE   99279253
PUBMED    10349636

REFERENCE 2
AUTHORS   Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
          Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
          prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE   20499374
PUBMED    11042159

REFERENCE 3
AUTHORS   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
          Konno, H., Akiyama, Y., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
          Sumi, N., Ishii, Y., Nakamura, S., Hazama, N., Nishino, T., Harada, A.,
          Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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QY	721	CCAGAAAGTGTGAGAAAGCCTACCCCGGCACATACACAGACCAATGATGTGTGCGACGCT	780
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QY	781	GCAGAAAGGGGGCAGAGACTCTTGCCAGAGGTGACTCGGGGGCCCTTGTCGTGTAAACCA	840
Db	794	TGCGAAAGAGGGGCAAGAGACTCTGTGACAGGATGAGACTGTGAGAGGCCCTCGTCTCAACGG	853
QY	841	GTCCTCTCAAGGCAATTAATCTCTGGGGGACAGATCCGTCGATCAACCCCAAAAGCCCTGG	900
Db	854	ATCTCTTCAAGGCAATCATCTCTGGGGGACAGGACCATGTGCTCCGTCACAGAAAGCCCTGG	913
QY	901	TGCTTACACGAAATCTGTCAATTAATGTGAGCTGGATCCAGAGAGAGATGAAGAAACAATTA	960
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QY	1021	TCACTCTGTTAATAAGAAACCCCTTAAGCAGAACCTTCTACGAAATTCCTTTGGGCTTCC	1079
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QY	1080	TGAGACTACAG----GAGATGCTGTCACTTAATTAATCAACTGGGGTTCCGAATC-AGTGA	1134
Db	1094	ATGAGTATAGATATAGGAGTGTCTTAATGATGATGACCTTGGGGCCCTGGAAATTAATCC	1153
QY	1135	GACCTGATTAATTCCTGCTTGAATTAATGTGACTCTGGGAAATGACMACACCTGTGT--	1192
Db	1154	TGACTGTGAATTAATTTGACTCTGACATGATCACACACTGTGTTTGTGTTTGGTTGT	1213
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DEFINITION	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310040F07 product:protease, serine, 20, full insert		
ACCESSION	AK009720	GI:12844688	
VERSION	AK009720		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PubMed	10349636		
REFERENCE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, R.,		
AUTHORS	2		

**TITLE**  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000).  
 20499374  
 11042159  
**REFERENCE**  
**AUTHORS**  
 3  
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Saeki, N., Carninci, P.,  
 Konno, H., Akiyama, Y., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M.,  
 Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashtwari, K.,  
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, K.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN Integrated Sequence Analysis (RISA) system-384-format  
 sequencing pipeline with 384 multichipillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
**JOURNAL**  
**MEDLINE**  
**PUBMED**  
 11076861  
**REFERENCE**  
**AUTHORS**  
 4  
 Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
 Aikawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,  
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondou, S., Yamana, I.,  
 Saito, T., Okazaki, Y., Gotojori, T., Bono, H., Kasukawa, T., Saito, R.,  
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,  
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 Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bul, C.,  
 Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,  
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 Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L.,  
 Wyszynski, B., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L.,  
 Wyszynski, B., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L.,  
 Hayashizaki, Y.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409 (6821), 685-690 (2001)  
 21085660  
 11217851  
**TITLE**  
 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**  
 6  
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,  
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 Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (10-JUN-2000) Yoshinori Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)  
**TITLE**  
 COMMENT  
 cDNA library was prepared and sequenced in Mouse Genome



REFERENCE 1 (bases 1 to 708)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgaphs-remail.nih.gov](mailto:cgaphs-remail.nih.gov)  
 Tissue Procurement: James Cleaver, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at: <http://image.llnl.gov>  
 Plate: LHM10699 row: a column: 21  
 High quality sequence stop: 704.  
 Location/Qualifiers  
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 /clone\_image="4803356"  
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 /clone\_lib="NCI CGAP\_Skn3"  
 /note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI CGAP Library."  
 BASE COUNT 147 a 262 c 183 g 116 t  
 ORIGIN  
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 Best Local Similarity 99.7%; Pred. No. 2.3e-57;  
 Matches 632; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 75 AGCTAGAGACCTGGGGCCGCTCCCTCCAGGCGATGAGATTCTGCACTAT 134  
 229 CCTGCTCTGTGGACAGAGGCTTGTAGGGGAGAGACGAGATCATCAAGGGTTCGA 288  
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 135 CCGTCTCTGTGGACAGAGGCTTGTAGGGGAGAGACGAGATCATCAAGGGTTCGA 194  
 289 GTGCAAGCTCTACCTCCAGCCCTGGAGAGAGCCCTGTTGAGAGAGCGGCTACTGTG 348  
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 195 GTGCAAGCTCTACCTCCAGCCCTGGAGAGAGCCCTGTTGAGAGAGCGGCTACTGTG 254  
 349 TGGGGCGAGCTCATCGCCCGAGATGGCTCCTGACAGAGCCGCTGCTCAACCCCG 408  
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 255 TGGGGCGAGCTCATCGCCCGAGATGGCTCCTGACAGAGCCGCTGCTCAACCCCG 314  
 409 CTACATAGTACCTGGGGAGACACACCTCCAGAGAGAGAGGCTGTGAGCAGACCG 468  
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 315 CTACATAGTACCTGGGGAGACACACCTCCAGAGAGAGAGGCTGTGAGCAGACCG 374  
 469 GACAGCCACTAGTCTTCCCGACCCGGGCTTCAACAACAGCCTTCCCAACAAGACCA 528  
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 375 GACAGCCACTAGTCTTCCCGACCCGGGCTTCAACAACAGCCTTCCCAACAAGACCA 434  
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 589 ACCCTCACCCTCTCTCAGCTGTGTGACATGCTGGACACAGCTGCTCATATTTCCGGGTG 648  
 495 ACCCTCACCCTCTCTCAGCTGTGTGACATGCTGGACACAGCTGCTCATATTTCCGGGTG 554  
 649 GGGAGACAGCTCAGCCCGCAAGTTACGCTTGGCTCAGACCTTGGATGCGCAACATAC 708  
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 555 GGGAGACAGCTCAGCCCGCAAGTTACGCTTGGCTCAGACCTTGGATGCGCAACATAC 614  
 709 CATCATTTAGACACGAGAGTGTGAGAAAGCTACCGCGGCAACATCAGAGACCATGTT 768  
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RESULT 14  
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 ACCESSION AK009659  
 VERSION AK009659.1 GI:12844589  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS Carninci, P., and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

REFERENCE  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159

REFERENCE  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861

REFERENCE  
 AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aikawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Salto, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Salto, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiya, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaio, I., Pesole, G., Quackenbush, J., Schriml, L. M., Stabli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarilli, J., Momberts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seva, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyokawa, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wyszewski, B., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohitsuki, S., and Hayashizaki, Y.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409 (6821), 685-690 (2001)  
 MEDLINE 21085660  
 PUBMED 11217851

REFERENCE  
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.





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1188	TTTTTGTGTTTCTGTTCTTTCTTCCACGCTTGAAGACAGTCCCGG-CATATCCACAGG	1246
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DEFINITION	UI-CF-DUI1-aam-j-17-0-UI-s1 UI-CF-DUI Homo sapiens cDNA clone	
ACCESSION	UI-CF-DUI1-aam-j-17-0-UI 3', mRNA sequence.	
VERSION	B0676834	
KEYWORDS	B0676834.1 GI:23522189	
SOURCE	EST.	
ORGANISM	Homo sapiens (human)	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE	1 (bases 1 to 654) Bonaldio,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene discovery Genome Res. 6 (3), 791-806 (1996)	
JOURNAL	Genome Res. 6 (3), 791-806 (1996)	
MEDLINE	9704447	
PUBMED	8889548	
COMMENT	Contact: McCray, PB McCrays lab University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA. Tel: 319 356 4866 Fax: 319 356 7171 Email: paul.mccray@uiowa.edu Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA library preparation: Dr. M. Bento Soares, University of Iowa CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com). The following repetitive elements were found in this cDNA sequence: 17-100->LINE2 (matched compliment) Seq primer: M13 FORWARD POLYA-Yes.	
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	/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-DUI1 is a normalized cDNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldio, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dr)18 tail. The sequence tag for this library is GGCTGTAGGC. TAG_Lib=UI-CF-DUI1 TAG_Tissue=Lung Epithelial Cells Tissue nos 359-368 TAG_Seq=GGCTGTAGGC"	

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Db	616	TACCCCTGCCCTCACACCTTGTGGGATGCGCCACATCTACCATCATTTAGAGACCAAGAGTGTG	557			
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Db	556	AGAACGCTTACCCCGGCAACATCAGACACACATGTTGTGTGCCAGGTGACGAAGAGG	497			
OY	792	GCAAGAGATCTCTGCCAGGGTGACTCCGGGGGCCCTCTGTGTGTAAACAGTCTCTTCAAG	851			
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Db	436	GCATTATCTCTCTGGGGCCAGGATCCGTGTGCGATCACCCGGAAGCCTGGTGTACACGA	377			
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Db	316	CCGACACAGCCCATCACCTCTCAATTTCCACTGGTGTGTGTCCTGTCACCTGTGTA	257			
OY	1032	ATTAAGAAACCCCTAAGCCCAAGACCTCTACGAACATTTTGGGCCCTCTGTGACACAGA	1091			
Db	256	ATTAAGAAACCCCTAAGCCCAAGACCTCTACGAACATTTTGGGCCCTCTGTGACACAGA	197			
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Best Local Similarity	100.0%;	Pred. No. 8.4e-56;			
Matches 616;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	672	TACCCCTGCCCTCACACCTTGGGATGCGCCACATTCACCATCATTTAGACACCAAGAGTGTG	731		
Db	616	TACGCTGCTCCCTCACACCTTGGGATGCGCCACATTCACCATCATTTAGAGCACAGAAAGTGTG	557		
OY	732	AGAACGCTTACCCCGGCAACATCAGACACACCATGATGTGTGCCAGGTGCAAGAAAGGG	791		
Db	556	AGAACGCTTACCCCGGCAACATCAGACACACCATGATGTGTGCCAGGTGCAAGAAAGGG	497		
OY	792	GCAAGAGCTCTGCGCAGGCTGACTCCGAGGGGCCCTCTGTGTGTAAACAGTCTCTTCAAG	851		
Db	496	GCAAGAGCTCTGCGCAGGCTGACTCCGAGGGGCCCTCTGTGTGTAAACAGTCTCTTCAAG	437		
OY	852	GCATTATCTCTGTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTCTACAGCA	911		
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OY	912	AAGCTGCAATATGTGAGCTGAGTCCAGGAGAGCATGTAAGAAACAATTAGACTGGACCA	971		
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Db	196	GATGCTGCACTTAATATCAACCTGGGGGTTCGAAATCAGTAGACCTGGATTCAAATTC	137		
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

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5843.068 Million cell updates/sec

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Delop 6.0 , Delext 7.0

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	756	31.9	250	1	KIKR_HUMAN
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8	650.5	27.4	293	1	KIKR_HUMAN
9	632.5	26.7	251	1	KIKR_HUMAN
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22	595	25.1	261	1	KIKR_HUMAN
23	594	25.1	238	1	TRY3_SALSA
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#### ALIGNMENTS

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DT	16-OCT-2001	(rel. 40, Last sequence update)			
DT	15-SEP-2003	(rel. 42, Last annotation update)			
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GN	KIK11 OR PRSS20 OR TLSP.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
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RA	Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;				
RT	"CDNA cloning and expression of a novel serine protease, TLSP.,"				
RL	Biochim. Biophys. Acta 1399:225-228(1998).				
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RC	TISSUE=Hippocampus, and Prostate;				
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RA	Mitsu S., Yamada T., Okui A., Komiyama K., Uemura H., Yamaguchi N.;				
RT	"A novel isoform of a kallikrein-like protease, TLSP/hippocastin,				
RL	(PRSS20), is expressed in the human brain and prostate."				
RN	Biochem. Biophys. Res. Commun. 272:205-211(2000).				
RP	[3]				
RC	SEQUENCE FROM N.A. (ISOFORM 1).				
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RA	Yousef G.M., Scorilas A., Diamandis E.P.;				
RT	"Genomic organization, mapping, tissue expression, and hormonal				
RL	regulation of trypsin-like serine protease (TLSP PRSS20), a new				
RN	member of the human kallikrein gene family."				
RL	Genomics 63:88-96(2000).				
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RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuag J.;				
RT	Moss P., Paepers B., Wang K.;				

"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region." [5]

SEQUENCE FROM N.A. (ISOFORM 1).

RA Iamertin J.E., McCreedy P.M., Skowronski E., Wiswanathan V.,  
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 RA Phan H., Velasco N., De L., Regala W., Terry A., Brower A., Ganes J.,  
 RA Dangnan L., Eiler A., Christensen M., Georgescu A., Avila J., Liu S.,  
 RA Andreise T., Trankheim M., Altix C., Amico-Keller G., Coffield J.,  
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  
 RA Ariellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
 RA Olsen A.S., Carrano A.V.,  
 RT "Sequence analysis of chromosome 19q13.4."  
 RT Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.

SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE-Testis;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usslin T.B., Toshylyuk S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smallus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- FUNCTION: POSSIBLE MULTIFUNCTIONAL PROTEASE. EFFICIENTLY CLEAVES  
 BE-PHE-ARG-4-METHYLCOMARYL-7-AMIDE, A KALLIKREIN SUBSTRATE, AND  
 WEAKLY CLEAVES OTHER SUBSTRATES FOR KALLIKREIN AND TRYPSIN.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named Isoforms-2:

CC Name=1;  
 CC IsoId=09UBX7-1; Sequence-Displayed;  
 CC Name=2;  
 CC IsoId=09UBX7-2; Sequence-VSP\_005402;

CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKIN AND PROSTATE. ISOFORM  
 CC 1 IS EXPRESSED PREFERENTIALLY IN BRAIN; ISOFORM 2 IN PROSTATE.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.

CC -----

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 CC or send an email to [license@lsb-sib.ch](mailto:license@lsb-sib.ch)).

CC -----

DR EMBL; AB012917; BAA33404.1; ALT\_INIT.  
 DR EMBL; AB013730; BAA8713.1; -  
 DR EMBL; AB041036; BAA96797.1; -  
 DR EMBL; AF164623; AAD47815.1; -  
 DR EMBL; AF243527; AAG33364.1; -  
 DR EMBL; AC011473; AAG23257.1; -  
 DR EMBL; BC022068; AAH22068.1; -  
 DR HSSP; P00763; IDPO.  
 DR MEROPS; S01.257; -  
 DR Genew; HGNC:6359; KLK11.  
 DR MIM; 604434; -  
 DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR Pfam; PF00089; trypsin\_1.  
 DR PRINTS; PRO0722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolyse; Serine protease; Glycoprotein; Signal; zymogen;  
 KW Alternative splicing.

FT SIGNAL 1  
 FT PROPEP 19 21  
 FT CHAIN 22 250  
 FT ACT\_SITE 62 62  
 FT ACT\_SITE 110 110  
 FT ACT\_SITE 203 203  
 FT DISULFID 28 163  
 FT DISULFID 47 63  
 FT DISULFID 135 237  
 FT DISULFID 142 209  
 FT DISULFID 174 188  
 FT DISULFID 199 224  
 FT CARBOHYD 99 165  
 FT CARBOHYD 165 165  
 FT CARBOHYD 181 181  
 FT CARBOHYD 210 210  
 FT VARSPLIC 1  
 FT FT 1

SEQUENCE 250 AA: 27466 MW: 1929108BCDC7A56 CRC64:  
 /FTid=VSP\_005402.

Alignment Scores:  
 Pred. No: 2,4e-81 Length: 250  
 Score: 1355.00 Matches: 250  
 Percent Similarity: 100.00% Conservative: 0  
 Best local Similarity: 100.00% Mismatches: 0  
 Query Match: 57.17% Indels: 0  
 Ds: 1 Gaps: 0

US-09-856-320a-1 (1-1301) x KLRB\_HUMAN (1-250)

QY 209 ATGAGGATTCGACGATTAATCCGCTGCTGGCGCAACAGGGCTTGAGGGAGAGAGACC 268  
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 Db 1 MetArgIleuLeuGlnleuIleuLeuLeuAlaLeuAlaThrGlyGlyGluThr 20

QY 269 AGCATCATCAAGGGGTTCGAGTCCAAAGCTCACTCCAGCCCTGGAGCAGCAGCCGTTC 328  
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 Db 21 ArgIleIleuGlyPheGlnGlyPheGlnGlyPheGlnGlyPheGlnGlyPheGlnGlyPhe 40

QY 329 GAGAAAGCGGGCTACTCTGTGGGGGAGCCCTATGCGCCCAAGATGGCTCTGACAGCA 388  
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 Db 41 GluIysThrArgIleuLeuGlyAlaThrIleuLeuAlaProArgTrpLeuThrAla 60

QY 389 GCCCACTGCTCAAGCCCGCTACATAGTCCATGGGGGAGCAACCCCAAGAGGAG 448  
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 Db 61 AlaHisCysLeuIysProAlaGlyTyrIleValHisLeuGlyGlnHisAsnLeuGlnGly 80

QY 449 GAGGGGTTCGAGCAGACCCGAGCAGCCAGTCTCTCCCAAGCCCGGCTTCAACAC 508  
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 Db 81 GluGlyCysLeuGlnThrArgThrAlaThrIleuSerPheProHisProGlyPheAsnAsn 100

QY 509 AGCCTCCCAACAAGACCAAGCAGCCATGACATCATGCTGTGGAAGTGGATGCCAGTCC 568  
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 Db 101 SerIleuProAsnIysAspHisAlaArgAsnAspIleMetLeuValIysMetAlaSerProVal 120

QY 569 TCCATACCTGGGCTGTGGACCCCTCAGCTCTCTCAGCGCTGTGTCTGCTGACACC 628  
 |||||||  
 Db 121 SerIleThrTrpAlaValArgProLeuThrIleuSerSerArgCysValThrAlaGlyThr 140

QY 629 AGCTGCCTCATTCGCGGTGGGAGCAGCTCCAGCCCAAGTACGCTGCTGACACC 688  
 |||||||  
 Db 141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnIleuArgLeuProHisThr 160

QY 689 TTGCGATGGCCCAACATCATCATGAGACACAGAGTGTGAGAACGCTTACCCGGC 748



Db 109 AsnAspSerPleMetLeuIleArgLeuProArgGlnAlaArgLeuSerProAlaValGln 128  
 QY 590 CCCCCTACACCTCTCTCAGCCTGTGTGACAGTGTGGACACACCTCCATTTCCGGCTGG 649  
 Db 129 ProLeuAsnLeuSerGlnThrCysValSerProGlyMetGlnCysLeuIleSerGlyTrp 148  
 QY 650 GGCAGCAGCCGACCCCGCAGTTCAGCCTGCTCAGACCTTGGCATGCGCCAAATACAC 709  
 Db 149 G1YAlaValSerSerProLysAlaLeuPheProAlaThrLeuGlnCysAlaAsnIleSer 168  
 QY 710 ATCATTCAGACACACAGAGTGTGAGAGCCCTACCCCGGCAACACACAGACCATGGTG 769  
 Db 169 IleLeuGlnAsnLysLeuGlnCysHisThrPalaIleTrpProGlnHisIleSerAspSerMetLeu 188  
 QY 770 TGTGCCAGCCTGCAGGAGGGGGCAGACTCTGCCAGGGGTGACTCCGGGGCCCTCTG 829  
 Db 189 CysAlaIleGlyLeuTrpGlnGlyArgGlySerCysGlnGlyAspSerGlyGlyProLeu 208  
 QY 830 GTCGTGAACCAAGTCTCTTCAAGGATATATCTCCCTGGGGCCAGATCCGCTGTGCATCAC 889  
 Db 209 ValCysAsnGlyThrLeuAlaGlyValValSerGlyLeuAlaGluProCysSerArgPro 228  
 QY 890 CGAAGCCTGGTGTCTACACAGAAAGTGTGCAATATGTGTGACATGATCCAGACAGCATG 949  
 Db 229 ArgArgProAlaValIleTrpThrSerValCysHisThrLeuAspTrpIleGlnGluIleMet 248  
 QY 950 AAGAAC 955  
 Db 249 GluAsn 250

RESULT 3  
 NRPN\_RAT  
 ID NRPN\_RAT STANDARD: PRT: 260 AA.  
 AC 088780;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuropilin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine  
 protease 1)  
 GN KIK8 OR PRS19 OR NRPN OR BSP1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Fischer; TISSUE=Brain;  
 RX MEDLINE=98389725; PubMed=9722524;  
 RA Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;  
 RT "Serine proteases in rodent hippocampus";  
 RL J. Biol. Chem. 273:23004-23011(1998).  
 CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND  
 CC HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST  
 CC FIBRONECTIN (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO HIPPOCAMPUS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: AI005641; CA006643.1; -  
 DR HSP; Q61955; INPM.  
 DR MEROPS; S01.244; -  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR001254; Ser.protease\_Try.  
 DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYP\_SPE; 1.  
 DR PROSITE; PS00240; TRYPsin\_DOM; 1.  
 DR PROSITE; PS00134; TRYPsin\_HIS; 1.  
 DR PROSITE; PS00135; TRYPsin\_SER; 1.  
 KW Hydrolyase; Serine protease; Glycoprotein; zymogen; signal.  
 FT SIGNAL 1 28  
 FT PROPEP 29 32  
 FT CHAIN 33 260  
 FT ACT\_SITE 73 73  
 FT ACT\_SITE 120 120  
 FT ACT\_SITE 212 212  
 FT DISULFID 39 173  
 FT DISULFID 58 74  
 FT DISULFID 145 246  
 FT DISULFID 152 218  
 FT DISULFID 184 198  
 FT DISULFID 208 233  
 FT CARBOHYD 110 110  
 SQ SEQUENCE 260 AA; 28510 MW; 58DF4F0602A0BF5 CRC64; (POTENTIAL).  
 N-LINKED (GLCNAC... ) (POTENTIAL).  
 Alignment Scores:  
 Pred. No.: 1,18e-38 Length: 260  
 Score: 701.50 Matches: 129  
 Percent Similarity: 66.67% Conservative: 35  
 Best Local Similarity: 52.44% Mismatches: 75  
 Query Match: 29.60% Indels: 7  
 DB: 1 Caps: 3  
 US-09-856-320A-1 (1-1301) x NRPN\_RAT (1-260)  
 QY 227 ATCTGCTGCTCTGGGACACAGGCTGTAGGGGACAGACAGC----- 271  
 Db 13 IleLeuLeuPheLeuLeuMetGlyAlaIlePalaGlyLeuThrAlaGlnGlySerLys 32  
 QY 272 ATCATCAAGGGGTTGAGTGAAGCCTCATCCAGCCCTGGAGGAGCGCTGTGAG 331  
 Db 33 IleLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 52  
 QY 332 AAGAGGGGCTACTCTGTGGGGCGAGCCTCATCCGCCAGATGGCTCTGACAGACC 391  
 Db 53 GlyLysLysLeuValLysGlyGlyValLeuValGlyAspArgTrpValLeuThrAlaAla 72  
 QY 392 CACTGCTCAAGCCCCCTCATATGTCACCTGGGGCAGACACACCTCCAGAGAGAG 451  
 Db 73 HisCysLysLysAspLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 92  
 QY 452 GCGTGTGAGGAGACCCCGACAGCCATGATGCTCCCGCCAGCCCGGCTTCACACACAG 511  
 Db 93 GluProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 112  
 QY 512 CTCGCCAACAAGACACCCCAATGATCATGCTGTGGAAGATGGCATGCCAGTCTCC 571  
 Db 113 AsnPro---GluAspHisSerHisAspIleMetLeuIleArgLeuGlnAsnSerAlaAsn 131  
 QY 572 ATACCTGGGCTGTGGACCCCTCATCCCTCTCTCATCCGCTGTGTGACCTGTGCAC 631  
 Db 132 LeuGlyAspLysValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 151  
 QY 632 TGCTCATTTCCGGCTGGGACAGCGTGCAGGCCCGCCAGTTCAGCCCTGCACACCTG 691  
 Db 152 CysIleIleSerGlyTrpGlyThrValThrSerProGlnGlnAsnPheProAsnThrLeu 171  
 QY 692 CGATCGCCCAATCATCATCATGAGCAGACAGAGTGTGAGAGCGCTACCCCGGAC 751  
 Db 172 AsnGlyAlaGlnValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 191  
 QY 752 ATCAGACACACATGTGTGTGCGAGCGTGCAGAGAGGGGAGAGCTCTCCACAGGT 811  
 Db 192 IleThrGlnGlnLysMetValCysAlaGly---SerSerAsnLysAlaAspThrCysGlnGly 210  
 QY 812 GACTCCGGGGGCGCTCTGCTGTATACCAATCTCTTCAAGCATATATCTCTGGGGCAG 871  
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Db 211 AspSerGlyGlyProLeuValCysAsnGlyValLeuGlnGlyIleThrThrTrpGlySer 230  
 QY 872 GATCCGTGTGCATACCCGGAAGCCTGTGTACACGAAAGTCTGCAATATGTGAC 931  
 Db 231 AspProCysGlyLysProGluIulysProGlyValTyrThrLysIleCysArgTyrThrAsn 250  
 QY 932 TGATCCAGGAGCAGT 949  
 Db 251 TrpIleLysLysThrMet 256  
 RESULT 4  
 NRP.N.MOUSE  
 ID NRP.N.MOUSE STANDARD: PRT: 260 AA.  
 AC 061955;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neutropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8).  
 GN KLK8 OR PRSS19 OR NRP.N.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C; TISSUE-Hippocampus;  
 RX MEDLINE=95348817; PubMed=7623137;  
 RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,  
 Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;  
 RT "Expression and activity-dependent changes of a novel limbic-serine  
 protease gene in the hippocampus.";  
 RL J. Neurosci. 15:5088-5097(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;  
 RT "Cloning and assignment of mouse neutropsin gene, Prss19 to chromosome  
 7B4.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBI databases.  
 RN [3]  
 RP SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.  
 RC STRAIN-BALB/C; TISSUE-Brain;  
 RX MEDLINE=9825202; PubMed=9556608;  
 RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,  
 Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;  
 RT "Characterization of recombinant and brain neutropsin, a  
 plasticity-related serine protease.";  
 RL J. Biol. Chem. 273:11189-11196(1998).  
 RN [4]  
 RP X-RAY CRYSTALOGRAPHY (2.1 ANGSTROMS) OF 33-257.  
 RC TISSUE-Hippocampus;  
 RX MEDLINE=99134351; PubMed=9933620;  
 RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,  
 Shiosaka S., Hakoshima T.;  
 RT "Crystal structure of neutropsin, a hippocampal protease involved in  
 kindling epileptogenesis.";  
 RL J. Biol. Chem. 274:4220-4224(1999).  
 CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND  
 HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST  
 FIBRONECTIN.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.  
 CC -1- ENZYME REGULATION: STRONGLY INHIBITED BY DIISOPROPYL  
 FLUOROPHOSPHATE, LEUPEPTIN AND (4-AMIDINOPHENYL)METHANESULFONYL 1-  
 FLUORIDE.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE LIMBIC SYSTEM OF  
 MOUSE BRAIN AND IS LOCALIZED AT HIGHEST CONCENTRATION IN PYRAMIDAL  
 NEURONS OF THE HIPPOCAMPAL CA1-3 SUBFIELDS.  
 CC -1- MASS SPECTROMETRY: MW=26613; METHOD-MALDI; RANGE=29-260.  
 CC -1- MASS SPECTROMETRY: MW=26229; METHOD-MALDI; RANGE=33-260.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: D30785; BAA06451.1; -.  
 DR EMBL: AB032202; BAA92435.1; -.  
 DR PIR: I56559; I56559.  
 DR PDB: INPM; 23-MAR-99.  
 DR MEROPS: S01.244; -.  
 DR MGD: MGI:892018; Klk8.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYPSIN\_SPC; 1.  
 DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 DR HydroLase: Serine protease; Glycoprotein; zymogen; signal;  
 KW 3D-structure.  
 KM  
 FT SIGNAL. 1 28  
 FT PROPEP 29 32  
 FT CHAIN 33 260  
 FT ACT\_SITE 73 73  
 FT ACT\_SITE 120 120  
 FT ACT\_SITE 212 212  
 FT DISULFID 39 173  
 FT DISULFID 58 74  
 FT DISULFID 145 246  
 FT DISULFID 152 218  
 FT DISULFID 184 198  
 FT DISULFID 208 233  
 FT CARBOHYD 110 110  
 FT STRAND 34 34  
 FT STRAND 37 38  
 FT TURN 41 42  
 FT TURN 45 46  
 FT STRAND 47 52  
 FT TURN 53 54  
 FT STRAND 55 64  
 FT TURN 65 66  
 FT STRAND 67 70  
 FT HELIX 72 74  
 FT STRAND 80 83  
 FT STRAND 87 87  
 FT TURN 88 89  
 FT STRAND 96 98  
 FT STRAND 100 105  
 FT TURN 107 108  
 FT TURN 114 115  
 FT TURN 118 119  
 FT STRAND 122 126  
 FT STRAND 140 141  
 FT TURN 148 149  
 FT STRAND 151 156  
 FT STRAND 170 170  
 FT STRAND 171 178  
 FT HELIX 181 187  
 FT TURN 189 191  
 FT TURN 194 195  
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 FT TURN 212 213  
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 FT STRAND 221 228  
 FT STRAND 235 235  
 FT TURN 236 237  
 FT STRAND 238 238  
 N-LINKED (GLCNAC. .) (POTENTIAL).  
 NEUROPSIN.  
 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT STRAND 240 244  
 SEQUENCE 245 256  
 260 AA; 28523 MM; BE5F6F6BE37CD60E CRC64;  
 Alignment Scores:  
 Pred. No.: 1,85e-38 Length: 260  
 Score: 698.50 Matches: 129  
 Percent Similarity: 56.13% Conservative: 35  
 Best Local Similarity: 52.02% Mismatches: 77  
 Query Match: 29.47% Indels: 7  
 Gaps: 3  
 DB: 1  
 US-09-856-320a-1 (1-1301) x NRPN\_MOUSE (1-260)  
 QY 227 ATCTGCTGCTGCTGCGAAGAGGCTGTTAGGGGAGAGACAGC----- 271  
 Db 13 lIleuLeuLeuLeuLeuPheMetGlyAlaTrpAlaGlyLeuThrArgAlaGlnGlySerLys 32  
 QY 272 ATCATCAAGGGGTTTCAGAGTGCAGACCTCCTCCAGCCCTGGGAGGAGCCCTTTCGAG 331  
 Db 33 lIleuLeuGlnGlyArgGlnGlyCysIleProHisSerGlnProTrpGlnAlaAlaLeuPheGln 52  
 QY 332 AAGACGGGCTACTCTGTGGGGAGCGCTCATCGCCCGCCAGATGCTGTCAGACAGCC 391  
 Db 53 GlyIuArgLeuIleCysGlyGlyValLeuValGlyAspArgTrpValLeuThrAlaAla 72  
 QY 392 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGAGAGCAACCTCCAGAGAGAG 451  
 Db 73 HisCysIysIysGlnIysIysSerValArgLeuGlnIysHisSerLeuGlnSerArgAsp 92  
 QY 452 GGCCTGAGAGACCGCGGAGAGCGACGAGTCTCCCGCCCGGCTTCACAAACAGC 511  
 Db 93 GlnProGlnGlnGlnIleGlnValAlaGlnSerIleGlnHisProCysTyrAsnAsnSer 112  
 QY 512 CTCGCCAAGAGAGAGCGCATGATGATGATGATGATGATGATGATGATGATGATGATG 571  
 Db 113 AsnPro---GlnAspHisSerHisAspIleMetLeuLeuArgLeuGlnAsnSerAlaAsn 131  
 QY 572 ATACCTGGGCTGTGGCAGCCCGCTCACCCTCTCCACGCTGTGCTGCTGCGACAGC 631  
 Db 132 LeuGlnIysIysValIysProValGlnLeuAlaAsnLeuCysProLysValGlnGlnLys 151  
 QY 632 TGCTCATTTCCGGCTGGGGAGCGATCCAGCCCGAGTTAGCCCTCCACACCTTG 691  
 Db 152 CysIleIleSerGlyTrpGlnIysValIysSerProGlnGlnAsnProAsnThrLeu 171  
 QY 692 CGATGCCCAACATCATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 751  
 Db 172 AsnCysAlaGlnValIysIleTyrSerGlnAsnIysCysGlnAlaIaTyrProGlnLys 191  
 QY 752 ATCAGACAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 811  
 Db 192 lIleThrGlnGlnMetValCysAlaGlnLys---SerSerAsnGlnAlaAspThrCysGlnGly 210  
 QY 812 GACTCCGGGGGCTCTGTGCTGTGATACCACTCTTCAAGGATTAATCTCTGGGGCAG 871  
 Db 211 AspSerIleGlyProLeuValIysAspGlyMetLeuGlnGlyIleThrSerTrpGlnSer 230  
 QY 872 GATCCGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 931  
 Db 231 AspProCysGlnIysProGlnIysProGlnIysValIysThrIysIleCysArgTyrThrThr 250  
 QY 932 TGGATCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955  
 Db 251 TrpIleIysIysThrMetAspAsn 258

DE kallikrein 15 precursor (EC 3.4.21.-) (ACO protease).  
 GN KIK15.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.  
 RX PubMed=11010966;  
 RA Yousef G.M., Scorillas A., Jung K., Ashworth L.K., Diamandis E.P.;  
 RT "Molecular cloning of the human kallikrein 15 gene (KIK15). Up-  
 RT regulation in prostate cancer."  
 RL J. Biol. Chem. 276:53-61(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20510030; PubMed=11054574;  
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuag J.,  
 RA Moss P., Paepers B., Wang K.;  
 RT "Sequencing and expression analysis of the serine protease gene  
 RT cluster located in chromosome 19q13 region."  
 RL Gene 257:119-130(2000).  
 RN [3]  
 RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=94289486; PubMed=8018728;  
 RA Dhanich M.E., Spleas M.;  
 RT "A novel serine protease-like sequence from human brain."  
 RL Biochem. Biophys. Acta 1218:225-228(1994).  
 CC -1- FUNCTION: Protease whose physiological substrate is not yet known.  
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1;  
 CC IsoId=Q9H2R5-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9H2R5-2; Sequence=VSP\_005405;  
 CC Name=3;  
 CC IsoId=Q9H2R5-3; Sequence=VSP\_005406, VSP\_005407;  
 CC Name=4;  
 CC IsoId=Q9H2R5-4; Sequence=VSP\_005404;  
 CC -1- TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also  
 CC expressed in the prostate, salivary, and adrenal glands and in the  
 CC colon testis and kidney.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AF242195; AAC09469.1; -;  
 DR EMBL: AF242195; AAC09470.1; -;  
 DR EMBL: AF242195; AAC09471.1; -;  
 DR EMBL: AF242195; AAC09472.1; -;  
 DR EMBL: AF243527; AAC33354.1; -;  
 DR EMBL: X75363; CAA53145.1; ALT\_SEQ.  
 DR HSBP; P00763; IDPO.  
 DR MEROPS; S01.081; -;  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR001254; Ser-protease\_Try.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; FALSE\_NG.  
 KW Hydrolase; Serine protease; Glycoprotein; Signal; Zymogen;  
 KW Alternative splicing.  
 FT SIGNAL 1  
 POTENTIAL. 16





```

CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
CC HIPPOCAMPAL PLASTICITY.
CC -1- CATABOLIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms-2;
CC Name-1;
CC IsoId=060259-1; Sequence=Displayed;
CC CC
CC IsoId=060259-2; Sequence=VSP_005401;
CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS PREDOMINANTLY EXPRESSED IN THE
CC PANCREAS WHILE ISOFORM 2 IS EXPRESSED IN ADULT BRAIN AND
CC HIPPOCAMPI. BOTH FORMS ARE ALSO FOUND IN FETAL BRAIN AND
CC PLACENTA. NOT DETECTED IN KIDNEY, SPLEEN, LIVER AND LUNG.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC CC
CC -----
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CC CC
CC EMBL; AB009849; BAA28673.1; -
CC EMBL; AB012761; BAA28676.1; -
CC EMBL; AB010780; BAA82664.1; -
CC EMBL; AB008390; BAA82665.1; -
CC EMBL; AB008927; BAA82666.1; -
CC EMBL; AF095982; AAD56050.1; -
CC EMBL; AF095742; AAD59709.1; -
CC EMBL; AF095743; AAD29574.1; -
CC EMBL; AF243527; AAG33361.1; -
CC EMBL; AC011473; AAG32354.1; -
CC HSSP; Q61955; INPM.
CC DR MEROPS; S01.244; -.
CC DR Genew; HGNC:6369; KLR8.
CC MIM; 605644; -.
CC DR GO; GO:0007399; P:neurogenesis; TNS.
CC InterPro; IPR001314; Chymotrypsin.
CC DR InterPro; IPR001254; Ser_protease_Try.
CC pfam; PF00089; trypsin; 1.
CC DR PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00020; Tryp_Spc; 1.
CC DR PROSITE; PS00240; TRYPsin_DOM; 1.
CC DR PROSITE; PS00134; TRYPsin_HIS; 1.
CC DR PROSITE; PS00135; TRYPsin_SER; 1.
CC KW Hydroxylase; Serine protease; Glycoprotein; Zymogen; Signal;
CC Alternative splicing.
CC FT SIGNAL; 1
CC FT PROPEP; 29
CC FT CHAIN; 33
CC FT ACET_SITE; 73
CC FT ACET_SITE; 120
CC FT ACET_SITE; 212
CC FT DISULFID; 39
CC FT DISULFID; 58
CC FT DISULFID; 145
CC FT DISULFID; 152
CC FT DISULFID; 184
CC FT DISULFID; 208
CC FT CARBOHYD; 110
CC FT VANSPLIC; 23
CC FT FT
CC FT FT
CC SEQUENCE 260 AA; 28048 MW; EF439E5B8C83E660 CMC64;

Alignment Scores:
Pred. No.: 6.63e-38
Score: 690.00
Percent Similarity: 66.93%
Best Local Similarity: 49.21%
Query Match: 29.11%

Length: 260
Matches: 125
Conservative: 45
Mismatch: 80
Indels: 4

```

[illegible]



RT "Purification, molecular cloning and expression of a human stratum  
RT cornutum trypsin-like serine protease with possible function in  
RT desquamation.";  
RL J. Biol. Chem., 274:30033-30040(1999).  
RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20118156; PubMed=10652563;  
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;  
RT "Identification of novel human kallikrein-like genes on chromosome  
RT 19q13.3-q13.4.";  
RL Anticancer Res. 19:2843-2852(1999).  
RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20510030; PubMed=11054574;  
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McNulty J.,  
RA Moss P., Paepke B., Wang K.;  
RT "Sequencing and expression analysis of the serine protease gene  
RT cluster located in chromosome 19q13 region.";  
RL Gene 257:119-130(2000).  
RN  
RP SEQUENCE FROM N.A.  
RC TISSUE-Ovary;  
RX MEDLINE=22386257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Bluet K.H., Schaefer C.F., Bat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ugin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rosa S.S., Loquelano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bohak S.A., McEwen F.U., McKernan K.C., Malek A.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schnutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smallus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.W., Maier M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: MAY BE INVOLVED IN DESQUAMATION.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN SKIN, BREAST, BRAIN AND TESTIS.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, KALLIKREIN SUBFAMILY.  
-----  
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DR EMBL; AF168768; AAFF03101.1; -  
DR EMBL; AF168768; AAD264429.1; -  
DR EMBL; AF243527; AAG33358.1; -  
DR EMBL; BC008036; AAHO8036.1; -  
DR HSSP; P00763; IDPO.  
DR MEROPS; S01\_017; -  
DR GenPept; HGNC:6366; KLK5.  
DR MTM; 605643; -  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0008544; P:epidermal differentiation; TAS.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
DR InterPro; IPRO01314; Chymotrypsin.  
DR InterPro; IPRO01254; Ser.protease\_Try.  
DR Pfam; PF00089; trypsin; 1  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; TRYP\_SPC; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.

[illegible]



QY	752	ATCAGACAGACCCTGGTGTGTGTCCAGCGCAGGAGGGGCAAGAGATCCTGCCAGGT	81.11
Db	183	IllethThProglYmethylCysAlaIglYalProGInglYglYlYsAspSerCysGInglY	2020
QY	812	GACTCGGGGGCCCTCTGGTGTGTGAACCACTCTTCAAGGCATTATCTCTGGGGCCAG	87.11
Db	223	GlutRGcysAlaLeuProglYlYTrProglYalYlYrIAsnLeuCyslYsYrIArgSer	242.2
QY	932	TGGATCCAGAGAGACGATGAAGAC 955	
Db	243	TrpIleGlucIuGluThrMetArgasp 250	
RESULT 10			
KLKC_HUMAN	STANDARD:	PRT;	248 AA.
AC	09UKR0; 09UKR1;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5)		
DE	(KLK-L5).		
GN	KLK12 OR KLK15.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RX	MEDLINE=20118156; PubMed=10652563;		
RA	Yousef G.M., Luo L.-Y., Diamandis E.P.;		
RT	*Identification of novel human kallikrein-like genes on chromosome		
RT	19q13.3-q13.4.*;		
RL	Anticancer Res. 19:2843-2852(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).		
RA	Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;		
RT	*Cloning of new alternatively spliced forms of the kallikrein-like		
RT	gene 5 (KLK-L5).*		
RL	Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RX	MEDLINE=20510030; PubMed=11054574;		
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuall J.,		
RA	Moss P., Paepert B., Wang K.;		
RT	*Sequencing and expression analysis of the serine protease gene		
RT	cluster located in chromosome 19q13 region.*;		
RL	Gene 257:119-130(2000).		
RN	[4]		
RP	SEQUENCE FROM N.A. (ISOFORM 2).		
RA	Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,		
RA	Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,		
RA	Pan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.,		
RA	Dangman L., Eler A., Christensen M., Georgescu A., Avila J., Liu S.,		
RA	Dnarese T., Frankheim M., Attix C., Amico-Keller G., Coefield J.,		
RA	Dnarese S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,		
RA	Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,		
RA	Olsen A.S., Carrano A.V.;		
RT	*Sequence analysis of chromosome 19q13.4.*;		
RL	Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: Secreted (Probable).		
CC	-1- ALTERNATIVE PRODUCTS:		
CC	Event-Alternative splicing; Named isoforms-2;		
CC	Name-1;		
CC	isoId=09UKR0-1; Sequence-Displayed;		
CC	Name-2;		
CC	isoId=09UKR0-2; Sequence-VSP_005403;		
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.		

[illegible]

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OY 515 CCCAACAAAGACCCGACATGATCATATGCTGTGAGATGACATCCGACCTTCATC 574
    ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 102 ---SerThrSerHisGlnHisAspLeuArgLeuArgLeuArgLeuProVal 120
OY 575 ACCCTGGGCTGGCGACCCCTCACCTCTCCCTGACCGCTGTGACGTGGACACCACTGC 634
    ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 121 ThrSerSerValGlnProLeuProLeuProAsnAspCysAlaThrAlaGlyThrGluCys 140
OY 635 CTCATTTCCGCTGGGCGACGACGTCACGACCCGACGTTACGCTGCTCACACCTTGGCA 694
    ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 141 HisValSerGlyTyrGlyIleThrAsnHisProAlaGlnProPheProAspLeuGln 160
OY 695 TCCGCGACATCATCATCATATGAGACGACGAAAGTGTGAGAACCCCTACCCCGGCAACATC 754
    ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 161 CysLeuAsnLeuSerIleValSerHisAlaThrCysHisAlaGlyValTyrProGlyArgIle 180
OY 755 ACAGACACCATGTGTGTGTGCCAGCTGCAGGAGGCGACAGAGACTCTGCTCCAGGGTGC 814
    ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 181 ThrSerAsnMetValCysAlaGly---GlyValProGlyGlnAspAlaCysGlnGlyAsp 199
OY 815 TCCGGGGGCGCTGTGCTGTGTATACCAAGTCTCTCAAGGATATATCTCCGCGGCGACG--- 871
    ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 200 SerGlyGlyProLeuValCysGlyGlyValLeuGlnGlyLeuValSerTyrProIleVal 219
OY 872 GATCCGCTGTGATCACCCGAAAGCTGTGTCTACACGAAAGTGTGCAATATGTGGAC 931
    ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 220 GlyProCysGlyGlnAspGlyIleProGlyValTyrThrTyrIleCysGlySerValAsp 239
OY 932 TGGATCCAGACGACATGACGAACAAT 958
    ||| ::::: ||| ::::: ||| ::::: |||
Db 240 TrrIleArgMetIleMetArgAsnAsn 248

RESULT 11
KLK7_RAT STANDARD: PRT: 261 AA.
AC P36373;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE glandular kallikrein 7, submandibular/renal precursor (EC 3.4.21.35)
DE (Tissue kallikrein) (RGR-7) (RSG-7) (Esterase B) (Proteinase A).
GN KLK7 OR KLK-7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8908074; PubMed=2849988;
RA Chen Y.-P., Chao J., Chao L.;
RT "Molecular cloning and characterization of two rat renal kallikrein
RT genes."
RL Biochemistry 27:7189-7196(1988).
RN [2]
RP SEQUENCE OF 25-75.
RC TISSUE-Submandibular gland;
RC MEDLINE=8198057; PubMed=3482210;
RA Kato H., Nakatani E., Enjoji K., Hayashi I., Oh-Ishi S., Iwanaga S.;
RT "Characterization of serine proteinases isolated from rat
RT submandibular gland: with special reference to the degradation of rat
RT kininogens by these enzymes."
RL J. Biochem. 102:1389-1404(1987).
-1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS
-1- IN KININOGEN TO RELEASE LYS-BRADYKININ.
-1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in
-1- small molecule substrates. Highly selective action to release
-1- kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of
-1- Met-|-Xaa or Leu-|-Xaa.
-1- TISSUE SPECIFICITY: KIDNEY AND SUBMANDIBULAR GLAND.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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CC -----
DR EMBL: M19647; AAA1461.1; -.
DR PIR: A31136; A31136.
DR HSSP: P00759; 1TON.
DR MEROPS: S01.406; -.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR SMART: SM00020; TRYP-Spc; 1.
DR PROSITE: PS00240; TRYP-SIN_DOM; 1.
DR PROSITE: PS00134; TRYP-SIN_HIS; 1.
DR PROSITE: PS00135; TRYP-SIN_SER; 1.
KW Hydrolyase; Serine protease; Glycoprotein; Multigene family; Zymogen;
KW Signal.
FT SIGNAL 1 18 PROBABLE.
FT PROPEP 19 24 ACTIVATION PEPTIDE (PROBABLE).
FT CHAIN 25 261 GLANDULAR KALLIKREIN 7,
FT FT ACT_SITE 65 65 SUBMANDIBULAR/RENAL.
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM.
FT ACT_SITE 213 213 CHARGE RELAY SYSTEM.
FT DISULFID 31 173 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 152 219 BY SIMILARITY.
FT DISULFID 184 198 BY SIMILARITY.
FT DISULFID 208 234 BY SIMILARITY.
FT CARBOHYD 109 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 35 35 S -> D (IN REF. 2).
FT CONFLICT 46 46 T -> S (IN REF. 2).
SQ SEQUENCE 261 AA; 28972 MW; 4FB06C422F25AF16 CRC64;

Alignment Scores:
pred. No.: 3.11e-33 Length: 261
Score: 618.50 Matches: 114
Percent Similarity: 62.11% Conservative: 45
Best Local Similarity: 44.53% Mismatches: 86
Query Match: 26.10% Indels: 11
DB: Gaps: 2

US-09-856-320A-1 (1-1301) x KLK7_RAT (1-261) -----GGAGAGACCAAG 271
OY 224 TTAATCCCTGCTGCTGTGCAACAGGCGCTTGAAGG----- ||| ::::: |||
Db 5 IleLeuPheLeuAspLeuSerLeuGlnIleAspAlaAlaProProGlyGlnSerArg 24
OY 272 ATCATCAAGGGGTTGAGTGAAGCTGCTCCAGCCTCGGACGACGACCCCTGTTCGAG 331
    ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 25 ValIleGlyGlyTyrIleCysGlnIleAsnSerGlnProTyrGlnValAlaLeuTyrSer 44
OY 332 AAGACGCGCTACTGTGTGGGCGAGCTCATGCCGCCCAATGCGCTCTGACAGCAGCC 391
    ||| ::::: ||| ::::: ||| ::::: |||
Db 45 PheThrIleTyrLeuGlyGlyValLeuIleAspProSerTyrValIleThrAlaAla 64
OY 392 CAGTCCCTCAACCCCGCTACATGATGACCTGGGCGACAGACAACTCCAGAGAGAG 451
    ||| ::::: ||| ::::: ||| ::::: |||
Db 65 HisCysSerSerAsnIleGlnValIleThrLeuGlyArgAsnAsnLeuLeuIleAspGlu 84
OY 452 GGCTGTGAGACACCCGACAGCAGCTGATGCTCCCGCCGCGGCTTCAACAAAGACG 511
    ||| ::::: ||| ::::: ||| ::::: |||
Db 85 ProPheAlaGlnHisArgLeuValSerGlnSerPheProHisProAspTyrIleProPhe 104
OY 512 CTC-----CCCAACAAAGACACCCGACATGACATCATGCTGTG 550
    ||| ::::: ||| ::::: ||| ::::: |||
Db 105 LeuMetArgAsnHisThrArgTyrProGlyAspAspHisSerAsnAspLeuLeu 124
OY 551 AAGATGGCATGCCAGATGCCATGACCTGGGCTGGGCGACCCCTGACCTGCTGCACGC 610
    ::::: ||| ::::: ||| ::::: |||
Db 125 HisLeuSerGlnProAlaAspIleThrAspGlyValIleAspLeuProThrGlu 144

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OY 611 TGTGTCACTGCTGGACACAGCTGCTCATTTCCGGCTGGGGACAGACAGCCCCAC 670
DB 145 GlnProlyValGlySerThrCysLeuAlaSerGlyTrpGlySerThrLysProLeuIle 164
OY 671 TTACGCTGCTGACACCTGTCGATGGCGCCCAACATCAGCATGTGAGCAGACAGTGT 730
DB 165 TrpIuHeuProAspAspLeuGlnCysValAsnIleHsIleuSerAsnGlnLysCys 184
OY 731 GAGAGCGCTACCCCGGACATCAGACAGACATGCTGTGTGTCAGCGTGCAGAAAGG 790
DB 185 IleuAlaTrpLysGlnLysValThrAspLeuMetLeuLysAlaGlnLysGlnLys 204
OY 791 GCGAAGACGCTGCTGCGGCTGATCCGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 850
DB 205 GlyLysAspThrCysThrGlyAspSerGlyGlyProLeuLysCysAspGlyValLeuGln 224
OY 851 GCGATTTATCTGCTGGGGCGAGATCCGTCGATCCAGACCCGAGGCTGCTGCTGCTGCTG 910
DB 225 GlyIleuHsSerTrpGlySerValProCysAlaLysThrAsnMetProAlaIleTrpThr 244
OY 911 AAGCTGCGCAAAATATGTGACTGATCCAGACAGACATGAGAACAAAT 958
DB 245 LysIleuLysPheThrSerTrpIleLysGlnValMetLysGlnVal 260
RESULT 12
KIKL1_RAT STANDARD; PRT; 261 AA.
AC P00758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glandular kallikrein, pancreatic 1 precursor (EC 3.4.21.35) (Tissue
DE kallikrein) (PS kallikrein) (RKG-1).
GN KIKL1 OR KIK-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID-10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-83117659; PubMed-6961406;
RA Swift G.H., Dagorn J.-C., Ashley P.L., Cummings S.W., McDonald R.J.;
RT "Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid
RT sequence of the encoded preproenzyme.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7263-7267(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE-Submaxillary gland;
RX MEDLINE-86051477; PubMed-2998455;
RA Ashley P.L., Macdonald R.J.;
RT "Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide
RT sequences of four distinct types including tonin.";
RL Biochemistry 24:4512-4520(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE-Kidney;
RX MEDLINE-89327211; PubMed-2753879;
RA Inoue H., Fukui K., Miyake Y.;
RT "Identification and structure of the rat true tissue kallikrein gene
RT expressed in the kidney.";
RL J. Biochem. 105:834-840(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-89214217; PubMed-2708383;
RA Wines D.R., Brady J.M., Pritchett D.B., Roberts J.L., Macdonald R.J.;
RT "Organization and expression of the rat kallikrein gene family.";
RL J. Biol. Chem. 264:7653-7662(1989).
RN [5]
RP SEQUENCE OF 48-261 FROM N.A.
RX MEDLINE-86131678; PubMed-3004582;
RA Gerald W.L., Chao J., Chao L.;
RT "Immunological identification of rat tissue kallikrein cDNA and

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RT characterization of the kallikrein gene family.";
RL Biochim. Biophys. Acta 866:1-14(1986).
CC 1- FUNCTION: GLANDULAR KALLIKREIN'S CLEAVE MET-LYS AND ARG-SER BONDS
CC IN KININOMER TO RELEASE LYS-BRADYKININ.
CC 1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-I'-Xaa bonds in
CC small molecule substrates. Highly selective action to release
CC kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of
CC Met-I'-Xaa or Leu-I'-Xaa.
CC 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00758; -; NOT_ANNOTATED_CDS.
DR EMBL; M11563; AAA41464.1; ALP_INIT.
DR EMBL; M23876; AAA41462.1; -
DR EMBL; M23874; AAA41462.1; JOINED.
DR EMBL; M23875; AAA41462.1; JOINED.
DR EMBL; D00448; BAA00346.1; JOINED.
DR EMBL; D00446; BAA00346.1; JOINED.
DR EMBL; D00447; BAA00346.1; JOINED.
DR EMBL; X03560; CAA27247.1; -
DR PIR; A00944; KORTP.
DR HSSP; P00757; 1SGF.
DR InterPro; IPR001254; Ser_Protease_Try.
DR pfam; PF00089; trypsin_1.
DR SMART; SM00020; TRYPSIN_DOM.
DR PROSITE; PS02040; TRYPSIN_DOM.
DR PROSITE; PS0134; TRYPSIN_HIS.
DR PROSITE; PS00135; TRYPSIN_SER.
KW Hydrolyase; Serine protease; Glycoprotein; Multigene family; Zymogen;
KW signal.
FT SIGNAL 1 18 PROBABLE.
FT PROPEP 19 24 ACTIVATION PEPTIDE (PROBABLE).
FT CHAIN 25 261 GLANDULAR KALLIKREIN 1.
FT CHAIN 111 111 CHAIN 1.
FT CHAIN 112 261 CHAIN 2.
FT ACT_SITE 65 65 CHARGE RELAY SYSTEM.
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM.
FT ACT_SITE 213 213 CHARGE RELAY SYSTEM.
FT DISULFID 31 173 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 152 219 BY SIMILARITY.
FT DISULFID 184 198 BY SIMILARITY.
FT DISULFID 209 234 BY SIMILARITY.
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 261 AA; 28852 MW; F2F99C0227A7882B CRC64;
Alignment Scores:
Pred. No.: 3.61e-33 Length: 261
Score: 617.50 Matches: 112
Percent Similarity: 62.50% Conservative: 48
Best local Similarity: 43.75% Mismatches: 85
Query Match: 26.05% Indels: 11
Gaps: 2
US-09-856-320A-1 (1-1301) x KIKL1_RAT (1-261)
OY 224 TTATCTGCTGCTGCTGGACACAGGCTGTGAGGGGA-----GAGACAGG 271
DB 5 IleuHeuLeuAlaLeuSerLeuGlyTrpAsnAspAlaAlaProProValGlnSerArg 24
OY 272 ATCATCAAGGGGTTGAGTCAAGCCCTCACTCCAGCGCTGGACAGGAGCCCTGTTGAG 331
DB 25 ValValAlaGlyLysThrGlnCysGlnMetAsnSerGlnProTrpGlnValAlaValTrpTrp 44
OY 332 AAGACGGCGCTACTGTGTGGGGCGAGCGCTGATCCGCCCGCAGATGCTCTGACAGACGCC 391

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Db      45 pneglyglutylleucylglyvalleuileasprsertrpailletlalaia 64
QY      392 SACGSGCTCAAGCCCGTACATAGTTCACTGGGGCAGACACCTCCAGAGAGAG 451
Db      65 Hlscysalatlthraspntylrglnvaltrpleuglylalgaslnsleuylrglnasgly 84
QY      452 GGCTGTGACAGACCCGGACAGACCTAGTCTCTCCACCACCCGGCTTCAACAGACC 511
Db      85 Proplealaglnhlsargleuvalserglnserphrohisproglypheasnglnaspr 104
QY      512 CTC-----CCCAACAAAGACCCGAATACATCATCTGGTG 550
Db      105 Leuilletprasnhtltharglnproglyasrpsrtyserasnsprenleuileu 124
QY      551 AAGATGGCATCCGCAAGTCTCAACACCTGGCTGGCTCCGCTCCACCTCAACCTCAGCC 610
Db      125 Hlslseuserglnprohlsasprletlthrasprglyvallylvalleaspreurolleu 144
QY      611 TGTGTCACTGTGGCAGCAGTGTCTCATTTCCGGGTGGGAGCAGCAGTCCAGCCCGCAG 670
Db      145 Gluprollyvalglserthrcysleualaserglytrpglyserlthhrproasgly 164
QY      671 TTACGGCTGCTCACACCTTGGATGGCGCAACATCATCATGAGCAGACAGAGTCT 730
Db      165 Leugluleuserasphasprleuincysvalaslnleasprleuuserasnlyulscys 184
QY      731 GAGAACGCTTACCCCGGACATCACAGACACCATGTGTCTGCCAGCTGCAGAGAGG 790
Db      185 ValglualhlslygluglvalthrasprleuMetleucysalaglylmetasprgly 204
QY      791 GGCAGAGACTCTGCCAGGATGATCTCGGGGCGCTGTGTGTATACCATGCTCTTCAA 850
Db      205 Glylyasasprthrcyslyasprserglylproleuillcysasncllyalleugln 224
QY      851 GGCATTATCTCGTGGGGCAGATCGGTGGAGTACCCGAAAGCTGGTGTACAGAG 910
Db      225 Glylletlthsertrpglypheasprocgylglylulprolysproglylletytrh 244
QY      911 AAGTCTGCAATATGTGACTGTGATCCAGAGACAGATGAACAT 958
Db      245 Lysleuilellyserphethrprotrprietlysglvalmetlyglunsn 260

RESULT 13
TRY3_CHICK STANDARD; PRT; 248 AA.
AC 090629;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin II-P29 precursor (EC 3.4.21.4).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=95251611; PubMed=7733885;
RA Wang K., Gan L., Lee I., Hood L.E.;
RT Isolation and characterization of the chicken trypsinogen gene
family.*;
RL Biochem. J. 307:471-479(1995).
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg--|-Xaa, Lys--|-Xaa.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: HIGH LEVELS ARE SEEN IN THE PANCREAS WHILE
CC LOWER LEVELS ARE FOUND IN THE LIVER, SPLEEN AND THYMUS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -----
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CC -----
DR EMBL: U15157; AAA79914.1; -.
DR PIR: S55066; S55066.
DR HSSP: P00763; IDPO.
DR MEROPS: S01.151; -.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR KMW: Hydrolyase; Serine protease; Digestion; Pancreas; Zymogen; Signal;
KW Multigene family.
FT SIGNAL 1..16 BY SIMILARITY.
FT PROPEP 17..25 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 26..248 TRYPSIN II-P29.
FT ACT_SITE 65..65 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 109..109 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 202..202 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 32..162 BY SIMILARITY.
FT DISULFID 30..66 BY SIMILARITY.
FT DISULFID 134..235 BY SIMILARITY.
FT DISULFID 141..208 BY SIMILARITY.
FT DISULFID 173..187 BY SIMILARITY.
FT DISULFID 198..222 BY SIMILARITY.
FT SITE 196..196 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SQ SEQUENCE 248 AA; 26622 MW; E5E1B07622B58E CRC64;

Alignment Scores:
Pred. No.: 8, 22e-33 Length: 248
Score: 612.00 Matches: 121
Percent Similarity: 63.35% Conservative: 38
Best Local Similarity: 48.21% Mismatches: 82
Query Match: 25.82% Indels: 10
DB: 1 Gaps: 5

US-09-856-320A-1 (1-1301) x TRY3_CHICK (1-248)
QY 209 ATGAGGATTCCTGCAAGTAAATCTG-----CTGTCTGTGCAACAGGCTTGAGGGGA 262
Db      1 Metlyspheleupheleuileusercysleuglyalalvalalaphreproglyly 20
QY 263 -----GACACAGATCATCAAGGCTTCAGATGACCTCACTCCAGCCCTGGGAG 316
Db      21 Alaasrpsasprlylvallelyllytrhrcysprogluhlservalprotyrgln 40
QY 317 GCAGCCCTGTGAGAGACGGGCTACTGTGTGGGGCAGCGCTATCGCCCGCAGATGG 376
Db      41 Valserleu---Asnserllytrhspheycysglyserleuileasnsrglntrp 59
QY 377 CTCCTGACAGACGCCCATGTCTCAAGCCCGCTCAATAGTTTACCTGGGGCAGACAAAC 436
Db      60 Valleuseralalahlscystyrylserarglleglnvalargleuclglyluyraan 79
QY 437 CTCGAGAGAGAGGGCTGTGAGAGACCCGAGACGCCAGAGAGTACCTCCCGCACCC 496
Db      80 Ileasprvalglnglnasprserglvalalargsersevalillealrghispro 99
QY 497 GGCTTCACACAGAGCTCCCAACAAAGACCCCAATGATCATCTGTGGTGAAGAG 556
Db      100 Lyslyrserserlletlthreusn-----Asnspilletleuilelysleu 115
QY 557 GCATGCGCAGTCTCATCACTGCGGTGTGCACCCCTCAACCTCTCTCAGCTGTGTGTC 616
Db      116 AlaSerAlaValAlGluTyrSerAlaAspIleGlnProIleAlaLeuProSerSerCysAla 135
QY 617 ACTGTCGACAGAGCGCTCATTTCCGGCTGGGGCAGAGCTCAAGCCCGCAGATTACG 676
Db      136 LysAlaGlyThrGluCysLeuSerGlyTrpGlyAsnThrLeuSerAsnGlyTrpAsn 155

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QY 677 CTGCTCAGACCTTGGATGGCGCAACATCATATGAGCAGACAGAGTGAGAAC 736  
 DB 156 TyrProGluLeuGlnCysLeuAsnAlaProIleLeuSerAspGlnGluCysGlnGlu 175  
 QY 727 GCGTACCCCGCAACATGACAGACACCATGCTGGCAGCTCCAGAGAGGGGCGAG 796  
 DB 176 AlaTyrProGlyAspIleThrSerAsnMetIleCysValGlyPheLeuGlnGlyGlyLys 195  
 QY 797 GACTCTCCAGAGGAGTACCGGGGGCCCTGTGTCTGTAAACAGTCTTCAAGAGCAT 856  
 DB 196 AspSerCysGlnGlyAspSerCylGlyProValValCysAsnGlyGluLeuGlnGlyLe 215  
 QY 857 ATCTCTGGGGCGAGATCCGTGCTCCATCCAGACCCGAGCTGTGTCTACAGCAATC 916  
 DB 216 ValSerTyrGlyIleGly---CysAlaLeuLysGlyTyrProGlyValTyrThrLysVal 234  
 QY 917 TGCAATATGTGGACTGATCGAGAGAGAGCATG 949  
 DB 235 CysAsnTyrValAspTyrPheGlnGluThrIle 245

## RESULT 14

KLC\_RAT

ID KLC\_RAT STANDARD: PRT: 259 AA.

AC P36376: 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Glandular kallikrein 12, submandibular/renal precursor (EC 3.4.21.35)  
 DE (Tissue kallikrein) (RSCG-3).  
 GN KIK12 OR KIK-12.  
 OS Rattus norvegicus (rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP MEDLINE FROM N.A.  
 RX MEDLINE=89088074; PubMed=2849988;  
 RA Chen Y.-P., Chao J., Chao L.;  
 RT "Molecular cloning and characterization of two rat renal kallikrein genes";  
 RL Biochemistry 27:7189-7196(1988).  
 CC -1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS  
 CC IN KININOGEN TO RELEASE LYS-BRADYKININ.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in  
 CC small molecule substrates. Highly selective action to release  
 CC kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of  
 CC Met-|-Xaa or Leu-|-Xaa.  
 CC -1- TISSUE SPECIFICITY: KIDNEY AND SUBMANDIBULAR GLAND.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.  
 CC  
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 CC  
 CC EMBL: M19648; AAA51640.1; -;  
 DR EMBL: M22822; AAA51640.1; JOINED.  
 DR PIR: B31136; B31136.  
 DR HSSP: P00759; 1TON.  
 DR MEROPS: S01.160; -;  
 DR InterPro: IPR001254; Ser. protease\_Try.  
 DR Pfam: PF000089; trypsin\_1.  
 DR SMART: SM00020; tryp-Spec; 1.  
 DR PROSITE: PS02440; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KM Hydrolyase; Serine protease; Glycoprotein; Multigene family; Zymogen;  
 FT SIGNAL 1 18 PROBABLE.

FT PROPEP 19 24 ACTIVATION PEPTIDE (PROBABLE).  
 FT CHAIN 25 259 SUBMANDIBULAR/RENAL.  
 FT ACT\_SITE 63 63 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 118 118 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 211 211 CHARGE RELAY SYSTEM.  
 FT DISULFID 31 171 BY SIMILARITY.  
 FT DISULFID 48 64 BY SIMILARITY.  
 FT DISULFID 150 217 BY SIMILARITY.  
 FT DISULFID 182 196 BY SIMILARITY.  
 FT DISULFID 207 232 BY SIMILARITY.  
 FT CARBOHYD 91 91 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 106 106 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 259 AA; 28759 MW; 535ABBE25435144F CRC64;

## Alignment Scores:

Pred. No.: 8.9e-33 Length: 259  
 Score: 611.50 Matches: 112  
 Percent Similarity: 60.85% Conservative: 45  
 Best Local Similarity: 43.41% Mismatches: 88  
 Query Match: 25.80% Indels: 13  
 DB: 1 Gaps: 3

US-09-856-320A-1 (1-1301) x KLC\_RAT (1-259)

QY 218 CTGCAAGTTAATCTGCTTGTCTGGCAACAGGCTTGAGG-----GGAGAG 265  
 DB 3 LeuGlnIleLeuPheLeuValLeuSerValGlyIleAspAlaIleProIleGlyLys 22  
 QY 266 ACCAGGATCATCAAGGGGTTGAGTGCAGAGCTTCACTCCAGAGCCCTGGAGAGCCCTG 325  
 DB 23 SerAlaValAlaGlyGlyTyrLysCysGlnLysAsnSerGlnProTyrGlnAlaVal 42  
 QY 326 TTCGAGAAGAGCGGCTACTGTGTGGGCGAGCTGACGCGCCAGATGAGTGGCTTGACA 385  
 DB 43 Ile-----AsnAlaGlyTyrLeuGlyGlyGlyValLeuLeuAspProSerTyrValIleThr 60  
 QY 386 GCAGCCCACTGCTTCAAGCCCGGCTGACATGATTCACCTGGGCGAGCAACCTCCAGAG 445  
 DB 61 AlaAlaIleCysTyrSerHisAsnTyrHisValLeuLeuGlyAlaGlnAsnLeuPheLys 80  
 QY 446 GAGAGGCGCTGTGAGCAGACCCCGGACAGCCAGCTAGTCCCTCCCGGAGCCGCTTAAAC 505  
 DB 81 AspIleProPheAlaGlnTyrAlaValAlaMetIleSerPheProHisProAspTyrAsn 100  
 QY 506 -----AACAGGCTCCCAACAAAGACCCAGCAATGACATCATG 544  
 DB 101 ProPheMetLysAsnHisThrLeuPheProGlyAspAspHisSerAsnAspLeuMet 120  
 QY 545 CTGCTGAAGATGCGATGCCAGTCTCCATGACCTGGGCTGTGGAGCCCTCACCTTCC 604  
 DB 121 LeuLeuHisLeuSerGlnProAlaAspIleThrAspGlyValLysValIleAspLeuPro 140  
 QY 605 TCACGCGTGTGACCTGTGGCAGCAGCTGCTTCCGCGTGGGCGAGCAGCAGCTCCAGC 664  
 DB 141 ThrIleGlnProLysValGlySerThrCysLeuAlaSerIleTyrPheSerTyrLysPro 160  
 QY 665 CCCAGTTAGCGCTGCTGACACCTTGCAGATGGCCCAACATCCACCATATGAGACACAG 724  
 DB 161 LeuGlnTyrPheGlnPheProAspAspLeuGlnCysValAsnIleAsnIleLeuSerAsnGln 180  
 QY 725 AAGTGTGAGAACGCTTACCCCGGCAACATGACAGACACATGCTGTGGCTGAGCAG 784  
 DB 181 LysCysIleLysAlaHisThrGlnMetValThrAspValMetLeuCysAlaGlyLysLeu 200  
 QY 785 GAAGGGGCAAGAGCTCTGCGCAGAGTACCGGGGGCCCTGTGCTGTAAACAGCTCT 844  
 DB 201 GlnIleGlyLysAspThrCysAsnGlyAspSerCylGlyProLeuLeuCysAspGlyVal 220  
 QY 845 CTTCAGAGCATTTATCTCTGGGCGCAGAGTCCGCTGCTGATCCAGCAAGCCGTGCTGTC 904  
 DB 221 LeuGlnIleTyrIleThrSerTyrPheSerValProCysGlyLysIleThrAsnArgProAlaIle 240





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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 15, 2003, 20:04:15 ; Search time 35.6662 Seconds  
(without alignments)  
7015.902 Million cell updates/sec

Title: US-09-856-320A-1  
Perfect score: 2370  
Sequence: 1 ctgccttcgtccacacctg.....aaaaaaaaaaaaaaaaaaaaa 1301

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 566616

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_n2p.model -DEV=xlp  
-O=/cgn2.1/USPTO.spool.P/US09856320/r/unatc\_15102003.105640.8549/app.query.fasta\_1.2318  
-DB=PIR.76 -OFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR.SCOR=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=plot -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09856320@cgn.1.1.74@runatc\_15102003.105640.8549 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
1: PIR.76:\*  
2: pir1:\*  
3: pir2:\*  
4: pir3:\*  
5: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	698.5	29.5	260	2	I56559 neuropsin - mouse
2	618.5	26.1	261	2	A31136 tissue kallikrein
3	617.5	26.1	265	1	KORP tissue kallikrein
4	612	25.8	248	2	S55066 trypsin (EC 3.4.21
5	611.5	25.8	259	2	B31136 tissue kallikrein
6	611.5	25.8	261	1	NGMSG 7S nerve growth fa
7	604.5	25.5	263	2	S15686 tissue kallikrein
8	602.5	25.4	246	1	TRPRT2 trypsin (EC 3.4.21
9	601.5	25.4	261	2	A34079 tissue kallikrein
10	600.5	25.3	246	1	TRRT1 trypsin (EC 3.4.21
11	596.5	25.2	261	2	A29586 tissue kallikrein
12	595.5	25.1	259	1	KORPtn tonin (EC 3.4.21.-
13	595	25.1	261	2	A29745 tissue kallikrein
14	594	25.1	238	2	S31779 trypsin (EC 3.4.21

15	591.5	25.0	261	2	S45303 tissue kallikrein
16	585.5	24.7	246	2	B25528 trypsin (EC 3.4.21
17	585	24.7	261	2	A25606 tissue kallikrein
18	580.5	24.5	261	1	KOMSI tissue kallikrein
19	580	24.5	231	1	TRPCTR trypsin (EC 3.4.21
20	580	24.5	262	1	KORH tissue kallikrein
21	578.5	24.4	244	2	A44284 tissue kallikrein
22	578	24.4	232	1	KOPC tissue kallikrein
23	576	24.3	247	1	TRDG tissue kallikrein
24	572.5	24.2	257	2	S33772 tissue kallikrein
25	572.5	24.2	261	2	S01971 tissue kallikrein
26	571.5	24.1	253	2	A53968 serine proteinase
27	569	24.0	229	1	TRBOTR trypsin (EC 3.4.21
28	567	23.9	247	2	A27547 trypsin (EC 3.4.21
29	565	23.8	243	2	A35871 trypsin (EC 3.4.21
30	565	23.8	256	1	NGMSA 7S nerve growth fa
31	564.5	23.8	261	2	A41020 tissue kallikrein
32	564	23.8	259	2	A23746 tissue kallikrein
33	563	23.8	247	2	S13813 trypsin (EC 3.4.21
34	563	23.8	248	2	S55067 trypsin (EC 3.4.21
35	562.5	23.7	261	1	A32297 semenogelase (EC 3
36	559.5	23.6	261	1	S35711 trypsin (EC 3.4.21
37	559	23.6	242	2	S49489 trypsin (EC 3.4.21
38	559	23.6	247	2	S05494 trypsin (EC 3.4.21
39	558.5	23.6	259	2	D23863 tissue kallikrein
40	558.5	23.6	261	1	TRMSM5 tissue kallikrein
41	558	23.5	261	2	A24378 tissue kallikrein
42	557.5	23.5	304	2	S33496 trypsin (EC 3.4.21
43	556	23.5	246	1	TRDGC trypsin (EC 3.4.21
44	555.5	23.4	231	2	S31778 trypsin (EC 3.4.21
45	553	23.3	261	2	JE0236 tissue kallikrein

ALIGNMENTS

RESULT 1  
I56559  
neuropsin - mouse  
C:Species: Mus musculus (house mouse)  
C.Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #extl\_change 21-Jul-2000  
C.Accession: I56559  
R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momoto, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nis  
J. Neurosci. 15, 5088-5097, 1995  
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease  
A:Reference number: I56559; MID:95348817; PMID:7623137  
A:Accession: I56559  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-260 <RES>  
A:Cross-references: GB:D30785; NID:91648847; PIDN:BA06451.1; PID:g1020091  
A:Superfamily: trypsin; trypsin homology  
F:33-252/Domain: trypsin homology <TRY>

Alignment Scores:

Pred. No.: 1.1e-38  
Score: 698.50  
Percent Similarity: 66.13%  
Best Local Similarity: 52.02%  
Query Match: 29.47%  
DB: 2  
Gaps: 3

US-09-856-320A-1 (1-1301) x I56559 (1-260)	
OY	227 ATCTGCTGCTCTGTGCAACAGGCGTGTGAGGGGAGAGCCAGG----- 271
DB	13 IIELEULEULEULEUPHEMETGLYALATPRALAGLYLEUPTHARGYLAAGINLYSERIYS 32
OY	272 ATCATCAAGGGTGTGAGTGCAGGCTCAGCTCCAGCCCTGGCAGGAGCCCTGTTGAG 331
DB	33 IIELEUGLUGLYARGGLUCYSATLEPRONHSSEKINPOTRGLALALALEUPHEGIN 52
OY	332 AAGACGGCGTACTGTGTGGGGCGAGCGTCATGCGCCCGGAGATGGCTCTCTGACAGCAGCC 391

Db 53 GLYLGLNAGLEUILLIECSYLIGLYVALLEUVALGLYASPRATGTRPVALLLEUTHRALIALA 72

QY 392 CACTGGCTTCACACCCCGCTACATAGTTCACCTGGGGGACACAACTCCAGAGAGAG 451

Db 73 HCTGSLYSLSGLINLSYTSYSERVALTRGLEUGLYASPHISERLEUINSERATGASR 92

QY 452 GGCTGTGAGACACCCCGACACCTAGTGCCTTCCCGCCCGGGCTTCACACACAC 511

Db 93 GLNPRGGLNGLGLLLEGLNVALAGINSERILEGLNHISPRGYSYTRASNANSE 112

QY 512 CTCGCCAACAAAGACCCGACATGACATCATGCTGTGAATGGATGACATCGCAGTCC 571

Db 113 ASNPRO---GLASPHISERHISASPIEMETLEUILLIARGLEUINSERIALASN 131

QY 572 ATCACCCTGGGCTGGCGACCCCTCACCCCTGCTGTCACGTCACCTGGCACAC 631

Db 132 LEUGLYASPLYSVALLYSPROVALGLNLEUALAASNLEUCYSPROLYVALGLNLS 151

QY 632 TGGCTCATTTCCGGCTGGGGGACAGCTCCACCCCAATTACGCTGGCTACACCTTG 691

Db 152 CYSILEILIESERGLYTRPILYTRVALTRSERPROGLNGLUASNPHEPROASNTRLEU 171

QY 692 CCATCGCGCCAAATACATCACCTATGAGACACAGAAAGGAGGAGACCCGACCC 751

Db 172 ASNCYSIALAGLIVALLYSILERYSERGLASNLYSCGLNARGHIALATYTRPROGLYLS 191

QY 752 ATCAGACAGACCATGGTGTGTGTCAGCCGTCAGAGAAAGGGGACAGACCTGCCAGGCT 811

Db 192 ILIETHRGLGLYMETVALCYSLAGLY---SERSERASNGLYALASPHRYCSGLNGLY 210

QY 812 GACTCCGGGGGGCTCTGGTCTGTAACTGCTTTCAAGCGATTATCTCCGGGGCCAG 871

Db 211 ASPSERGLYGLYPROLEUVALCYSLASPLGYMETLEUGLNGLYILETHSERTRPGLYSER 230

QY 872 GATCCGTGTGCGATCACCACCCGAAGCCGTGTCTACACAGAAAGCTGCAATATGNGAG 931

Db 231 ASPRPGCYGLYLYSPROGLULYSPROGLYVALTYRTHLYSLIECSARGYTRHTHR 250

QY 932 TGGATCCAGAGAGCATGAGAAGAC 955

Db 251 TRPILLYSLYSTHMETASPSN 258

RESULT 2

A11136

tissue kallikrein (EC 3.4.21.35) 7 precursor, submandibular - rat

N.Alternate names: glandular prokallikrein 7, submandibular; proteinase A

C.Species: Rattus norvegicus (Norway rat)

C.Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #ext-change 22-Jun-1999

C.Accession: A11136; S10658; S10699; D41429; B41429; S09315

R.Chen, Y.P.; Chao, J.; Chao, L.

Biochemistry 27, 7189-7196, 1988

A.Title: Molecular cloning and characterization of two rat renal kallikrein genes.

A.Reference number: A11136; MUID:89088074; PMID:2849988

A.Accession: A11136

A.Molecule type: DNA

A.Residues: 1-261 <CHE>

A.Cross-references: GB:M19647; GB:J02837; NID:9204999; PIDN:AAA4161.1; PID:9205000

R.Elouajeh, A.; Gutman, N.; Brillard, M.; Gauthier, F.

FEBS Lett. 265, 137-140, 1990

A.Title: Substrate specificity of two kallikrein family gene products isolated from the

A.Reference number: S10698; MUID:90306305; PMID:2194829

A.Accession: S10698

A.Molecule type: Protein

A.Residues: 25-36 <ELM>

A.Accession: S10699

A.Molecule type: Protein

A.Residues: 112-139 <EL2>

R.Kato, H.; Nakamshi, E.; Enjyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.

J. Biochem. 102, 1389-1404, 1987

A.Title: Characterization of serine proteinases isolated from rat submaxillary gland: w

A.Reference number: A41429; MUID:88198057; PMID:3482210

A.Accession: D41429

A.Molecule type: Protein

[illegible]

QY 851 GGCAATATCTCCTGGGGCCAGATCCGTGCGATACCCGAAAGCTGTCTACAG 910  
 DB 225 GYIIIEthSerTrpIySerValProCysAlaLysThsAsnMetProIalIeYrThr 244  
 QY 911 AAGTCTGCAATATGCTGATCGATCCAGAGAGAGATGAGACAT 958  
 DB 245 LysLeuIleLysPheThrSerTrpIleYrGluValMetLysGluAsn 260

RESULT 3  
 KORTP  
 tissue kallikrein (EC 3.4.21.35) precursor - rat  
 N:Alternate names: glandular kallikrein; kininogenin; true tissue kallikrein  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 05-Apr-1983 #sequence\_revision 05-Apr-1983 #text-change 16-Jun-2000  
 C:Accession: A00944; A41429; A25137; JX0073; A23863; A33359  
 R:Smith, G.H.; Dagorn, J.C.; Ashley, P.L.; Cummings, S.W.; Macdonald, R.J.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982  
 A:Title: Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence of  
 A:Reference number: A00944; MUID:83117659; PMID:6961406  
 A:Accession: A00944  
 A:Molecule type: mRNA  
 A:Residues: 1-265 <SMI>  
 A:Experimental source: pancreatic  
 R:Kato, H.; Nakamishi, E.; Enjoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.  
 J. Biochem. 102, 1389-1404, 1987  
 A:Title: Characterization of serine proteinases isolated from rat submaxillary gland: w  
 A:Reference number: A41429; MUID:88198057; PMID:3482210  
 A:Accession: A41429  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 29-53, 'X', 55-87 <KAT>  
 R:Gerald, W.L.; Chao, J.; Chao, L.  
 Biochem. Biophys. Acta 866, 1-14, 1986  
 A:Title: Immunological identification of rat tissue kallikrein cDNA and characterization  
 A:Reference number: A25137; MUID:86131678; PMID:3004582  
 A:Accession: A25137  
 A:Molecule type: mRNA  
 A:Residues: 115-265 <GER>  
 R:Inoue, H.; Fukui, K.; Miyake, Y.  
 J. Biochem. 105, 834-840, 1989  
 A:Title: Identification and structure of the rat true tissue kallikrein gene expressed  
 A:Reference number: JX0073; MUID:89922721; PMID:2753879  
 A:Accession: JX0073  
 A:Molecule type: DNA  
 A:Residues: 1-265 <IND>  
 A:Cross-references: GB:D00448; NID:9220792; PIDN:BAA00346.1; PID:9220794  
 A:Experimental source: kidney  
 R:Ashley, P.L.; Macdonald, R.J.  
 Biochemistry 24, 4512-4520, 1985  
 A:Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of  
 A:Reference number: A23863; MUID:86051477; PMID:2998455  
 A:Accession: A23863  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-265 <ASH>  
 A:Cross-references: GB:M1563; NID:9205029; PIDN:AAA1464.1; PID:9205030  
 A:Experimental source: submaxillary gland  
 R:Wiles, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; Macdonald, R.J.  
 J. Biol. Chem. 264, 7653-7662, 1989  
 A:Title: Organization and expression of the rat kallikrein gene family.  
 A:Reference number: A33359; MUID:89214217; PMID:2708383  
 A:Accession: A33359  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 5-265 <MIN>  
 A:Cross-references: GB:M23874; GB:J04701; GB:M23875; GB:M23876; NID:9205007; PIDN:AAA14  
 C:Comment: The kallikreins liberate lysyl-bradykinin, a vasoactive decapeptide, from kin  
 C:Comment: The protein presumably assumes the two-chain form by cleavage between residu  
 C:Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release  
 C:Genetics:  
 A:Introns: 20/1; 73/2; 169/1; 214/3  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: hydrolase; pancreas; serine proteinase; zymogen

F:1-17/Domain: signal sequence #status predicted <SIG>  
 F:18-28/Domain: activation peptide #status predicted <AP>  
 F:29-265/Product: tissue kallikrein, pancreatic #status predicted <MP>  
 F:29-257/Domain: trypsin homology <TRY>  
 F:35-177, 54-70, 156-223, 188-202, 213-238/Disulfide bonds: #status predicted  
 F:69,124,217/Active site: His, Asp, Ser #status predicted

Alignment Scores:

	Pred. No.:	2,53e-33	Length:	265
Score:	617.50	Matches:	112	
Percent Similarity:	62.508	Conservative:	48	
Best Local Similarity:	43.758	Mismatches:	85	
Query Match:	26.058	Indels:	11	
DB:	1	Gaps:	2	

US-09-856-320A-1 (1-1301) x KORTP (1-265)

QY 224 TTAATCTCTCTGCTGCGATACCCGAAAGCTGTCTACAG-----GAGACGAG 271  
 DB 9 IIELeuPheLeuAlaLeuSerLeuGlyArgAsnAspAlaAlaProProValGlnSerArg 28  
 QY 272 ATCATCAAGGGGTTCGAGTCAAGCCTCACTCCAGCCCTGGAGGAGCCGCTCGAG 331  
 DB 29 ValValGlyGlyTrpAsnGlyMetAsnSerGlnProTrpValAlaValIleYrThr 48  
 QY 332 AAGACGGGCTACTCTGTGGGGGAGCTATCGCCCGCCAGATGGCTCTCGACAGAGCC 391  
 DB 49 PheGlyGlyLeuLeuGlyValLeuIleAspProSerTrpValIleThrAlaIle 68  
 QY 392 CACTGCTCAAGCCCGCTACATATGTCACCTGGGAGACACACACCTCCAGAGAGAG 451  
 DB 69 HiscysAlaThrAspAsnTrpGlnValTrpLeuGlyArgAsnAsnLeuYrGluAsn 88  
 QY 452 GGCTGTGACAGACCCCGGAGAGCCATGATGATGCTCCCGCCAGCCGCTCAACAGAGC 511  
 DB 89 ProPheAlaGlnHisArgLeuValSerGlnSerPheProHisProIlePheAsnGlnAsp 108  
 QY 512 CTC-----CCCAACAAAGACACCGGACCATGATCATGCTGTG 550  
 DB 109 LeuIleTrpAsnHisThrArgGlnProGlyAspAspTrpSerAsnAspLeuLeu 128  
 QY 551 AAGATGGATCGCCGATCCATCCATCGCTGGTGGGACCCCTACCTCTCTCAGCG 610  
 DB 129 HisLeuSerGlnProAlaAspIleThrAspGlyValIleAspLeuProIleGln 148  
 QY 611 TGTGTCACTGTGGGACGACGATGCTCCATTCCTGGTGGGAGGACGACGACCCGAG 670  
 DB 149 GluProLysValGlySerThrCysLeuAlaSerGlyTrpGlySerIleThrProAspGly 168  
 QY 671 TTACGCTGCTCTACACCTTGGATGCGCCACATCCATCATTTGAGGACGAGAGTGT 730  
 DB 169 LeuGlnLeuSerAspAspLeuGlnCysValAsnIleAspLeuLeuSerAsnGlyCys 188  
 QY 731 GAGAACGCTACCCGCGGACATCACAGACACCATGCTGTGGCCAGCCTGACGAGAGG 790  
 DB 189 ValGluAlaHisLysGluGluValThrAspLeuMetLeuCysAlaGlyIleMetAspGly 208  
 QY 791 GGCAAGGACTCTGCGAGGATGACATCCCGGGGCGCTGGTGTGTAACAGATCTGTCA 850  
 DB 209 GlyLysAspThrCysLeuSerGlyAspSerGlyGlyProLeuIleCysAsnLysValLeuGln 228  
 QY 851 GGCAATATCTCCTGGGGCCAGATCCGTGCGATACCCGAAAGCTGTCTACAG 910  
 DB 229 GYIIIEthSerTrpIySerValProCysAlaLysThsAsnMetProIalIeYrThr 248  
 QY 911 AAGTCTGCAATATGCTGATCGATCCAGAGAGATGAGACAT 958  
 DB 249 LysLeuIleLysPheThrProTrpIleYrGluValMetLysGluAsn 264

RESULT 4  
 S55066  
 trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken  
 N:Alternate names: trypsinogen II





```

Db      121 LeuLeuHisLeuSerGluProAlaAspIleThrAspGlyValIleValIleAspLeuPro 140
QY      605 TCACGCTGTGTACAGCTGTCCGACACAGCTCCATTCCTCCGGTGGGGGACAGCTCCAC 664
      ::::::::::::::::::::
Db      141 ThrGluGluProLysValGlySerThrCysLeuAlaSerGlyTyrPheSerThrIlePro 160
QY      665 CCCGAGTTACGGCTGCTTCACACCTTCGATCGGCAACATCACCATCTCATGAGCCAG 724
      ::::::::::::::::::::
Db      161 LeuGluTyrGluPheThrProAspAspLeuGlnCysValAsnIleAsnIleLeuSerAsnGln 180
QY      725 AAGTGTGAGACGCGCTACCCCGGCAACATCAGACACACATCGGTGTGTCAGCGTCAG 784
      ::::::::::::::::::::
Db      181 LysCysIleLeuAlaHisThrGlnMetValIleThrAspValMetLeuCysAlaGlyIleLeu 200
QY      785 GAAGGGGCGACAGACTCTCTCCAGGCTGATCTCCGGGGGCGCTGTGCTGTATACCACTGT 844
      ::::::::::::::::::::
Db      201 GluGlyGlyLysAspThrCysAsnGlyAspSerGlyGlyProLeuLeuCysAspGlyVal 220
QY      845 CTTCAGAGCATATATCTCCCTGGGGGCGAGATCCGTGTGCATACCCGAAAGCTGTGTTC 904
      ::::::::::::::::::::
Db      221 LeuGlnGlyIleThrSerThrPheSerValProCysGlyGluThrAsnArgProAlaIle 240
QY      905 TCACAGAACTGTGCAATATGTGACCTGTGACAGAGACAGATGAGAACAAT 958
      ::::::::::::::::::::
Db      241 TyrThrLysLeuIleLysPheThrSerThrIleLysGluValMetLysGluAsn 258

```

## RESULT 6

```

NGMSG
7S nerve growth factor gamma chain (EC 3.4.21.-) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Dec-1981 #sequence revision 17-May-1985 #text change 18-Jun-1999
C:Accession: A91005; A90949; A93510; A92341; A00942; A21093; A22705
R:Evans, B.A.; Richards, R.I.
EMBO J. 4, 133-138, 1985
A:Title: Genes for the alpha and gamma subunits of mouse nerve growth factor are contig
A:Reference number: A91005; MUID:85257431; PMID:3848399
A:Accession: A91005
A:Molecule type: DNA
A:Residues: 1-261 <EVA>
R:Ullrich, A.; Gray, A.; Wood, W.I.; Hayflick, J.; Seeburg, P.H.
DNA 3, 387-392, 1984
A:Title: Isolation of a cDNA clone coding for the gamma-subunit of mouse nerve growth fa
A:Reference number: A90949; MUID:85076169; PMID:6548955
A:Accession: A90949
A:Molecule type: mRNA
A:Residues: 1-261 <UL>
A:Cross-references: GB:X01389; NID:953373; PIDN:CAA25645.1; PID:953374
R:Howles, P.N.; Dickinson, D.P.; DiCaprio, L.L.; Woodworth-Gutai, M.; Gross, K.W.
Nucleic Acids Res. 12, 2791-2805, 1984
A:Title: Use of a cDNA recombinant for the gamma-subunit of mouse nerve growth factor to
A:Reference number: A93510; MUID:84169573; PMID:620835
A:Accession: A93510
A:Molecule type: mRNA
A:Residues: 127-202, 'E', 204-261 <HON>
A:Cross-references: GB:X00472; NID:954260; PIDN:CAA25154.1; PID:954261
A:Experimental source: Inbred strain DBA/2J
R:Thomas, K.A.; Baglan, N.C.; Bradshaw, R.A.
J. Biol. Chem. 256, 9156-9166, 1981
A:Title: The amino acid sequence of the gamma-subunit of mouse submaxillary gland 7 S ne
A:Reference number: A92341; MUID:81264363; PMID:7263706
A:Accession: A92341
A:Molecule type: protein
A:Residues: 25-107, 112-261 <THO>
A:Experimental source: outbred strain Swiss Webster
C:Comment: 7S nerve growth factor is composed of two alpha chains, a beta dimer composed
C:Comment: The active form of the gamma chain occurs naturally as combinations of either
C:Genetic:
A:Map position: 7
A:Introns: 16/1; 69/2; 165/1; 210/3
A:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; growth factor; hydrolase; serine proteinase; submandibular gla
F:1-18/Domain: signal sequence #status predicted <SIG>
F:25-253/Domain: trypsin homology <TRY>

```

```

F:25-107/Domain: segment B1 <GB1>
F:25-107,112-261/Product: nerve growth factor gamma chain (active form) #status exper
F:112-261/Domain: segment A <GAA>
F:112-164/Domain: segment C <GCC>
F:165-261/Domain: segment B2 <GB2>
F:31-173,50-66,152-219,184-198,209-234/Disulfide bonds: #status predicted
F:55,120,213/Active site: His, Asp, Ser #status predicted
F:102/Binding site: carbohydrate (Asn) (covalent) #status experimental

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## Alignment Scores:

	Pred. No.:	6, 31e-33	Length:	261
Score:		611.50	Matches:	110
Percent Similarity:		63.288	Conservative:	52
Best Local Similarity:		42.978	Mismatches:	83
Query Match:		25.808	Indels:	11
DB:	1	Gaps:	2	

US-09-856-320A-1 (1-1301) x NGMSG (1-261)

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QY      224 TTAATCTGCTGTCTGTGCGAACAGGCGCTGTAGGGGA-----GAGACGAG 271
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Db      5 IleLeuPheLeuAlaLeuSerLeuGlyIleAspAlaIleProValGlnSerArg 24
QY      272 ATCATCAAGGGGTGAGTGCAGCTCACTCCACCTCCAGGACCGCTGTTCAG 331
      ::::::::::::::::::::
Db      25 IleValGlyLysPheLysCysGlnLysAsnSerGlnProThrPheValAlaValTyrArg 44
QY      332 AAGACGGGCTACTGCTGTGGGGGAGAGCGCTCATGCCCGGAGATGGCTGCTGCAGACGCG 391
      ::::::::::::::::::::
Db      45 TyrThrGlnTyrLeuLysGlyValIleLeuAspProAsnThrValLeuThrAlaIle 64
QY      392 CACTGCGCTCAAGCGCGCTACATAGTTCACTGCGGAGACACACCACTCCAGAGAGAG 451
      ::::::::::::::::::::
Db      65 HisCysTyrAspAspAsnTyrLysValTyrPheGlyLysAsnIleLeuPheLysAspGln 84
QY      452 GGCTGTGACACAGACCGGAGAGGACCTGAGTCTTCCGCCCGCGGCTTCACAAACAGC 511
      ::::::::::::::::::::
Db      85 ProSerAlaGlnHisArgPheValSerLysAlaIleProHisProGlyPheAsnMetSer 104
QY      512 CTCGCCCAAGAAA-----GACCACCGGCAATGACATGATGCTGTGG 550
      ::::::::::::::::::::
Db      105 LeuMetArgLysHisIleArgPheLeuGluTyrAspTyrSerAsnAspLeuMetLeuLeu 124
QY      551 AAGATGCGATCGCCACTCTCCATCAGCTGAGTGGAGACCCCTGCTCTGTCAGCG 610
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Db      125 ArgLeuSerLysProAlaAspIleThrAspThrValLysProIleThrProThrGln 144
QY      611 TGTGTACAGTGTGGACACAGCTGCTCATTTCCGGTGGGAGACAGCTCCAGCCCGCAG 670
      ::::::::::::::::::::
Db      145 GluProLysLeuGlySerThrCysLeuAlaSerGlyTyrPheLysThrIleThrProThrLys 164
QY      671 TTACGCTGCTGCACACCTTGGCGATCGGCGACACATCAGCATGATGAGCAGAGATGT 730
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Db      165 PheGlnPheThrAspAspLeuTyrCysValAsnIleLysLeuLeuProAsnGlnAspCys 184
QY      731 GAGAACGCTTACCCCGGCAACATCAGACAGACCATGGTGTGCCAGCTGCAGAGAGG 790
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Db      185 AlaLysAlaHisIleGluLysValIleThrAspAlaMetLeuCysAlaGlyIleMetAspGly 204
QY      791 GGCAGAGATCTCTGCGCAGGCTGACTCCGGGGGCGCTCTGTCTGTACCAAGTCTGTCA 850
      ::::::::::::::::::::
Db      205 GlyLysAspThrCysLysGlyAspSerGlyGlyProLeuIleCysAspGlyValLeuGln 224
QY      851 GGCATATCTGCTGGGGGAGAGATCGGTGTGCGATCAGCCGAAAGCGTGTGTACAGG 910
      ::::::::::::::::::::
Db      225 GlyIleThrSerThrProLysIleThrProCysGlyGluProAspMetProGlyValTyrThr 244
QY      911 AAGTCTGCAAAATATGTGAGTGCATGCAGAGACATGAGAACAAT 958
      ::::::::::::::::::::
Db      245 LysLeuAsnLysPheThrSerThrIleLysAspThrMetAlaLysAsn 260

```

## RESULT 7

S1586

tissue kallikrein (EC 3.4.21.35) precursor, renal - multimammate rat (*Mastomys natalensis*)  
 C:Species: *Mastomys natalensis*  
 C:Date: 09-Jun-1994 #sequence\_revision 10-Nov-1995 #text\_change 22-Jun-1999  
 C:Accession: I83227, S15686  
 R:Fahnestock, M.  
 DNA Cell Biol. 13, 293-300, 1994  
 A:Title: Characterization of kallikrein cDNAs from the African rodent *Mastomys*.  
 A:Reference number: 160208; MUID:94226702; PMID:7909667  
 A:Accession: I83227  
 A:Status: preliminary; translated from GR/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-263 <RES>  
 A:Cross-references: EMBL:X17352; NID:955526; PIDN:CAA35232.1; PID:955527  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: hydrolase; serine proteinase  
 F:25-255/Domain: trypsin homology <TRY>  
 F:65,121,215/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Pred. No.:	1,83e-32	Length:	263
Score:	604.50	Matches:	111
Percent Similarity:	62.02%	Conservative:	49
Best local Similarity:	43.02%	Mismatches:	85
Query Match:	25.51%	Indels:	13
DB:	2	Gaps:	3

US-09-856-320a-1 (1-1301) x S15686 (1-263)

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OY 224 TTAATCGTGTGCTGCTGCGAAGAGGCTGTAGGGGA-----GAGACGAG 271
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 272 ATCAACAAGGGGTGAGTGCACACCTTCACCTCCAGCCCTGGAGGACCCCTGTGAG 331
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 25  ILEELGGLGYPHEASCYSGILULYASNSERTINPROTRPHASVALALVALTYARG 44
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 332 AAGAGGGGCTACTCTGTGGGGGAGAGGCTATCGCCGCCCAATGAGCTCCAGAGCC 391
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 45  PHEALARGTYGTGILNCSGLYGLVALLEULASPLASALANTRVALLEUTHRALALA 64
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 392 CACTGCTCAAGCCCGCTACATPAGTTCACCTGGGAGGACACAACTCCAGAGAGAG 451
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 65  HICSGTYRANARPLYTYGLNVALTPREULYASNAANALGRPHGLUASPLU 84
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 452 GCGTGTGACAGACCCGAGACGACGAGTGCCTCCGCCACCCGCGCTTACACAGC 511
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 85  PROSERLAGLINSGLINLEULLESERLYSALALEPROGLIYRPHASNMESER 104
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 512 CTCCSCAAGAGCCAC-----CGCATGACATCATGCTG 547
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 105 LEULASNLYSASPHNISTHPRONISPROGLIYASPRTYSERASNAASPLAEMLEU 124
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 548 GTAGAGATGCGATGCCAGTGTCCATGACCTGGGCTGGGACCCCTACACCTTCTCA 607
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 125 VALARGLEULYSYSPROALAGLILIEHTHASPVALYALLYSPTOLIEASPLEUPROTH 144
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 608 CGGTGTGACAGTGTGGACGACGCTGCTATGTCGCGTGGGAGACAGCTGC--AGC 664
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 145 GLIULIUPROTHVALIGLYSERARGCYSEULASERGLYTRGLYSERTHPROTH 164
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 665 CCCAGTTAGCCCGCTGACACTTGGAGTGGCGCAACATGACATCATTTGACACAG 724
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 165 GLIULIUPROTHVALIGLYSERARGCYSEULASERGLYTRGLYSERTHPROTH 184
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 725 AAGTGTGAGAGAGCCGCTACACCTTGGAGTGGCGCAACATGACATCATTTGACACAG 784
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 185 VALCYSLALYSALAHNISTHGLULYVALTHRSPHRHMETLEUCYSLAAGLYGLMET 204
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 785 GAAGGGGCAAGAGCTCTGCGACGAGTGCAGCGGGGCGCTGTGTTGTAACAGCT 844
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 205 ASPGLIYLYASPRTHNCSYVALIGLYASPSERGLYGLYPROLEULIECYASPSGLYVAL 224
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 845 CTTCAGAGCATATCTCTGGGGCCAGAGATCCGCTGTCGATCACCCGAAAGCCCTGCTC 904
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  
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Db 225 LEULINGLYLIEHNSERTIPGLYPROTHPRCDYSALALEUPROAENVALPROGLYILE 244  
 OY 905 TACAGAAAGTCTGCATATATGTGACTGATTCAGAGACGATGAGACAAAT 958  
 Db 245 TYRTHRYSLEULIEGLIUTYRARGSETRIPLEYSAPVALMETALASNAAN 262

RESULT 8  
 TRRT2  
 trypsin (EC 3.4.21.4) II precursor - rat  
 N:Alternate names: trypsinogen II  
 C:Species: *Rattus norvegicus* (Norway rat)  
 C:Date: 05-Apr-1993 #sequence\_revision 30-Sep-1987 #text\_change 18-Jul-1997  
 C:Accession: A22657; A00949  
 R:Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.  
 J. Biol. Chem. 259, 14255-14264, 1984  
 A:Title: Structure of two related rat pancreatic trypsin genes.  
 A:Reference number: A22657; MUID:85054880; PMID:6094547  
 A:Accession: A22657  
 A:Molecule type: DNA  
 A:Residues: 1-246 <CRA>  
 R:MacDonald, R.J.; Stary, S.J.; Swift, G.H.  
 J. Biol. Chem. 257, 9724-9732, 1982  
 A:Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences  
 A:Reference number: A00948; MUID:82265624; PMID:6896710  
 A:Accession: A00949  
 A:Molecule type: mRNA  
 A:Residues: 9-246 <MAC>  
 C:Comment: The trypsin II mRNA is present in much lower quantities than the trypsin I  
 C:Genetics:  
 A:Introns: 14/1: 67/2  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-23/Domain: activation peptide #status predicted <AP>  
 F:24-246/Product: trypsin II #status predicted <END>  
 F:24-239/Domain: trypsin homology <TRY>  
 F:30-160,48-64,132-253,139-206,171-185/Disulfide bonds: #status predicted  
 F:63,107,200/Active site: His, Asp, Ser #status predicted  
 F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:

Pred. No.:	2,49e-32	Length:	246
Score:	602.50	Matches:	119
Percent Similarity:	62.45%	Conservative:	39
Best local Similarity:	47.04%	Mismatches:	88
Query Match:	25.42%	Indels:	7
DB:	1	Gaps:	4

US-09-856-320a-1 (1-1301) x TRRT2 (1-246)

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OY 200 CTCGAGCCAGATGAGATCTGCAAGCTTATGCTGTCGGCAACAGGGCTGTGAGG 259
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1 MetArgAlaLeuLeuPheLeuAlaLeuValGlyAlaValAlaPhePro---ValAsp 19
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 260 GGAGAGACAGGATCATCAAGGGTTCGAGTGCAGAGCTGCTCCAGCCCTGGACAGA 319
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 20 ASPASPSPYSILVALIGLYLYTYRTHCYSGINLUNASERVALPROTYGLNVAL 39
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 320 GCCCTGTTCCAGAAAGCGCGCTACTGTGGGGCGACGCTGATGCCCCCAATGGCTC 379
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 40 SerLeu---AsnSerGlyThrHisAspHisCysGlyGlySerLeuLeuAsnAspGlnTrpVal 58
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 380 CTGACAGCAGCCCGCTGCTCAAGCCCGCTACATGTTACCTGAGGGGAGACAACTTC 439
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 59 ValSerLeuAlaHisCysGlyTrpLysSerArgIleGlnValArgLeuGlyGlnHisAsnIle 78
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 440 CAGAAAGAGAGGGCTGTGAGCAGACCCGGACAGCACTGATGCTTCCCAACCCGGC 459
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 79 AsnValLeuGlnGlyAspArgGlnPheIleAsnAlaValIleLeuLysHisProAsn 98
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 500 TTCAACAACAGCTCCCAACAAAGACACCCGATGACATGCTGCTGGTGAAGATGGCA 559
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  
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Db 99 pheapahgylstThleuasn-----asnaspIleMetleuIlelylseuser 114  
 QY 560 TCGCCAGTCTCCATCACCCTGGCGTGGCAGCCCTCCACCTCTCCATCGCTGTGCTACT 619  
 Db 115 SerProvalylsleuAsnAlaIryAlaIaThrValAlaIeuproSerSerCysAlaPro 134  
 QY 620 GCTGGCAGCAGCTGCTCTATTTCGGCTGGGAGACAGCTCCAGCCCCAGTTACGCCCTG 679  
 Db 135 AlaglyThrGlnCysleuIleSerIleIleIleIleIleIleIleIleIleIleIleIle 154  
 QY 680 CCTCACACCTGGCAGTGGCGCCCAACATCACCATTGAGACAGAGAGTGGAGAACGCC 739  
 Db 155 ProAspLeuIleuGlnCysleuAspAlaProleuIleuProGlnAlaIleuIleuIleuIle 174  
 QY 740 TACCCCGGCAACATCAGACACACATGCTGTGCTGCAGCGTGCAGAGAGGGGCAAGCAG 799  
 Db 175 TyrProGlyIleIleThrAspAsnMetValCysValGlyPheIleuGlnGlyIleIleIle 194  
 QY 800 TCCTGCGCAGGCTGACTCCGGGGGCGCTCTGGTCTGTACACAGCTCTTCAAGGCATATTC 859  
 Db 195 SerCysGlnGlyAspSerIleIleIleIleIleIleIleIleIleIleIleIleIleIle 214  
 QY 860 TCCTGGGGCGAGAGCCGCTGCTGCATCCGAAAGCCGCTGTACAGCAAGCTTCG 919  
 Db 215 SerTyrGlyTyrGly----CysAlaIleuProAspAsnProGlyValIleIleIleIleIle 233  
 QY 920 AATATGTGACTGGATCCAGCAGACAGATGAAGAACAT 958  
 Db 234 AsnTyrValAspTyrPheIleGlnAspThrIleAlaIleAsn 246

## RESULT 9

A34079  
 tissue kallikrein (EC 3.4.21.35) P1 precursor - rat  
 A:Alternate names: kallikrein-related proteinase k8  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Mar-1990 #sequence\_revision 30-Mar-1990 #text\_change 22-Jun-1999  
 C:Accession: A34079; S10700  
 R:Brady, J.M.; Wines, D.R.; MacDonald, R.J.  
 Biochemistry 28, 5203-5210, 1989  
 A:Title: Expression of two kallikrein gene family members in the rat prostate.  
 A:Reference number: A34079; MUID:89352606; PMID:2765531  
 A:Accession: A34079  
 A:Status: preliminary  
 A:Molecule type: DNA; mRNA  
 A:Molecule type: protein  
 A:Residues: 1-261 <BRA>  
 A:Cross-references: GB:M27215; GB:M27216; GB:M27217; NID:g206638; PIDN:AAA42036.1; PID:g  
 A:Experimental source: prostate  
 R:Elmoujehed, A.; Gutman, N.; Brillard, M.; Gauthier, F.  
 FEBS Lett. 265, 137-140, 1990  
 A:Title: Substrate specificity of two kallikrein family gene products isolated from the  
 A:Reference number: S10698; MUID:90306305; PMID:2194829  
 A:Accession: S10700  
 A:Molecule type: protein  
 A:Residues: 25-43;112-138 <ELM>  
 A:Experimental source: submaxillary gland  
 A:Note: 125-Lys was also found  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: hydrolase; serine proteinase  
 F:25-253/Domain: trypsin homology <TRY>  
 F:25-111/Product: tissue kallikrein P1 light chain #status experimental <MAT1>  
 F:112-261/Product: tissue kallikrein P1 heavy chain #status experimental <MAT2>  
 F:65;120;213/Active site: His, Asp, Ser #status predicted

## Alignment Scores:

Pred. No.: 2,89e-32 Length: 261  
 Score: 601.50 Matches: 111  
 Percent Similarity: 60.85% Conservative: 46  
 Best Local Similarity: 43.02% Mismatches: 90  
 Query Match: 25.38% Gaps: 11  
 DB: 2 Gaps: 2

US-09-856-320A-1 (1-1301) x A34079 (1-261)

QY 218 CTGCAATTATCTCTGCTCTGCGACAGGG-----CTGTAGGGGAGAG 265  
 Db 3 LeuIleuIleLeuPheIleuIleuSerIleuGlyTyrPasnAspAlaIaProProGlyIle 22  
 QY 266 ACCAGGATCATCAAGGGGTTCAGTGCAGAGCCTCATCTCCAGCCCTGGAGGACGCCCTG 325  
 Db 23 SerAlaGlyIleIleGlyIlePheAsnGlyIleIleIleIleIleIleIleIleIleIleIle 42  
 QY 326 TTGCAAGAGACCGCGCTACTCTGTGGGGGAGCGCTCATCTGCGCCCGAGATGGGCTCCGAGA 385  
 Db 43 TyrHisPheAsnGlnProGlnCysGlyValIleuIleHisProSerTyrPalleuIle 62  
 QY 386 GCAGGCCACTGCTCAGAGCCCGCTACATAGTTCATCTGGGAGACACACATCCAGAG 445  
 Db 63 AlaAlaHisCysTyrSerValAsnIleuIleIleIleIleIleIleIleIleIleIleIle 82  
 QY 446 GAGAGAGGCTGTGACAGACACCGGAGACAGGCACTGATCTTCCCGACCCCGGCTTCAAC 505  
 Db 83 AspGluProPheAlaGlnHisIleuValSerGlnSerPheProHisProIlePheAsn 102  
 QY 506 AACACGCTC-----CCCAACAAAGACACCGCAATGACATGATG 544  
 Db 103 LeuAspIleIleIleAsnHisThrArgIleProGlyAsnAspTyrSerAsnIleuMet 122  
 QY 545 CTGTGAGATGATCGCATCGCACTCTCATACCTGGGCTGCGAACCCCTCACTCTCC 604  
 Db 123 LeuIleuHisLeuIleuIleuThrProAlaAspIleThrAspGlyValIleValIleAspIleuPro 142  
 QY 605 TCACGCTGTGTCATCTGTGACACACAGCTCCATCTCCGCTGGGGGAGACAGCTCCAGC 664  
 Db 143 ThrGlnGluProIleuValGlySerThrCysLeuThrSerGlyTyrPoleuIleThrPro 162  
 QY 665 CCCCAAGTTACGCGCTGCTGCACACCTTGCGATCGCCCAACATCAACATGATGAGACCCAG 724  
 Db 163 LeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 182  
 QY 725 AAGTGTGAGACGCGCTTACCCCGCAACATCAGACACCATGATGTGTGTCAGCGTGCAG 784  
 Db 183 LysCysIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 202  
 QY 785 GAAAGGGCGAAGACTCTGCGCAGAGGTGATCTCCGGGGGCGCTCTGTCTGTACCACTGT 844  
 Db 203 AspGlyGlyIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 222  
 QY 845 CTTCAGGCATATCTGCTGGGGGCGCAGATCGCTGGCATCACCCGAAAGCGCTGTGTC 904  
 Db 223 LeuGlnGlyIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 242  
 QY 905 TACACGAAAGTGTGCAATATGTGATCTGATCCAGAGACAGATGAAGAACAT 958  
 Db 243 TyrThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 260

## RESULT 10

TRRT1  
 trypsin (EC 3.4.21.4) I precursor - rat  
 N:Alternate names: trypsinogen I  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 17-Dec-1982 #sequence\_revision 17-Dec-1982 #text\_change 24-Sep-1999  
 C:Accession: B22657; A00948  
 R:Crataik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.  
 J. Biol. Chem. 259, 14255-14264, 1984  
 A:Title: Structure of two related rat pancreatic trypsin genes.  
 A:Reference number: A22657; MUID:85054880; PMID:6094547  
 A:Accession: B22657  
 A:Molecule type: DNA  
 A:Residues: 1-246 <CRA>  
 A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508  
 A:Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue  
 J. Macdonald, R.J.; Stary, S.J.; Stary, G.H.  
 J. Biol. Chem. 257, 9724-9732, 1982  
 A:Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences  
 A:Reference number: A00948; MUID:82265624; PMID:6896710  
 A:Accession: A00948

A:Molecule type: mRNA  
 A:Residues: 1-246 <MAC>  
 A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508  
 C:Genetics:  
 A:introns: 14/1; 67/2; 152/1; 197/3  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: hydrolyase; pancreas; protein digestion; serine proteinase; zymogen  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-23/Domain: activation peptide #status predicted <APT>  
 F:24-246/Product: trypsin I #status predicted <ENZY>  
 F:24-239/Domain: trypsin homology <TRY>  
 F:30-160,48-64,133-233,139-206,171-185/Disulfide bonds: #status predicted  
 F:63,107,200/Active site: His, Asp, Ser #status predicted  
 F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:  
 Pred. No.: 3,38e-32 Length: 246  
 Score: 600.50 Matches: 118  
 Percent Similarity: 62.45% Conservative: 40  
 Best Local Similarity: 46.64% Mismatches: 88  
 Query Match: 25.34% Indels: 7  
 Gaps: 4

US-09-856-320a-1 (1-1301) x TRPT1 (1-246)

```

OY      200 CTCACGCGCATGAGAGATTCTGACATATCTGCTGCTGCGCAACAGGCGTTGTAGCG 259
Db      1 MetSerAlaLeuIleLeuAlaLeuValGlyAlaAlaValAlaPheProLeu---Glu 19
OY      260 GGAGAGACAGCATCAACAGGGGTTCAGTGCAGACGCTCCAGCCCTGGCAGGCA 319
Db      20 AspaSapbryslIleValGlyGlyTyrThrCysProGluHisSerValProTyrGluVal 39
OY      320 GCCCTGTTCGAGAACGCGGCTACTCTGTGGGGGAGACGCTATGCGCCCGCATGGCTC 379
Db      40 SerLeu---AsnSerGlyTyrHisPheCysGlyGlySerLeuIleAsnAspGlnTyrVal 58
OY      380 CTGACAGACGCGCCCTGCTCAACGCCCTACATAGTTCACTGGGGGAGACAAACCTC 439
Db      59 ValSerAlaAlaHisCysTyrTyrLeuSerArgTlleGlnValAlaGlyLeuGlyHisAsnIle 78
OY      440 CAGAGAGAGAGGCGCTGAGCAGACAGCCGAGACGCTGAGTCTCCCGCCCGCGGC 499
Db      79 AsnValIleuGlnGlyAspGlnGlnPheIleAsnAlaAlaGlyIleIleLysHisProAsn 98
OY      500 TTCAACAACAAGCGCTCCCAACAAGACCGCAATGATCATGTGGTGAAGATGCA 559
Db      99 TyrSerSerTrrPrlLeuAsn-----AsnAspIleMetLeuIleLysLeuSer 114
OY      560 TCGCAGTCTGCATCACCCTGGGCTGTGCGACCCCTCAACCTCTCTCAACGCTGTCACT 619
Db      115 SerProValIlyLeuAsnAlaArgValAlaProValAlaLeuProSerAlaCysAlaPro 134
OY      620 GCTGGCAGCAGCTCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCGCAGTTGCGCTG 679
Db      135 AlagIyhrGlnCysLeuIleSerGlyTrrPrlYasnThrLeuSerAsnGlyValAsnAsn 154
OY      680 CCTCAACACTTGGCGATCGCCCAACATCATCATCTTGAAGCAGCAAGAGTGTGAACGCC 739
Db      155 ProAspLeuLeuGlnCysValAspAlaProValLeuSerGlnAlaAspGlnAlaAla 174
OY      740 TACCCGCGCAACATCAAGACACATGCTGTGCCAGCTGCAGGAAGGGGGCAAGAG 799
Db      175 TyrTrpGlyGlnIleThrSerSerMetIleCysValGlyPheLeuGlnGlyGlyAsp 194
OY      800 TCGTGGCAGGAGTACTCGGGGGGCGCTGTGTTGTAACCAAGTCTTCAAGGATTATC 859
Db      195 SerCysGlnIlyAspSerGlyGlyProValValCysAsnGlyGlnLeuGlnGlyIleVal 214
OY      860 TCGTGGGCGCAGATCCGCTGGCATCACCGGAAGCGCTGTGTTCAAGAAAGTGTGC 919
Db      215 SerTrpIlyTyrGly---CysAlaLeuProAspAsnProGlyValTyrThrLysValCys 233

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OY 920 AAATATGTGACTGGATTCAGAGACGATGAAAGCAAT 958  
 Db 234 AsnDheValGlyTrrPrlGlnAspTrrPrlAlaAlaAsn 246

RESULT 11  
 A29586  
 tissue kallikrein (EC 3.4.21.35) hK-1 precursor - human  
 N:Alternate names: glandular kallikrein  
 C:Species: Homo sapiens (man)  
 C:Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 22-Jun-1999  
 C:Accession: A29586  
 R:Schmedlich, L.J.; Bennetts, B.H.; Morris, B.J.  
 DNA 6, 429-437, 1987  
 A:Title: Primary structure of a human glandular kallikrein gene.  
 A:Reference number: A29586; MUID:88054467; PMID:2824146  
 A:Accession: A29586  
 A:Molecule type: DNA  
 A:Residues: 1-261 <SCCH>  
 A:Cross-references: GB:M18157; NID:g186640; PIDN:AA74454.1; PID:g386842  
 A:Note: the authors translated the codon TAC for residue 43 as Trp  
 C:Genetics:  
 A:introns: 16/1; 69/2; 165/1; 210/3  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: hydrolyase; serine proteinase  
 F:25-253/Domain: trypsin homology <TRY>  
 F:65,120,213/Active site: His, Asp, Ser #status predicted

Alignment Scores:  
 Pred. No.: 6.2e-32 Length: 261  
 Score: 596.50 Matches: 111  
 Percent Similarity: 62.11% Conservative: 48  
 Best Local Similarity: 43.36% Mismatches: 86  
 Query Match: 25.17% Indels: 11  
 Gaps: 2

US-09-856-320a-1 (1-1301) x A29586 (1-261)

```

OY      224 TTAATCTGCTGTGCTGCGCAACAGGCGTTGTAGGGGA-----GAGACCGAG 271
Db      5 ValLeuSerIleAlaLeuSerValGlyCysThrGlyAlaValProLeuIleGlnSerArg 24
OY      272 ATGATCAAGGAGTTCGAGTGCAGACCCCTACCTCCAGCCCTGGGAGCAGACGCCCTTCGAG 331
Db      25 IleValIleGlyTrrPrlGlnCysGlyLysHisSerGlnProTrrPrlValAlaValTyrSer 44
OY      332 AAGACGCGGCTACTGTGTGGGCGGACGCTGATCGCCCGCAGAGGCTCTGAGAGAGCC 391
Db      45 HisGlyTrrPrlAlaHisCysGlyGlyValIleValHisProGlnTrrPrlValIleAla 64
OY      392 CACTGGCTCAAGCCCGCTCAATAGTTCACTGGGGGAGCAGCAACCTCCAGAGAGAG 451
Db      65 HisCysLeuLysLysAsnSerGlnValTrrPrlGlnGlyArgHisAsnLeuPheGlnProGln 84
OY      452 GCGTGTAGAGAGACCGCGAGACGACGATCTCTCCCGCCCGCGCTTCACAAACAGC 511
Db      85 AspThrGlyGlnArgValProValSerHisSerPheProIleProLeuTyrAsnMetSer 104
OY      512 CTC-----CCCAACAAGACCGCCGATGACATCATGTGTG 550
Db      105 LeuLeuLysHisGlnSerLeuArgProAspGlnAspSerSerHisAspLeuMetLeu 124
OY      551 AAGATGGCATGGCAGTCTCATACCTGGGCTGTGCGACCCCTCAACCTCTCTCAACG 610
Db      125 ArgLeuSerGlnProAlaLysIleThrAspValIlyValIleGlyLeuProThrGln 144
OY      611 TGTGTACTCTGTGGCAGCAGACTCCCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCGAG 670
Db      145 GluProAlaLeuIlyThrThrCysTyrAlaSerGlyTrrPrlSerIleGlnProGlnGln 164
OY      671 TTACGCGCTGCGTCAACCGTTCGATGCGCAACATGATCATCTTGAAGCAGCAAGTGT 730
Db      165 PheLeuArgProArgSerLeuGlnCysValSerLeuHisLeuLeuSerAsnAspMetCys 184

```

QY 731 GAGAACGCTACCCCGGACATCAACACACCAATGCTGTGCCAGCTGCAGAGAGG 790  
 Db 185 AAlaArgAlaTyrSerGluLysValThrGlnPheMetLeuCysAlaGlyLeuThrPthrgly 204  
 QY 791 GGCAGAGACTCTCTCCAGGAGTACCTCCGGGGCCCTCGTGTGTATACCAAGCTCTGTCA 850  
 Db 205 GilyAspPrhTrpCysGlyGlyAspSerGlyGlyProLeuValCysAsnGlyValLeuGln 224  
 QY 851 GGCATATTCCTCGGGGCGAGATCCGTGTGCATCACCCGACCTGTGTCTACACG 910  
 Db 225 GlyIleThrSerTrpGlyProGluProCysAlaLeuProGluLysProAlaValYtrhr 244  
 QY 911 AAGCTCTGCAATATGTGACCTGCGATCCAGAGAGAGAGAGAGAGAGAT 958  
 Db 245 LysValValHisTyrArgLysTrpIleLysAspPrhIleAlaAlaAsn 260  
 RESULT 12  
 KORTN  
 tonin (EC 3.4.21.-) precursor - rat  
 N:Alternate names: esterase 1  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 25-Feb-1985 #sequence revision 02-Dec-1994 #text change 18-Jun-1999  
 C:Accession: B33359; A32340; C23863; A93323; A94635; A34050; A30971; A00945  
 R:Wines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; MacDonald, R.J.  
 J. Biol. Chem. 264, 7653-7662, 1989  
 A:Title: Organization and expression of the rat kallikrein gene family.  
 A:Reference number: A33359; MUID:89214217; PMID:2708383  
 A:Accession: B33359  
 A:Molecule type: DNA  
 A:Residues: 1-259 <MIN>  
 A:Cross-references: GB:M2877; GB:J04702; GB:M23878; NID:9207411; PIDN:AAA42259.1; PID:9  
 R:Shal, S.Y.; Woodley-Miller, C.; Chao, J.; Chao, L.  
 Biochemistry 28, 5334-5343, 1989  
 A:Title: Characterization of genes encoding rat tonin and a kallikrein-like serine prote  
 A:Reference number: A32340; MUID:89375248; PMID:2550051  
 A:Accession: A32340  
 A:Molecule type: DNA  
 A:Residues: 1-259 <SHA>  
 A:Cross-references: GB:M26533; NID:9206775; PIDN:AAA42081.1; PID:9206776; GB:J02860  
 R:Ashley, P.L.; MacDonald, R.J.  
 Biochemistry 24, 4512-4520, 1985  
 A:Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of  
 A:Reference number: A33863; MUID:86051477; PMID:2998455  
 A:Accession: C23863  
 A:Molecule type: mRNA  
 A:Residues: 1-259 <ASH>  
 A:Cross-references: GB:M11565; NID:9205033; PIDN:AAA41466.1; PID:9205034  
 R:Lazure, C.; Leduc, R.; Seidah, N.G.; Thibault, G.; Genest, J.; Chretien, M.  
 Nature 307, 555-558, 1984  
 A:Title: Amino acid sequence of rat submaxillary tonin reveals similarities to serine pr  
 A:Reference number: A93323; MUID:84117504; PMID:6320014  
 A:Accession: A93323  
 A:Molecule type: protein  
 A:Residues: 25-259 <LAI>  
 R:Lazure, C.  
 submitted to the Protein Sequence Database, March 1985  
 A:Reference number: A94635  
 A:Contents: carbohydrate-binding site; revisions  
 A:Accession: A94635  
 A:Molecule type: protein  
 A:Residues: 104-119 <LA2>  
 R:Kanada, M.; Furukata, N.; Yamaguchi, T.; Ikeita, M.; Kizuki, K.; Moriya, H.  
 Biochem. Biophys. Res. Commun. 166, 231-237, 1990  
 A:Title: Observation of tissue prokallikrein activation by some serine proteases, argini  
 A:Reference number: A34050; MUID:90147705; PMID:2302205  
 A:Accession: A34050  
 A:Molecule type: protein  
 A:Residues: 25-30, 'X', 32-34 <KAN>  
 R:Lazure, C.; Leduc, R.; Seidah, N.G.; Thibault, G.; Genest, J.; Chretien, M.  
 Biochem. Cell Biol. 65, 321-337, 1987  
 A:Title: The complete amino acid sequence of rat submaxillary gland tonin does contain t  
 A:Reference number: A30971; MUID:87271223; PMID:3038148  
 A:Accession: A30971

A:Molecule type: protein  
 A:Residues: 25-259 <LA2>  
 C:Comment: This protein is found in submaxillary gland. It has both trypsin- and chym  
 C:Genetics:  
 A:Introns: 16/1; 67/2; 163/1; 208/3  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: glycoprotein; hydrolase; serine proteinase  
 F:1-17/Domain: signal sequence #status predicted <SIG>  
 F:18-24/Domain: propeptide #status predicted <PRO>  
 F:25-259/Product: tonin #status experimental <MAT>  
 F:31-171, 48-64, 150-217, 182-196, 207-232/Disulfide bonds: #status predicted  
 F:63, 118, 211/Active site: His, Asp, Ser #status predicted  
 F:106, 189/Binding site: carbohydrate (Asn) (covalent) #status experimental

Alignment Scores:  
 Pred. No.: 7 22e-32  
 Score: 595.50  
 Percent Similarity: 62.02%  
 Best Local Similarity: 42.25%  
 Query Match: 25.13%  
 Db: 1  
 Gaps: 3

US-09-856-320a-1 (1-1301) x KORTN (1-259)  
 QY 218 CTGCAATTAACTCTGCTGCTGCGCAACAGGGCTTGAGG-----GGAGG 265  
 Db 3 LeuGlnIleLeuSerLeuValLeuSerValGlyArgIleAspAlaIleProProIleGln 22  
 QY 266 ACCAGATATCAAGAGGGTTGAGTGCAGAGCTCATCTCCAGCTGCGAGGACCCG 325  
 Db 23 SerArgIleValGlyGlyTyrIleCysGlyLysAsnSerGlnProTrpIleValAlaVal 42  
 QY 326 TTGAGGAAGAGCGGCTCTGCTGTGGGGGAGCGACGTCATCGCCAGATGGCTGTGCA 385  
 Db 43 IleAsnGlu-----TyrLeuCysGlyValLeuIleAspProSerTrpIleThr 60  
 QY 386 GCAGCCCACTGCTCAAGCCCGCTACATGATGTTACCTGGGGAGACACAACTCCAGAG 445  
 Db 61 AlaAlaHisCysTyrSerAsnAsnTyrGlnValLeuGlyArgAsnIleuLeuHeys 80  
 QY 446 GAGGAGGGCTGTGACACAGCCGAGACAGCTAGTCTTCCACCCCGGCTTC--- 502  
 Db 81 AspGluProPheIleGlnArgIleuValArgGlnSerPheArgIleAspProIle 100  
 QY 503 -----AACAAAGCCCTCCCAACAAAGCCGCAATGATCATG 544  
 Db 101 ProLeuIleValIleThrAsnAspTrpGlnProValIleAspHisSerAsnIleuMet 120  
 QY 545 CTGTTGAAGATGTCATCGCATCTGCATACCTGGGCTGTGCGACCCCTACCTCTCC 604  
 Db 121 LeuIleuHisLeuSerGlnProIleAspIleThrGlyValIleValIleAspLeuPro 140  
 QY 605 TCACCTGTGTGATCTGCGACACAGCTGCTCATTTCCGGTGGGAGACAGCTGCAGC 664  
 Db 141 ThrLysGluProLysValGlySerThrCysLeuAlaSerGlyTyrGlySerThrAsnPro 160  
 QY 665 CCCGAGTTACGCTCTGCATACCTGGAGTGGAGCCGCAATGATGATGAGACAG 724  
 Db 161 SerGlnMetValValSerHisAspLeuIleCysValAsnIleHisLeuIleuSerAsnIle 180  
 QY 725 AAGTTGAGAAAGCTTACCCCGGCAACATCAACAGACACATGTTGTGCGACGTCGAG 784  
 Db 181 LysCysIleGluThrTyrLysAspAsnValIleAspValMetLeuCysAlaGlyIleuMet 200  
 QY 785 GAGGGGCAAGACTCTCCAGGAGTATCTCGGGGCGCTGTGTGTATACCAAGTCT 844  
 Db 201 GluGlyGlyLysAspTrpCysAlaGlyAspSerGlyGlyProLeuIleCysAspGlyVal 220  
 QY 845 CTTCAGGATTAATCTCTGGGGCCAGAGATCGTGTGCAGATCCCGAAAGCTGTGTC 904  
 Db 221 LeuGlnGlyIleThrSerGlyValAlaThrProCysAlaLysProLysThrProAlaIle 240











GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 16:00:49 ; Search time 475.114 Seconds  
(without alignments)  
7105.351 Million cell updates/sec

Title: US-09-856-320A-1

Perfect score: 1301  
Sequence: 1 ctgccttgcctccacacctg.....aaaaaaaaaaaaaaaaaaaa 1301Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1271.4	97.7	1292	12	US-09-933-767-189 Sequence 189, App
2	1271.4	97.7	1292	14	US-10-023-282-189 Sequence 189, App
3	1198	92.1	1204	11	US-09-946-374-169 Sequence 169, App
4	1198	92.1	1204	12	US-10-015-387A-169 Sequence 169, App
5	1198	92.1	1204	12	US-10-137-870-505 Sequence 505, App
6	1198	92.1	1204	12	US-10-140-018-505 Sequence 505, App
7	1198	92.1	1204	12	US-10-140-021-505 Sequence 505, App
8	1198	92.1	1204	12	US-10-140-274-505 Sequence 505, App
9	1198	92.1	1204	12	US-10-140-471-505 Sequence 505, App
10	1198	92.1	1204	12	US-10-140-807-505 Sequence 505, App
11	1198	92.1	1204	12	US-10-140-922-505 Sequence 505, App
12	1198	92.1	1204	12	US-10-140-924-505 Sequence 505, App
13	1198	92.1	1204	12	US-10-140-926-505 Sequence 505, App
14	1198	92.1	1204	12	US-10-141-698-505 Sequence 505, App
15	1198	92.1	1204	12	US-10-141-702-505 Sequence 505, App
16	1198	92.1	1204	12	US-10-141-704-505 Sequence 505, App

17	1198	92.1	1204	12	US-10-142-421-505 Sequence 505, App
18	1198	92.1	1204	12	US-10-142-432-505 Sequence 505, App
19	1198	92.1	1204	12	US-10-142-767-505 Sequence 505, App
20	1198	92.1	1204	12	US-10-143-033-505 Sequence 505, App
21	1198	92.1	1204	12	US-10-144-994-505 Sequence 505, App
22	1198	92.1	1204	12	US-10-145-628-505 Sequence 505, App
23	1198	92.1	1204	12	US-10-145-631-505 Sequence 505, App
24	1198	92.1	1204	12	US-10-145-633-505 Sequence 505, App
25	1198	92.1	1204	12	US-10-145-746-505 Sequence 505, App
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## ALIGNMENTS

RESULT 1  
US-09-933-767-189  
Sequence 189, Application US/09933767  
General Information:  
Publication No. US20030181692A1  
APPLICANT: NI et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P2  
CURRENT FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: PCT/US01/05614  
PRIOR FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: 60/184,836  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: 60/193,170  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: 09/205,258  
PRIOR FILING DATE: 1998-12-04  
PRIOR APPLICATION NUMBER: PCT/US98/11422  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/048,885  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/049,375  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,881  
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PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,896  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/049,020  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,876  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,895  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,884  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 60/048,894





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QY 661 CAGCCCCAGTTACGCTGCTCCACACCTTTCGATGCGGCAACATCATATGAGCA 720  
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Db 1259 TGTATAATGAAAAAAAAAAAAAAAAAAAA 1287

RESULT 3  
US-09-946-374-169  
Sequence 169, Application US/09946374  
Publication No. US20030073129A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C1  
CURRENT APPLICATION NUMBER: US/09/946,374  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
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PRIOR FILING DATE: 1998-09-02  
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PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101479  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101915  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102207

PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102240  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102307  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102330  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102487  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102571  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102684  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102687  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102965  
PRIOR FILING DATE: 1998-10-02  
PRIOR APPLICATION NUMBER: 60/103258  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103314  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103315  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103328  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103395  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103396  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103401  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103633  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103678  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103711  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/104257  
PRIOR FILING DATE: 1998-10-14  
PRIOR APPLICATION NUMBER: 60/104987  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105002  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105104  
PRIOR FILING DATE: 1998-10-21  
PRIOR APPLICATION NUMBER: 60/105169  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105266  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105693  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105694  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105807

Query Match 92.1%; Score 1198; DB 11; length 1204;  
Best Local Similarity 100.0%; Pred. No. 8,8e-312;  
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 GTTCGCGAGATGACAGAGTTGAGGTGGCTGGCGGAGCTGGAAGTCATCGGCGAGAGCTGTC 163  
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Db 1 GTTCCGAGATGACAGAGTTGAGTGGCTGGGGGACTGGAAGTATCGGGGACAGAGTCTC 60  
QY 164 ACACGACCCAGAGAACTGGGGGCGCTCTCCGCCCTCCAGGGCATGAGATTCTGCAG 223  
Db 61 ACACGACCCAGAGAACTGGGGGCGCTCTCCGCCCTCCAGGGCATGAGATTCTGCAG 120  
QY 224 TTATCTGCTGCTGCTGGGCAACGAGGCTTGTAGGGGAGAGACAGGATATCAAGGGG 283  
Db 121 TTTAATCTGCTGCTGGGCAACGAGGCTTGTAGGGGAGAGACAGGATATCAAGGGG 180  
QY 284 TTGAGTGCAGAACTCTCACTCCACAGGCTGGGAGGACAGCCCTGTCGAAAGACCGGCTA 343  
Db 181 TTGAGTGCAGAACTCTCACTCCACAGGCTGGGAGGACAGCCCTGTCGAAAGACCGGCTA 240  
QY 344 CTCTGTGGGGGCGAGCTCATGCGCCCAAGATGGCTCTGACAGCAGCCCATGCTCAAG 403  
Db 241 CTCTGTGGGGGCGAGCTCATGCGCCCAAGATGGCTCTGACAGCAGCCCATGCTCAAG 300  
QY 404 CCCCCTCATAGTATTCACCTGGGGGAGCAGAACTCCAGAAAGAGAGGGCTGTGAGCAG 463  
Db 301 CCCCCTCATAGTATTCACCTGGGGGAGCAGAACTCCAGAAAGAGAGGGCTGTGAGCAG 360  
QY 464 ACCGGAGACGACATGAGTCTCTCCACAGCCCGGCTTCAACACAGAGCTCCCAACAAA 523  
Db 361 ACCGGAGACGACATGAGTCTCTCCACAGCCCGGCTTCAACACAGAGCTCCCAACAAA 420  
QY 524 GACCAACCGCAATGACATCATGCTGTGAGAGATGGCATGCGCATCTCATCACTGGGCT 583  
Db 421 GACCAACCGCAATGACATCATGCTGTGAGAGATGGCATGCGCATCTCATCACTGGGCT 480  
QY 584 GTGGACCCCTCATGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 643  
Db 481 GTGGACCCCTCATGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
QY 644 GGGTGGGGGCGAGAGCTGTCAGAGCCCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 703  
Db 541 GGGTGGGGGCGAGAGCTGTCAGAGCCCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
QY 704 ATACCATCATGATGAGACACAGAAAGTGTGAGAACGCTTACCCCGGCAACATCACAGAC 763  
Db 601 ATACCATCATGATGAGACACAGAAAGTGTGAGAACGCTTACCCCGGCAACATCACAGAC 660  
QY 764 ATGATGTGTGCGAGCGCTGAGAGAAAGGGGAGAGAGTGTGAGAGAGTGTGAGAGAGT 823  
Db 661 ATGATGTGTGCGAGCGCTGAGAGAAAGGGGAGAGAGTGTGAGAGAGTGTGAGAGAGT 720  
QY 824 CTTCTGTGTGTGTAACAGTCTCTTCAAGGCAATATCTCTGAGGGGCGAGATCCGCTGCG 883  
Db 721 CTTCTGTGTGTGTAACAGTCTCTTCAAGGCAATATCTCTGAGGGGCGAGATCCGCTGCG 780  
QY 884 ATACCCCGGAAAGCTGTGTCTACAGAAAGTGTGCAAAATATGTGATGATGATCAGAG 943  
Db 781 ATACCCCGGAAAGCTGTGTCTACAGAAAGTGTGCAAAATATGTGATGATGATCAGAG 840  
QY 944 AGCATGAAGAACTGTGATGATGAGACACAGCAGCCATCATCACTCATTTCCACT 1003  
Db 841 AGCATGAAGAACTGTGATGATGAGACACAGCAGCCATCATCACTCATTTCCACT 900  
QY 1004 TGGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1063  
Db 901 TGGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
QY 1064 CATCTTTTGGGCTCTCTGAGACTACAGAGATGCTGTACATTAATCAACTGGGGTTC 1123  
Db 961 CATCTTTTGGGCTCTCTGAGACTACAGAGATGCTGTACATTAATCAACTGGGGTTC 1020  
QY 1124 GAATATGATGAGACTGATGATTAATTTGCTGAATTTGATGATGATGATGATGATGATG 1183  
Db 1021 GAATATGATGAGACTGATGATTAATTTGCTGAATTTGATGATGATGATGATGATGATG 1080  
QY 1184 ACACCTGGTTTGTCTCTGCTGTATCCCAAGCCCAAGACAGCTCTGCGCATATATCA 1243  
Db 1081 ACACCTGGTTTGTCTCTGCTGTATCCCAAGCCCAAGACAGCTCTGCGCATATATCA 1140

QY 1244 AGTTTCATTAATTAATTTGCTAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1301  
Db 1141 AGTTTCATTAATTAATTTGCTAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198  
RESULT 4  
US-10-015-387A-169  
; Sequence 169, Application US/10015387A  
; Publication No. US20030135034A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C54  
; CURRENT APPLICATION NUMBER: US/10/015.387A  
; PRIORITY FILING DATE: 2001-12-12  
; PRIOR Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 169  
; LENGTH: 1204  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-015-387A-169  
Query Match 92.1%; Score 1198; DB 12; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 8.8e-312;  
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 104 GTTCCGAGATGACAGAGTTGAGTGGCTGGGGGACTGGAAGTATCGGGGACAGAGTCTC 163  
Db 1 GTTCCGAGATGACAGAGTTGAGTGGCTGGGGGACTGGAAGTATCGGGGACAGAGTCTC 60  
QY 164 ACACGACCCAGAGAACTGGGGGCGCTCTCCGCCCTCCAGGGCATGAGATTCTGCAG 223  
Db 61 ACACGACCCAGAGAACTGGGGGCGCTCTCCGCCCTCCAGGGCATGAGATTCTGCAG 120  
QY 224 TTATCTGCTGCTGCTGGGCAACGAGGCTTGTAGGGGAGAGACAGGATATCAAGGGG 283  
Db 121 TTTAATCTGCTGCTGGGCAACGAGGCTTGTAGGGGAGAGACAGGATATCAAGGGG 180  
QY 284 TTGAGTGCAGAACTCTCACTCCACAGGCTGGGAGGACAGCCCTGTCGAAAGACCGGCTA 343  
Db 181 TTGAGTGCAGAACTCTCACTCCACAGGCTGGGAGGACAGCCCTGTCGAAAGACCGGCTA 240  
QY 344 CTCTGTGGGGGCGAGCTCATGCGCCCAAGATGGCTCTGACAGCAGCCCATGCTCAAG 403  
Db 241 CTCTGTGGGGGCGAGCTCATGCGCCCAAGATGGCTCTGACAGCAGCCCATGCTCAAG 300  
QY 404 CCCCCTCATAGTATTCACCTGGGGGAGCAGAACTCCAGAAAGAGAGGGCTGTGAGCAG 463  
Db 301 CCCCCTCATAGTATTCACCTGGGGGAGCAGAACTCCAGAAAGAGAGGGCTGTGAGCAG 360  
QY 464 ACCGGAGACGACATGAGTCTCTCCACAGCCCGGCTTCAACACAGAGCTCCCAACAAA 523  
Db 361 ACCGGAGACGACATGAGTCTCTCCACAGCCCGGCTTCAACACAGAGCTCCCAACAAA 420  
QY 524 GACCAACCGCAATGACATCATGCTGTGAGAGATGGCATGCGCATCTCATCACTGGGCT 583  
Db 421 GACCAACCGCAATGACATCATGCTGTGAGAGATGGCATGCGCATCTCATCACTGGGCT 480



Db 841 ACAGTGAAGAAACATTAAGCTGAGACCCACCCACACACCCATCCATTCATTTCCACT 900  
OY 1004 TGGTGTGTTGTTCCCTGTTCACTGTTTAAAGAAACCCCTAAGCCAGACCCCTACGAA 1063  
Db 901 TGGTGTGTTGTTCCCTGTTCACTGTTTAAAGAAACCCCTAAGCCAGACCCCTACGAA 960  
OY 1064 CATTCCTTTGGGCTCTCTGAGTACAGAGATGCTGTCATTAATATACACCTGGGGTTC 1123  
Db 961 CATTCCTTTGGGCTCTCTGAGTACAGAGATGCTGTCATTAATATACACCTGGGGTTC 1020  
OY 1124 GAAATCAGTGAAGCTGATCAATTCGCTTGAATATGAGCTGAGCTGGAGATGCA 1183  
Db 1021 GAAATCAGTGAAGCTGATCAATTCGCTTGAATATGAGCTGAGCTGGAGATGCA 1080  
OY 1184 ACACCTGTTGTTCTCTGTTGTATCCCCAGCCCAAGACAGCTCTGGCCATATATCA 1243  
Db 1081 ACACCTGTTGTTCTCTGTTGTATCCCCAGCCCAAGACAGCTCTGGCCATATATCA 1140  
OY 1244 AGGTTTCAATTAATTTTCTTAATGAAAAAAGAAAAAAGAAAAAAGAAAAA 1301  
Db 1141 AGGTTTCAATTAATTTTCTTAATGAAAAAAGAAAAAAGAAAAAAGAAAAA 1198

## RESULT 6

US-10-140-018-505  
; Sequence 505, Application US/10140018  
; Publication No. US20030138885A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C158  
; CURRENT APPLICATION NUMBER: US/10/140,018  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 505  
; LENGTH: 1204  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-140-018-505

Query Match 92.1%; Score 1198; DB 12; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 8.8e-312;  
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 GTTCCGAGATGACAGAGTTGAGTGGCTGGGAGCTGAGATGATCGGGGAGAGGTCTC 163  
Db 1 GTTCCGAGATGACAGAGTTGAGTGGCTGGGAGCTGAGATGATCGGGGAGAGGTCTC 60  
OY 164 ACACGACGCAAGAACCTGGGGCCGCTCTCTCCGCCCTCCAGGCCATGAGATTCTGAC 223  
Db 61 ACACGACGCAAGAACCTGGGGCCGCTCTCTCCGCCCTCCAGGCCATGAGATTCTGAC 120  
OY 224 TTATCTGCTGCTGCTGGCAACGAGGCTGTAGAGGAGAGACAGATCATTAAGGG 283  
Db 1198

Db 121 TTAATCTGCTGCTGCTGGCAACAGGGCTTGTAGAGGGGAGAGACAGATCATTAAGGG 180  
OY 284 TTGAGTGAAGACCTCACTCCACAGCCCTGGCAGGAGCCGCTTGGAGAGAGCGGCTA 343  
Db 181 TTGAGTGAAGACCTCACTCCACAGCCCTGGCAGGAGCCGCTTGGAGAGAGCGGCTA 240  
OY 344 CTCTGTGGGGGAGAGCTCATATGCCCCAGATGAGCTCTGACAGGACCCATGCTCAG 403  
Db 241 CTCTGTGGGGGAGAGCTCATATGCCCCAGATGAGCTCTGACAGGACCCATGCTCAG 300  
OY 404 CCCCCGTAACATGATGACCTGGGGGAGACAGACCTCCAGAGAGGAGGGCTGTAGACAG 463  
Db 301 CCCCCGTAACATGATGACCTGGGGGAGACAGACCTCCAGAGAGGAGGGCTGTAGACAG 360  
OY 464 ACCCGAGAGCAGCAGTGAAGTCTTCCCGACCCCGGCTTCAACAACACCTCCCAACAA 523  
Db 361 ACCCGAGAGCAGCAGTGAAGTCTTCCCGACCCCGGCTTCAACAACACCTCCCAACAA 420  
OY 524 GACCAACGCAATGATCATGCTGTGGAAGATGGCATGCGCATGCTCATACCTGGGCT 583  
Db 421 GACCAACGCAATGATCATGCTGTGGAAGATGGCATGCGCATGCTCATACCTGGGCT 480  
OY 584 GTGGAGCCCTCAGCCCTCTCTCAAGCTGTGTCACTGTGGACACAGCTGCTCATTTCC 643  
Db 481 GTGGAGCCCTCAGCCCTCTCTCAAGCTGTGTCACTGTGGACACAGCTGCTCATTTCC 540  
OY 644 GGGTGGGGGAGACAGCTGACAGCCCGCAGTACGCTGCTGCTACACCTTGGAGGCCAAC 703  
Db 541 GGGTGGGGGAGACAGCTGACAGCCCGCAGTACGCTGCTGCTACACCTTGGAGGCCAAC 600  
OY 704 ATCAACATCATTTGAGACACAGAAAGTGTGAGAAAGCTTACCCCGCAACATACAGACAC 763  
Db 601 ATCAACATCATTTGAGACACAGAAAGTGTGAGAAAGCTTACCCCGCAACATACAGACAC 660  
OY 764 ATGCTGTGTGCGACAGCTGACAGAGAGGGGCGAAGAGACTCTGCCAGAGTACTCGGGGGC 823  
Db 661 ATGCTGTGTGCGACAGCTGACAGAGAGGGGCGAAGAGACTCTGCCAGAGTACTCGGGGGC 720  
OY 824 CCTGTGCTGTGTAACAGCTCTCTCAAGGATTAATCTCTGGGGCGAGATCCGTGCGC 883  
Db 721 CCTGTGCTGTGTAACAGCTCTCTCAAGGATTAATCTCTGGGGCGAGATCCGTGCGC 780  
OY 884 ATCAACGCAAGAGCTGTGTACAGAAAGTGTGCAATATGTGACTGATCCAGAG 943  
Db 781 ATCAACGCAAGAGCTGTGTACAGAAAGTGTGCAATATGTGACTGATCCAGAG 840  
OY 944 ACAGTGAAGAAACATTTAGACTGAGACCCACACACAGCCATGACCTCCATTTCCACT 1003  
Db 841 ACAGTGAAGAAACATTTAGACTGAGACCCACACACAGCCATGACCTCCATTTCCACT 900  
OY 1004 TGGTGTGTTGTTCTCTGTTCACTGTTTAAAGAAACCCCTAAGCCAGACCCCTACGAA 1063  
Db 901 TGGTGTGTTGTTCTCTGTTCACTGTTTAAAGAAACCCCTAAGCCAGACCCCTACGAA 960  
OY 1064 CATTCCTTTGGGCTCTCTGAGTACAGAGATGCTGTCATTAATATCAACTGGGGTTC 1123  
Db 961 CATTCCTTTGGGCTCTCTGAGTACAGAGATGCTGTCATTAATATCAACTGGGGTTC 1020  
OY 1124 GAAATCAGTGAAGCTGATCAATTCGCTTGAATATGAGCTGAGCTGGAGATGCA 1183  
Db 1021 GAAATCAGTGAAGCTGATCAATTCGCTTGAATATGAGCTGAGCTGGAGATGCA 1080  
OY 1184 ACACCTGTTGTTCTCTGTTGTATCCCCAGCCCAAGACAGCTCTGGCCATATATCA 1243  
Db 1081 ACACCTGTTGTTCTCTGTTGTATCCCCAGCCCAAGACAGCTCTGGCCATATATCA 1140  
OY 1244 AGGTTTCAATTAATTTTCTTAATGAAAAAAGAAAAAAGAAAAAAGAAAAA 1301  
Db 1141 AGGTTTCAATTAATTTTCTTAATGAAAAAAGAAAAAAGAAAAAAGAAAAA 1198

## RESULT 7

US-10-140-021-505

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Sequence 505, Application US/10140021
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C167
CURRENT APPLICATION NUMBER: US/10/140,021
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 505
LENGTH: 1204
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-021-505

Query Match      92.1%; Score 1198; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8,8e-312;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 GTTCCGACAGATCAGAGGTTGAGTGGCTGCGGAGCTGAGATCGGCGAGAGGCTTC 163
DB 1 GTTCCGACAGATCAGAGGTTGAGTGGCTGCGGAGCTGAGATCGGCGAGAGGCTTC 60
QY 164 ACAGAGCGCAAGGAACCTGGGGGCGGCTCCCTCCCTCCAGCCATGAGATTTGCGAG 223
DB 61 ACAGAGCGCAAGGAACCTGGGGGCGGCTCCCTCCCTCCAGCCATGAGATTTGCGAG 120
QY 224 TTAATCTGCTGCTCTGCGCAACAGGCTTGTAGGGGGAGAGACCAGATCATCAAGGG 283
DB 121 TTAATCTGCTGCTCTGCGCAACAGGCTTGTAGGGGGAGAGACCAGATCATCAAGGG 180
QY 284 TTGAGTGCAGAGCTTCACTCCAGCCCTGGCAGGAGCCCTGTTGAGAAAGAGCGGCTA 343
DB 181 TTGAGTGCAGAGCTTCACTCCAGCCCTGGCAGGAGCCCTGTTGAGAAAGAGCGGCTA 240
QY 344 CTCTGTGGGGGAGAGCTCATGCCCCCAGATGGCTCTGACAGGAGCCCATGCTCAAG 403
DB 241 CTCTGTGGGGGAGAGCTCATGCCCCCAGATGGCTCTGACAGGAGCCCATGCTCAAG 300
QY 404 CCCCCTACATATGTTACACTGGGGGAGAGCAACCTCCAGAAAGAGAGGGCTGTAGAGAG 463
DB 301 CCCCCTACATATGTTACACTGGGGGAGAGCAACCTCCAGAAAGAGAGGGCTGTAGAGAG 360
QY 464 ACCGGAGACAGCCACTGAGTCTTCCCAACCCCGGCTTCACACAGAGCTCCCAACAAA 523
DB 361 ACCGGAGACAGCCACTGAGTCTTCCCAACCCCGGCTTCACACAGAGCTCCCAACAAA 420
QY 524 GACCAACCCGATGATATGCTGTGAAGATGAGATGCGATGCGCATCATCACTGGGGCT 583
DB 421 GACCAACCCGATGATATGCTGTGAAGATGAGATGCGATGCGCATCATCACTGGGGCT 480
QY 584 GTGCGACCCCTACCTCTCTCTGACGCTGTGTACATGCTGCGACCAAGCGCTCATTTCC 643
DB 481 GTGCGACCCCTACCTCTCTCTGACGCTGTGTACATGCTGCGACCAAGCGCTCATTTCC 540
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QY 644 GGCTGGGGGAGAGCAGTCCAGCCGCCAGGTTACGCTGCTCTACACCTTTGGATGCGGCAAC 703
DB 541 GGCTGGGGGAGAGCAGTCCAGCCGCCAGGTTACGCTGCTCTACACCTTTGGATGCGGCAAC 600
QY 704 ATACCATATATTGAGACACCAAGATGTGAAACGCTTACCCGGGCAACATCAGACAGACC 763
DB 601 ATACCATATATTGAGACACCAAGATGTGAAACGCTTACCCGGGCAACATCAGACAGACC 660
QY 764 ATGTGTGTGCCAGGCTGAGAGAAAGGGGAGAGATCTCTGCGAGGATGATCCGGGGGC 823
DB 661 ATGTGTGTGCCAGGCTGAGAGAAAGGGGAGAGATCTCTGCGAGGATGATCCGGGGGC 720
QY 824 CCTGTGCTGTATACCAAGTCTCTTCAAGGCAATTAATCTCTGGGGCCAGGATCGGTGGC 883
DB 721 CCTGTGCTGTATACCAAGTCTCTTCAAGGCAATTAATCTCTGGGGCCAGGATCGGTGGC 780
QY 884 ATCACCAGCAAGCCCTGCTGTCTACACGAAAGTCTGCAATTAATGTGATGATCCAGAG 943
DB 781 ATCACCAGCAAGCCCTGCTGTCTACACGAAAGTCTGCAATTAATGTGATGATCCAGAG 840
QY 944 ACAGTGAAGAACAAATTAGACTGGACCCAGCCAGCCAGCCATCAACCCCTCATTTCCACT 1003
DB 841 ACAGTGAAGAACAAATTAGACTGGACCCAGCCAGCCAGCCATCAACCCCTCATTTCCACT 900
QY 1004 TGGTGTGTTGCTCTGCTCTCTCTGTTAATAAGAAACCTTAAGCCAAAGACCTTAAGAA 1063
DB 901 TGGTGTGTTGCTCTGCTCTCTCTGTTAATAAGAAACCTTAAGCCAAAGACCTTAAGAA 960
QY 1064 CATTTCTTTGGGCTCTCTGAGCTACAGAGAGATGCTGACTTAATTAATCAACTGGGGTTC 1123
DB 961 CATTTCTTTGGGCTCTCTGAGCTACAGAGAGATGCTGACTTAATTAATCAACTGGGGTTC 1020
QY 1124 GAATCAGTGAAGACCTGATTAATTAATTTGCTGCAATTAATGTGATGATGGAATGAGA 1183
DB 1021 GAATCAGTGAAGACCTGATTAATTAATTTGCTGCAATTAATGTGATGATGGAATGAGA 1080
QY 1184 ACACCTGTTGTTCTCTGCTGTATCCAGGCCCAAGAGACGCTCTGGCCATATATCA 1243
DB 1081 ACACCTGTTGTTCTCTGCTGTATCCAGGCCCAAGAGACGCTCTGGCCATATATCA 1140
QY 1244 AGCTTTCATTAATTAATTTGCTTAATGAAAAAATTTGCTTAATGAAAAAATTTGCT 1301
DB 1141 AGCTTTCATTAATTAATTTGCTTAATGAAAAAATTTGCTTAATGAAAAAATTTGCT 1198

RESULT 8
US-10-140-274-505
Sequence 505, Application US/10140274
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C161
CURRENT APPLICATION NUMBER: US/10/140,274
Prior Application removed - See File Wrapper or Palm
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NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 505  
LENGTH: 1204  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-140-274-505

Query Match 92.1%; Score 1198; DB 12; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 8.8e-312;  
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 104 GTTCGCGATGACAGAGTTGAGTGGCTGCGGAGCTGAAGTCAATCGGGAGAGGTCTC 163
DB 1 GTTCGCGATGACAGAGTTGAGTGGCTGCGGAGCTGAAGTCAATCGGGAGAGGTCTC 60
OY 164 ACAGACGCAAGAAAGCTGGGGCCGCTCTCCCTCCAGAGCCATGAGATTCTGCAG 223
DB 61 ACAGACGCAAGAAAGCTGGGGCCGCTCTCCCTCCAGAGCCATGAGATTCTGCAG 120
OY 224 TTAATCTGCTTGTCTGGCAAGAGGCTTTAGGGGAGAGACAGATCATCAAGGG 283
DB 121 TTAATCTGCTTGTCTGGCAAGAGGCTTTAGGGGAGAGACAGATCATCAAGGG 180
OY 284 TTCGAGTGCAGACCTCACTCCAGCCCTGGCAGAGCCGCTTGCAGAAAGAGCGGCTA 343
DB 181 TTCGAGTGCAGACCTCACTCCAGCCCTGGCAGAGCCGCTTGCAGAAAGAGCGGCTA 240
OY 344 CTCTGTGGGGGCGACGCTCATGCCCCAGATGCTCTGACAGACGCCATGCTCAAG 403
DB 241 CTCTGTGGGGGCGACGCTCATGCCCCAGATGCTCTGACAGACGCCATGCTCAAG 300
OY 404 CCCCAGTACATAGTTCACTCTGGGGGACACAACTCCAGAAAGAGAGGGGCTGTGACAG 463
DB 301 CCCCAGTACATAGTTCACTCTGGGGGACACAACTCCAGAAAGAGAGGGGCTGTGACAG 360
OY 464 ACCCGAGACGACCTGAGTCTCTCCACCCCGCTTCAACAACAGCCCTCCCAACAAA 523
DB 361 ACCCGAGACGACCTGAGTCTCTCCACCCCGCTTCAACAACAGCCCTCCCAACAAA 420
OY 524 GACCAACGCAATGACATCATCTGTGTGAAGATGGCATATGCCAGTCTCATACCTGGGCT 583
DB 421 GACCAACGCAATGACATCATCTGTGTGAAGATGGCATATGCCAGTCTCATACCTGGGCT 480
OY 584 GTGGACCCCTCAGCCCTCTCTCTGCGGTGTCAGTCTGTGGCAGACAGTGCCTATTTC 643
DB 481 GTGGACCCCTCAGCCCTCTCTCTGCGGTGTCAGTCTGTGGCAGACAGTGCCTATTTC 540
OY 644 GGCTGGGGCAGACAGTCCAGCCCGCAGTTACGCTGCTCTACACCTTGCATGGCCAAAC 703
DB 541 GGCTGGGGCAGACAGTCCAGCCCGCAGTTACGCTGCTCTACACCTTGCATGGCCAAAC 600
OY 704 ATCAACCATATGAGCAACAGAGTGTGAGAACGCTTACCCCGCAACATCACAGACACC 763
DB 601 ATCAACCATATGAGCAACAGAGTGTGAGAACGCTTACCCCGCAACATCACAGACACC 660
OY 764 ATGGTGTGTGCGACGCGAGAGAGGGGGAGAGNCTCTGCGAGGGGTGATCCGGGGGG 823
DB 661 ATGGTGTGTGCGACGCGAGAGAGGGGGAGAGNCTCTGCGAGGGGTGATCCGGGGGG 720
OY 824 CCTGTGTGTGAACAGTCTCTTCAAGGCAATTAATCTCTGGGGCAGAGATCCGTGTGCG 883
DB 721 CCTGTGTGTGAACAGTCTCTTCAAGGCAATTAATCTCTGGGGCAGAGATCCGTGTGCG 780
OY 884 ATCAACCGGAAAGCTGTGTCTACAGAAAGTGTGCAAAATATGTGAGATCCAGAG 943
DB 781 ATCAACCGGAAAGCTGTGTCTACAGAAAGTGTGCAAAATATGTGAGATCCAGAG 840
OY 944 ACGATGAAGAACAATTGAGTGCAGCCACCCACAGCCCAATCAACCTCATTTCCACT 1003
DB 841 ACGATGAAGAACAATTGAGTGCAGCCACCCACAGCCCAATCAACCTCATTTCCACT 900
OY 1004 TGGTGTGTGCTCTGTTCACTGTATTAAGAAACCTTAAGCAGACCTCTACGAA 1063
DB 1004 TGGTGTGTGCTCTGTTCACTGTATTAAGAAACCTTAAGCAGACCTCTACGAA 1063
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DB 901 TGGTGTGTGCTCTGTTCACTGTATTAAGAAACCTTAAGCAGACCTCTACGAA 960
OY 1064 CATTCCTTTGGGCTCTCTGAGTACAGAGATGCTGTCAATTAATCAACTGGGGTTC 1123
DB 961 CATTCCTTTGGGCTCTCTGAGTACAGAGATGCTGTCAATTAATCAACTGGGGTTC 1020
OY 1124 GAAATCAGTGAAGACCTGGATTCAATTTCTGCTTGAATATTTGACTGTGGAAATGACA 1183
DB 1021 GAAATCAGTGAAGACCTGGATTCAATTTCTGCTTGAATATTTGACTGTGGAAATGACA 1080
OY 1184 ACACCTGATTTGTTCTCTGTTGATCCCAAGCCCAAGACAGCTCCTGGCATATATCA 1243
DB 1081 ACACCTGATTTGTTCTCTGTTGATCCCAAGCCCAAGACAGCTCCTGGCATATATCA 1140
OY 1244 AGGTTCAATTAATATTTGCTTAATGAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1301
DB 1141 AGGTTCAATTAATATTTGCTTAATGAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1198

RESULT 9
US-10-140-471-505
; Sequence 505, Application US/10140471
; Publication No. US2003013887A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C163
; CURRENT APPLICATION NUMBER: US/10/140,471
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-140-471-505

Query Match 92.1%; Score 1198; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.8e-312;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1124 GAAATCAGTGAAGCTGTGATCAAAATTTGCTTGAATATTTGTGACTGTGGGAATGACA 1183
    |||
Db 1021 GAAATCAGTGAAGCTGTGATCAAAATTTGCTTGAATATTTGTGACTGTGGGAATGACA 1080
OY 1184 AACCTGCTGTTGCTCTCTTTGTATCCCAAGCCCAAGACAGCTCTCTGCAATATATCA 1243
    |||
Db 1081 AACCTGCTGTTGCTCTCTTTGTATCCCAAGCCCAAGACAGCTCTCTGCAATATATCA 1140
OY 1244 AGTTTCATTAATATTTGCTTAATGAAAAAATTTGCTTGAATATTTGTGACTGTGGGAATGACA 1301
    |||
Db 1141 AGTTTCATTAATATTTGCTTAATGAAAAAATTTGCTTGAATATTTGTGACTGTGGGAATGACA 1198

```

```

RESULT 12
US-10-140-924-505
; Sequence 505, Application US/10140924
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C177
; CURRENT FILING DATE: 2002-05-07
; Prior Apportionment removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-924-505

```

```

Query Match 92.1%; Score 1198; DB 12; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.8e-312;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 104 GTTCGGAGATGACAGAGTGTGAGTGTGGGAGTGAATGATTCGAGAGAGTCTC 163
    |||
Db 1 GTTCGGAGATGACAGAGTGTGAGTGTGGGAGTGAATGATTCGAGAGAGTCTC 60
OY 164 ACAGAGCCCAAGAACTGTGGGCGCGCTCTCCCTCCATGAGCATGATTTCTGAC 223
    |||
Db 61 ACAGAGCCCAAGAACTGTGGGCGCGCTCTCCCTCCATGAGCATGATTTCTGAC 120
OY 224 TTAATCTGCTGCTGTGCGCAACAGAGGCTTGTAGGGGGAGAGACAGATCATCAAGGGG 283
    |||
Db 121 TTAATCTGCTGCTGTGCGCAACAGAGGCTTGTAGGGGGAGAGACAGATCATCAAGGGG 180
OY 284 TTCGAGTGAACCTCTACCTCCAGCCCTGGCAGGAGCCCTTTTGAAGAAGCGGGCTA 343
    |||
Db 181 TTCGAGTGAACCTCTACCTCCAGCCCTGGCAGGAGCCCTTTTGAAGAAGCGGGCTA 240
OY 344 CTCTGTGGGGAGAGCTCATGCGCCCAAGATGGTCTCTGACAGACGCCCATGCTCAAG 403
    |||
Db 241 CTCTGTGGGGAGAGCTCATGCGCCCAAGATGGTCTCTGACAGACGCCCATGCTCAAG 300

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OY 404 CCCCGCTACATAGTTCACCTGTGGGGAGACACAACTTCAGAGAGAGAGGGCTGTGACAG 463
    |||
Db 301 CCCCGCTACATAGTTCACCTGTGGGGAGACACAACTTCAGAGAGAGAGGGCTGTGACAG 360
OY 464 ACCCGAGAGCCCACTGATCTCTCCCGACCCCGGCTTAACAAACAGCTCTCCCAACAA 523
    |||
Db 361 ACCCGAGAGCCCACTGATCTCTCCCGACCCCGGCTTAACAAACAGCTCTCCCAACAA 420
OY 524 GACACACCGCAATGACATCATGCTGGTGAATGGATGCGCCGATGCTCCATCACTCGGGCT 583
    |||
Db 421 GACACACCGCAATGACATCATGCTGGTGAATGGATGCGCCGATGCTCCATCACTCGGGCT 480
OY 584 GTGCAACCCCTCACTCTCTCTGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 643
    |||
Db 481 GTGCAACCCCTCACTCTCTCTGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
OY 644 GGCTGGGGAGAGAGCTGACGCGCCCGGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 703
    |||
Db 541 GGCTGGGGAGAGAGCTGACGCGCCCGGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
OY 704 ATCACCATCATTTGAGACAGCAGAAAGTGTGAAGAGCCTTACCCCGGCAATCAAGACAC 763
    |||
Db 601 ATCACCATCATTTGAGACAGCAGAAAGTGTGAAGAGCCTTACCCCGGCAATCAAGACAC 660
OY 764 ATGCTGTGTGCCAGGCTGACAGAGAGGGGCAAGAGACTCTGCCAAGGCTGACTCCGGGGG 823
    |||
Db 661 ATGCTGTGTGCCAGGCTGACAGAGAGGGGCAAGAGACTCTGCCAAGGCTGACTCCGGGGG 720
OY 824 CCTGTGTGTGTACACAGCTCTTCAAGGATTTATCTCTGGGGCCAGATCTCGTGTGCG 883
    |||
Db 721 CCTGTGTGTGTACACAGCTCTTCAAGGATTTATCTCTGGGGCCAGATCTCGTGTGCG 780
OY 884 ATCACCAGAGAGCTGTGTGTACACAGAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGT 943
    |||
Db 781 ATCACCAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
OY 944 ACAGTGAAGACAAATTTAGACTGTGAGCCACCAAGCCATCACTCCCTCACTTTCCACT 1003
    |||
Db 841 ACAGTGAAGACAAATTTAGACTGTGAGCCACCAAGCCATCACTCCCTCACTTTCCACT 900
OY 1004 TGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1063
    |||
Db 901 TGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
OY 1064 CATCTTTGGGCTCTGCTGACTACAGAGAGATGCTGCTCACTTAATATCAACTGGGGTTC 1123
    |||
Db 961 CATCTTTGGGCTCTGCTGACTACAGAGAGATGCTGCTCACTTAATATCAACTGGGGTTC 1020
OY 1124 GAAATCAGTGAAGCTGTGATCAAAATTTGCTTGAATATTTGTGACTGTGGGAATGACA 1183
    |||
Db 1021 GAAATCAGTGAAGCTGTGATCAAAATTTGCTTGAATATTTGTGACTGTGGGAATGACA 1080
OY 1184 AACCTGCTGTTGCTCTCTTTGTATCCCAAGCCCAAGACAGCTCTCTGCAATATATCA 1243
    |||
Db 1081 AACCTGCTGTTGCTCTCTTTGTATCCCAAGCCCAAGACAGCTCTCTGCAATATATCA 1140
OY 1244 AGTTTCATTAATATTTGCTTAATGAAAAAATTTGCTTGAATATTTGTGACTGTGGGAATGACA 1301
    |||
Db 1141 AGTTTCATTAATATTTGCTTAATGAAAAAATTTGCTTGAATATTTGTGACTGTGGGAATGACA 1198

```

```

RESULT 13
US-10-140-926-505
; Sequence 505, Application US/10140926
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.

```

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Collin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P330R1C187  
CURRENT APPLICATION NUMBER: US/10/140.926  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 505  
LENGTH: 1204  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-140-926-505

Query Match 92.1%: Score 1198; DB 12; Length 1204;

Best Local Similarity 100.0%: Pred. No. 8.8e-312;

Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 GTTCCGAGATGACAGAGTTGAGGTGGCTGGGAGCTGGAATCATGCGGAGAGTCTC 163  
1 GTTCCGAGATGACAGAGTTGAGGTGGCTGGGAGCTGGAATCATGCGGAGAGTCTC 60  
DB 164 ACAGACACCAAGAGAACTGGGGGCGCTCTCCCTCCAGGCAATGAGATTCTGCAG 223  
61 ACAGACACCAAGAGAACTGGGGGCGCTCTCCCTCCAGGCAATGAGATTCTGCAG 120  
QY 224 TTAATCTGCTGTGCTGGACACAGGGCTGTAGGGGAGAGACAGATCATCAAGGG 283  
121 TTAATCTGCTGTGCTGGACACAGGGCTGTAGGGGAGAGACAGATCATCAAGGG 180  
DB 284 TTGAGTGCAGAGCCCTCACTCCAGCCCTGGAGGACAGCCCTGTTCGAAAGACGGGCTA 343  
181 TTGAGTGCAGAGCCCTCACTCCAGCCCTGGAGGACAGCCCTGTTCGAAAGACGGGCTA 240  
QY 344 CTCTGTGGGGGAGAGCTCATGCGCCCAAGATGGCTCTGACAGAGCCCTGCTTAAG 403  
241 CTCTGTGGGGGAGAGCTCATGCGCCCAAGATGGCTCTGACAGAGCCCTGCTTAAG 300  
QY 404 CCCGCTACATTAAGTTCACTGGGGGACAGACAACCTCCAGAAAGAGAGGGCTGTGACAG 463  
301 CCCGCTACATTAAGTTCACTGGGGGACAGACAACCTCCAGAAAGAGAGGGCTGTGACAG 360  
QY 464 ACCGAGACCCCACTGAGCTCTTCCACCCCGGGCTTCAACAACAGCCTTCCCAACAA 523  
361 ACCGAGACCCCACTGAGCTCTTCCACCCCGGGCTTCAACAACAGCCTTCCCAACAA 420  
DB 524 GACACCGCAATGACATGCTGGTGAATGGATGCGCAGCTTCACACTTACCTGGGCT 583  
421 GACACCGCAATGACATGCTGGTGAATGGATGCGCAGCTTCACACTTACCTGGGCT 480  
QY 584 GTGCGACCCCTCAACCTCTCTCAAGCTGTGTCAGTCTGGACACAGCTCTCATTTTC 643  
481 GTGCGACCCCTCAACCTCTCTCAAGCTGTGTCAGTCTGGACACAGCTCTCATTTTC 540  
DB 644 GGGTGGGGGACAGAGTTCAGCCCACTTAAGCCCTGCTCACAACCTTGGATGGCCAAC 703  
541 GGGTGGGGGACAGAGTTCAGCCCACTTAAGCCCTGCTCACAACCTTGGATGGCCAAC 600  
QY 704 ATGACCATATGAGACACAGAAAGTGTGAAGAGCCCTACCCCGGCAATCATCAGACACC 763  
601 ATGACCATATGAGACACAGAAAGTGTGAAGAGCCCTACCCCGGCAATCATCAGACACC 660  
QY 764 ATGATGTGTCGACGCTGACAGAAAGGGGCAAGGACTCTGCAGGGGTGACTCGGGGGG 823  
|||||

DB 661 ATGATGTGTCGACGCTGACAGAAAGGGGCAAGGACTCTGCAGGGGTGACTCGGGGGG 720  
QY 824 CCTGTGCTGTACACAGCTCTTCAAGGCAATATCTCTGGGGCCAGATCCGTGGCC 883  
721 CCTGTGCTGTACACAGCTCTTCAAGGCAATATCTCTGGGGCCAGATCCGTGGCC 780  
QY 884 ATCACCAGAAAGCCTGTGTCTACAGAAAGTGTGAATATGTGACTGATCCAGAG 943  
781 ATCACCAGAAAGCCTGTGTCTACAGAAAGTGTGAATATGTGACTGATCCAGAG 840  
QY 944 ACGATGAAGAAATATGACTGACGACCCACACACAGCCCAATCACCCTCATTTCCACT 1003  
841 ACGATGAAGAAATATGACTGACGACCCACACACAGCCCAATCACCCTCATTTCCACT 900  
QY 1004 TGTGTGTGTTCTCTGTTCACTCTGTTAATAGAAACCTTAAGCAAGACCTCTACGAA 1063  
901 TGTGTGTGTTCTCTGTTCACTCTGTTAATAGAAACCTTAAGCAAGACCTCTACGAA 960  
DB 1064 CATCTTTGGGCTCTCTGACACTACAGAGATGCTGACTTAATATCAACTTGGGGTTC 1123  
961 CATCTTTGGGCTCTCTGACACTACAGAGATGCTGACTTAATATCAACTTGGGGTTC 1020  
QY 1124 GAAATCAGTACAGCTGATTCAAATCTGCTTGAATATGTGACTGTGGGAATGACA 1183  
1021 GAAATCAGTACAGCTGATTCAAATCTGCTTGAATATGTGACTGTGGGAATGACA 1080  
DB 1184 ACACCTGTTTCTCTCTGTATGCCAGCCCAAGACAGCTCTGCGCATATATCA 1243  
1081 ACACCTGTTTCTCTCTGTATGCCAGCCCAAGACAGCTCTGCGCATATATCA 1140  
QY 1244 AGTTTCAATTAATTTTGTAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1301  
1141 AGTTTCAATTAATTTTGTAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198

## RESULT 14

US-10-141-698-505

Sequence 505, Application US/10141698

Publication No. US20030134357A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Deforge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Flivaroif, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Collin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P330R1C206

CURRENT APPLICATION NUMBER: US/10/141.698

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 505

LENGTH: 1204

TYPE: DNA

ORGANISM: Homo Sapien

US-10-141-698-505

Query Match 92.1%: Score 1198; DB 12; Length 1204;  
Best Local Similarity 100.0%: Pred. No. 8.8e-312;  
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 12:59:38 : Search time 121.723 Seconds  
(without alignments)  
4717.579 Million cell updates/sec

Title: US-09-856-320A-1

Perfect score: 1301  
Sequence: 1 ctgccttcctccacacctcg.....aaaaaaaaaaaaaaaaaaaa 1301

Scoring table: IDENTITY\_MDC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/1na/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/1na/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/1na/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/1na/PCRTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/1na/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1283.4	98.6	1314	3	US-09-025-059-2
2	1271.4	97.7	1292	4	US-09-205-258-189
3	1114.4	85.7	1192	3	US-08-944-483-8
4	1063	81.7	1166	3	US-08-944-483-7
5	1029.2	79.1	1146	4	US-09-205-258-247
6	673.2	51.7	833	2	US-08-790-137-2
7	662.4	50.9	1052	4	US-09-386-642-10
8	551.8	42.4	662	4	US-09-702-705-109
9	551.8	42.4	662	4	US-09-736-457-109
10	478.8	36.8	618	4	US-09-280-116-3
11	441.8	34.0	472	4	US-09-280-116-136
12	409	31.4	409	4	US-09-702-705-1109
13	409	31.4	409	4	US-09-736-457-1109
14	368.4	28.3	406	3	US-08-944-483-6
15	262	20.1	262	3	US-08-944-483-5
16	250	19.2	250	3	US-08-944-483-4
17	237.4	18.2	239	3	US-08-944-483-3
18	228	17.5	994	3	US-09-008-271A-19
19	224.8	17.3	944	3	US-09-070-526-1
20	224	17.2	1049	4	US-09-386-642-9
21	196.4	15.1	1570	4	US-09-996-243-308
22	191.4	14.7	825	3	US-09-120-582-1
23	188.8	14.5	897	2	US-08-956-267A-1
24	187	14.4	1476	4	US-08-824-874-2
25	187	14.4	1476	4	US-09-210-084-2
26	187	14.4	1476	4	US-09-764-762-2
27	182.6	14.0	732	1	US-08-361-395-2

28	180.4	13.9	1341	4	US-08-983-075D-6	Sequence 6, Appl1
29	180.4	13.9	1358	4	US-08-983-075D-8	Sequence 8, Appl1
30	178.8	13.7	766	3	US-08-768-859A-9	Sequence 9, Appl1
31	178.8	13.7	766	3	US-08-767-820A-9	Sequence 9, Appl1
32	178.8	13.7	766	3	US-08-622-046B-6	Sequence 6, Appl1
33	178.8	13.7	766	3	US-08-622-046B-17	Sequence 17, Appl1
34	178.8	13.7	766	3	US-09-100-264-6	Sequence 6, Appl1
35	178.8	13.7	822	3	US-08-843-076D-6	Sequence 6, Appl1
36	178.8	13.7	822	3	US-09-100-264-8	Sequence 8, Appl1
37	178.8	13.7	832	3	US-08-768-859A-5	Sequence 5, Appl1
38	178.8	13.7	832	3	US-08-768-859A-20	Sequence 20, Appl1
39	178.8	13.7	832	3	US-08-767-820A-5	Sequence 5, Appl1
40	178.8	13.7	832	3	US-08-767-820A-20	Sequence 20, Appl1
41	178.8	13.7	832	3	US-08-622-046B-4	Sequence 4, Appl1
42	178.8	13.7	832	3	US-08-622-046B-15	Sequence 15, Appl1
43	178.8	13.7	832	4	US-08-843-076D-4	Sequence 4, Appl1
44	178.2	13.7	760	3	US-08-768-859A-7	Sequence 7, Appl1
45	178.2	13.7	760	3	US-08-767-820A-7	Sequence 7, Appl1

## ALIGNMENTS

RESULT 1  
US-09-025-059-2  
; Sequence 2, Application US/09025059  
; Patent No. 6075136  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,059  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0481 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELER:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1314 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: LUNG10T10  
; CLONE: 2723646  
; US-09-025-059-2  
Query Match 98.6%; Score 1283.4; DB 3; Length 1314;  
Best Local Similarity 99.9%; Pred. No. 4.2e-315;







Query Match	Best Local Similarity	85.7%	Score 1114.4	DB 3	Length 1192
Matches 1115	Conservative	0	Mismatches 1	Indels 0	Gaps 0
169	AGCCAGAGAACCTGGGGCCCGCTCTCCGCCCTCCAGGCCATGAGATTCTGCAGTTAAT	228			
67	AGCCTAGAGAACCTGGGGCCCGCTCTCCGCCCTCCAGGCCATGAGATTCTGCAGTTAAT	126			
229	CTGCTGTCCTGCGCAACAGGGCTGTGAGGGGGAGAGACCAGGATCATCAAGGGTTGCA	288			
127	CTGCTGTCCTGCGCAACAGGGCTGTGAGGGGGAGAGACCAGGATCATCAAGGGTTGCA	186			
289	GTGGAACCCCTCACTCCACGCGCTGGGAGAGAGCGCCGTTCGAGAAAGCCGGCTACTCTG	348			
187	GTGGAACCCCTCACTCCACGCGCTGGGAGAGAGCGCCGTTCGAGAAAGCCGGCTACTCTG	246			
349	TGGGGCAGACCTCATCGCCGCCAGATGAGCTCTGACAGGACCCATGCTCTCAAGGCCCG	408			
247	TGGGGCAGACCTCATCGCCGCCAGATGAGCTCTGACAGGACCCATGCTCTCAAGGCCCG	306			
409	CTACATAGTTCACTCGGGGAGCAGCAACCTCCAGAAAGGAGAGGGCTGTGACAGACCG	468			
307	CTACATAGTTCACTCGGGGAGCAGCAACCTCCAGAAAGGAGAGGGCTGTGACAGACCG	366			
469	GACAGCCACGATGCTCTCCGCCACCCGGGCTTCAACCAACAGCTCTCCCAACAAAGACCA	528			
367	GACAGCCACGATGCTCTCCGCCACCCGGGCTTCAACCAACAGCTCTCCCAACAAAGACCA	426			
529	CGCAATGACATGCTGTGTAAGATGGATGCGCAGCTCATCACTGAGGCTGTGG	588			

Db	427	CCGCAATGACATCATGCTGTGTGAAGATGGGATGSCCAAGTCTCATCACTGGGCTGTGG	486
QY	589	ACCCCTACACCTTCTCTCACGCTGTGTCACTGCTGGCACACAGTGGCTTATTTCCGGCTG	648
Db	487	ACCCCTACACCTTCTCTCACGCTGTGTGTCACTGCTGGCACACAGTGGCTTATTTCCGGCTG	546
QY	649	GGGAGAGACGTCACAGGCCCCAGTTAGGCGCTCTACACTTGGCGATGGGCCAATCTAC	708
Db	547	GGGAGAGACGTCACAGGCCCCAGTTAGGCGCTCTACACTTGGCGATGGGCCAATCTAC	606
QY	709	CATCATTTGAGACACAGAAAGTGTAGAAAGCGCTACCCCGGCAACATACAGACACATGAT	768
Db	607	CATCATTTGAGACACAGAAAGTGTAGAAAGCGCTACCCCGGCAACATACAGACACATGAT	666
QY	769	GTTGTCCACGCTGTACAGAAAGGGGGACAGGACTTCTCCAGAGGCTACCGGGGGCCCTCT	828
Db	667	GTTGTCCACGCTGTACAGAAAGGGGGACAGGACTTCTCCAGAGGCTACCGGGGGCCCTCT	726
QY	829	GGTCTGAACCACTCTCTTCANAGCATTTATCTCTGGGGCCAGAGATCCCTGTGCCATCAC	888
Db	727	GGTCTGAACCACTCTCTTCANAGCATTTATCTCTGGGGCCAGAGATCCCTGTGCCATCAC	786
QY	889	CCGAAAGCCCTGTGTGTACACGAAAGTCTGCAAAATATGTGACCTGATCAGAGACGAT	948
Db	787	CCGAAAGCCCTGTGTGTACACGAAAGTCTGCAAAATATGTGACCTGATCAGAGACGAT	846
QY	949	GAGAAACAATTTAGACTGAGACCCACCCACACACAGCCCATCACTCCATTTCCACTTGGTG	1008
Db	847	GAGAAACAATTTAGACTGAGACCCACCCACACACAGCCCATCACTCCATTTCCACTTGGTG	906
QY	1009	TTTGGTTCCGTCTCACTCTGTATTAAGAAACCTTAAGCAGAGCCCTCTAGAACATTC	1068
Db	907	TTTGGTTCCGTCTCACTCTGTATTAAGAAACCTTAAGCAGAGCCCTCTAGAACATTC	966
QY	1069	TTTGGGCGCTCTGGACTACAGAGATGCTGTCACTTAATATCAACTGGGTTGCAAT	1128
Db	967	TTTGGGCGCTCTGGACTACAGAGATGCTGTCACTTAATATCAACTGGGTTGCAAT	1026
QY	1129	CAGTGAAGCTGTGATTCAAATTTGCTTGAATATTTGACTCTGGGAATGACACACC	1188
Db	1027	CAGTGAAGCTGTGATTCAAATTTGCTTGAATATTTGACTCTGGGAATGACACACC	1086
QY	1189	TGTTTGTCTCTGTGTATCCCGACCCCAAGACAGTCCGCGCATATATCAAGTT	1248
Db	1087	TGTTTGTCTCTGTGTATCCCGACCCCAAGACAGTCCGCGCATATATCAAGTT	1146
QY	1249	TCAATAAATTTTGTCTAATGAAAAAAAAAAAAA 1284	
Db	1147	TCAATAAATTTTGTCTAATGAAAAAAAAAAAAA 1182	
RESULT 4			
US-08-944-483-7			
Sequence 7, Application US/08944483			
Patent No. 6232456			
GENERAL INFORMATION:			
APPLICANT: COHEN, MAURICE			
APPLICANT: COLETTIS, TRACEY L.			
APPLICANT: FRIEDMAN, PAULA N.			
APPLICANT: GRANADOS, EDWARD N.			
APPLICANT: KLISS, MICHAEL R.			
APPLICANT: RUSSELL, JOHN C.			
APPLICANT: STEWART, KENT D.			
APPLICANT: STROUPE, STEVEN D.			
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS			
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES			
NUMBER OF SEQUENCES: 76			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Abbott Laboratories			
STREET: 100 Abbott Park Road			
CITY: Abbott Park			
STATE: IL			

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? COUNTRY: USA
? ZIP: 60064-3500
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/944,483
? FILING DATE:
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Becker, Cheryl L.
? REGISTRATION NUMBER: 35,441
? REFERENCE/DOCKET NUMBER: 6183.US.01
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 847/935-1729
? TELEFAX: 847/938-2623
? TELEX:
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1166 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-08-944-483-7

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Query Match 81.7%; Score 1063; DB 3; Length 1166;

Best Local Similarity 99.3%; Pred. No. 2,1e-259;

Matches 1096; Conservative 2; Mismatches 3; Indels 3; Gaps 3;

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? 169 AGCCAAGGACCTGGGGCCGCTCCGCCCTCCAGGCGGAGAGATTCAGATTAT 228
? 63 AGCCTAGGAACTGGGGCCGCTCCGCCCTCCAGGCGGAGATTCAGATTAT 122
? 229 CCTGCTTGTCTGGCAACAGGGCTTGTAGGGGAGAGACCAGATCATCAAGGGTTGA 288
? 123 CTTGCTTGTCTGGCAACAGGGCTTGTAGGGGAGAGACCAGATCATCAAGGGTTGA 182
? 289 GTGCAAGCCTCTACCTCCAGCCCTGGCAGGACACCTGTTGGAAGAGCGGCTACTCTG 348
? 183 GTGCNAGCCTCTACCTCCAGCCCTGGCAGGACACCTGTTGGAAGAGCGGCTACTCTG 242
? 349 TGGGGCAGAGCTCATCGCCCCAGATGGCTCTGACAGAGCCACTGCTCAAGCCCG 408
? 243 TGGGGCAGAGCTCATCGCCCCAGATGGCTCTGACAGAGCCACTGCTCAAGCCCG 302
? 409 CTACATAGTTCACTGGGGCAGACACACCTCCAGAGAGAGAGGGCTGTGACAGACCG 468
? 303 CTACATAGTTCACTGGGGCAGACACACCTCCAGAGAGAGAGGGCTGTGACAGACCG 362
? 469 GACAGCCACTGATGCTTCTCCACCAGGGCTTCAACAAGACCTTCCCAACAAAGACA 528
? 363 GACAGCCACTGATGCTTCTCCACCAGGGCTTCAACAAGACCTTCCCAACAAAGACA 422
? 529 CCGCATATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 588
? 423 CCGCATATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 482
? 589 ACCCTCAACCTCTCTCAAGCTGTGTCACTGTGTCAGTGTGTCAGTGTGTCAGTGTG 648
? 483 ACCCTCAACCTCTCTCAAGCTGTGTCACTGTGTCAGTGTGTCAGTGTGTCAGTGTG 542
? 649 GGGCAGCAGCTCCACCCCAATGATGATGATGATGATGATGATGATGATGATGATGAT 708
? 543 GGGCAGCAGCTCCACCCCAATGATGATGATGATGATGATGATGATGATGATGATGAT 602
? 709 CATCATGAGCAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 768
? 603 CATCATGAGCAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 662

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? 769 GTGTGCCAGCTGTCAGAGAGGGGGCAAGGACTCTGTCAGAGGCTACCTCCGGGGCCCTCT 828
? 663 GTGTGCCAGCTGTCAGAGAGGGGGCAAGGACTCTGTCAGAGGCTACCTCCGGGGCCCTCT 722
? 829 GGTCTGTAAACAGCTCTCTTCAAGGCAATATCTCTGGGGCCAGAGATCCGTGTGCATCAC 888
? 723 GGTCTGTAAACAGCTCTCTTCAAGGCAATATCTCTGGGGCCAGAGATCCGTGTGCATCAC 782
? 889 CCGAAGCCTGGTGTGTACAGCAAGTGTGCAATATGTGAGTGTGATCCAGAGAGCAT 948
? 783 CCGAAGCCTGGTGTGTGTACAGCAAGTGTGCAATATGTGAGTGTGATCCAGAGAGCAT 842
? 949 GAAGAACAAATTAGTACTGAGACCCACCCACAGACCCCATACCTCCATTTCCTGCTGGTG 1008
? 843 GAAGAACAAATTAGTACTGAGACCCACCCACAGACCCCATACCTCCATTTCCTGCTGGTG 902
? 1009 TTTGGTCTCTGTCTACTCTGTATTAAGAAACCTTAAGCCAAAGACCTCTAGACATTC 1068
? 903 TTTGGTCTCTGTCTACTCTGTATTAAGAAACCTTAAGCCAAAGACCTCTAGACATTC 962
? 1069 TTTGGCCTCTGTGATACAGGAGATGCTGACTTAATATC-AACCTGGGGTTGGA 1127
? 963 TTTGGCCTCTGTGATACAGGAGATGCTGACTTAATATGAACTGGGGTTGGA 1022
? 1128 TC-AGTAGACCTGTGATTAATTTCTGCTGAAATATGTGACTGTGGAAATGACACAA 1186
? 1023 TCNAGTAGACCTGTGATTAATTTCTGCTGAAATATGTGACTGTGGAAATGACACAA 1082
? 1187 CCTGTTTGTCTCTGTATATCCACGCCC-AAAGACAGCTCTGAGCATATATCAAG 1245
? 1083 CCTGTTTGTCTCTGTATATCCACGCCC-AAAGACAGCTCTGAGCATATATCAAG 1142
? 1246 GTTCAATATATATTTGCTAAATG 1269
? 1143 GTTCAATATATTTTGTAAATG 1166

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RESULT 5

US-09-205-258-247

Sequence 247, Application US/09205258

Patent No. 6525174

GENERAL INFORMATION:

APPLICANT: Young et al.

TITLE OF INVENTION: 207 Human Secreted Proteins

FILE REFERENCE: P2007P1

CURRENT APPLICATION NUMBER: US/09/205,258

EARLIER FILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: PCT/US98/11422

EARLIER FILING DATE: 1998-06-04

EARLIER APPLICATION NUMBER: 60/048,885

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,881

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,880

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,896

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,020

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,876

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,895

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,884

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,894

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,971

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,964

EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 247  
LENGTH: 1146  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (20)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (35)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (36)  
OTHER INFORMATION: n equals a,t,g, or c

FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (37)  
; OTHER INFORMATION: n equals a,t,g, or c  
us-09-205-258-247  
Query Match 79.1%; Score 1029.2; DB 4; Length 1146;  
Best Local Similarity 98.7%; Pred. No. 7.56-251;  
Matches 1041; Conservative 4; Mismatches 8; Indels 2; Gaps 1;  
OY 237 CTCTGGCAACAGGGCTGTAGGGG--AGACACAGGATCATCAAGGGGTTCAGTCA 294  
Db CTGGCCACAGGGCTTGTAGGGGAGAGACCAGGATCATCAAGGGGTTCAGTCA 146  
OY 295 GCCTACTCCAGCCCTGGCAGGAGCCCTTTCAGAAAGAGCGGCTACTCTGTGGGC 354  
Db GCCTACTCCAGCCCTGGCAGGAGCCCTTTCAGAAAGAGCGGCTACTCTGTGGGC 206  
OY 355 GACGCTATGCCGCCAGATGGCTCTGACAGCAGCCCACTGCTCAAGCCCTCTCAT 414  
Db GACGCTATGCCGCCAGATGGCTCTGACAGCAGCCCACTGCTCAAGCCCTCTCAT 266  
OY 415 AGTCACCTGGGGAGAGACACACTCAAGAGAGAGGGCTGTAGGAGACCCGGACGC 474  
Db AGTCACCTGGGGAGAGACACACTCAAGAGAGAGGGCTGTAGGAGACCCGGACGC 326  
OY 475 CACTGAGTCTTCCCCACCCCGCTTCACACAGCCTCCCAACAAAGACACCGCAA 534  
Db CACTGAGTCTTCCCCACCCCGCTTCACACAGCCTCCCAACAAAGACACCGCAA 386  
OY 535 TGACATCATGTGTGTGAAGATGGCATGCCAGTCTCATACACTGGGCTGTGCACCC 594  
Db TGACATCATGTGTGTGAAGATGGCATGCCAGTCTCATACACTGGGCTGTGCACCC 446  
OY 595 CACCCTCTCTCAGCGTGTGTCAGTGTGGAGACAGTGGCTCATTTCCGGCTGGGACG 654  
Db CACCCTCTCTCAGCGTGTGTCAGTGTGGAGACAGTGGCTCATTTCCGGCTGGGACG 506  
OY 447 CACCCTCTCTCAGCGTGTGTCAGTGTGGAGACAGTGGCTCATTTCCGGCTGGGACG 506  
Db CACCCTCTCTCAGCGTGTGTCAGTGTGGAGACAGTGGCTCATTTCCGGCTGGGACG 566  
OY 715 TGACACCAAGAGTGTGAAGCCCTTACCCGGGCAACATCACAGACACATGTGTGTC 774  
Db TGACACCAAGAGTGTGAAGCCCTTACCCGGGCAACATCACAGACACATGTGTGTC 626  
OY 775 CAGCGTGAAGAGGGGCAAGGAGCTCTGCAAGGTGATCCGGGGGCCCTGTGGTCTG 834  
Db CAGCGTGAAGAGGGGCAAGGAGCTCTGCAAGGTGATCCGGGGGCCCTGTGGTCTG 686  
OY 627 CAGCGTGAAGAGGGGCAAGGAGCTCTGCAAGGTGATCCGGGGGCCCTGTGGTCTG 686  
Db CAGCGTGAAGAGGGGCAAGGAGCTCTGCAAGGTGATCCGGGGGCCCTGTGGTCTG 746  
OY 835 TAACCAAGTCTTCAAGGCAATTATCTCTGGGGCAAGATCCGTGCATCACCCGAA 894  
Db TAACCAAGTCTTCAAGGCAATTATCTCTGGGGCAAGATCCGTGCATCACCCGAA 746  
OY 895 GCCTGGTGTCTACACGAAAGTCTCAATATGTGTGATCTGGATCCAGAGACGATGAAG 954  
Db GCCTGGTGTCTACACGAAAGTCTCAATATGTGTGATCTGGATCCAGAGACGATGAAG 806  
OY 747 GCCTGGTGTCTACACGAAAGTCTCAATATGTGTGATCTGGATCCAGAGACGATGAAG 806  
Db GCCTGGTGTCTACACGAAAGTCTCAATATGTGTGATCTGGATCCAGAGACGATGAAG 1014  
OY 955 CAATTAGCTGAGCCACCCACACAGCCATCACCTCCATTCCATTGCTGTGTGTGT 1014  
Db CAATTAGCTGAGCCACCCACACAGCCATCACCTCCATTCCATTGCTGTGTGTGT 866  
OY 1015 TCCTGTCTACTGTGTATATAGAAACCTTAAGCCCAAGCCCTCTACGACATCTTTGGG 1074  
Db TCCTGTCTACTGTGTATATAGAAACCTTAAGCCCAAGCCCTCTACGACATCTTTGGG 926  
OY 1075 CCTCTGGACTACAGGAGATGCTGTCACTTAATATATCAACCTGGGGTTCGAATACGTGA 1134  
Db CCTCTGGACTACAGGAGATGCTGTCACTTAATATATCAACCTGGGGTTCGAATACGTGA 986  
OY 1135 GACCTGATCAATATCTGCTTGAATATTTGTGACCTGTGGAGATGACACACCTGTGTT 1194  
Db GACCTGATCAATATCTGCTTGAATATTTGTGACCTGTGGAGATGACACACCTGTGTT 1046

<b>QY</b>	<b>1195</b>	GTTCTCGTGTATACCCAGGCCAAAAGACAGCTCCTGGCATATATCAAGTTTCATA	<b>1254</b>
<b>Db</b>	<b>1047</b>	GTTCTCGTGTATACCCAGGCCAAAGACAGCTCTGCGCATATATCAAGTTTCATA	<b>1106</b>
<b>QY</b>	<b>1255</b>	AATATTTCCTAATGAAGAAAAAATAAAAAAAAA	<b>1289</b>
<b>Dd</b>	<b>1107</b>	AATATTTCCTAATGAAGAAAAAATAAAAAAAAA	<b>1141</b>

## RESULT 6

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US-08-790-137-2
Sequence 2, Application US/08790137
Patent No. 5840871
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goll, Suya K.
TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCI
TITLE OF INVENTION: KALIKREIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,137
FILING DATE: Filed Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0195 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 833 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-790-137-2

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Query Match	51.7%	Score 673.2;	DB 2;	Length 833;
Best Local Similarity	95.0%	Mismatches 706;	Conservative 0;	Indels 9;
				Gaps 1;

QY	264	AGACGACGATCATCAAGGGGTCTGAGTGCACAGCCTCACTCCCAACCTGGCAGGACGCC	323
Db	91	AGTCCCGGATTTTGGGAGGCTGGGAGTGTGAGACAGCATTTCCCAACCCCTGGCAGGCGGCTTC	150
QY	324	TGTTTCAGAGACAGCGGGCTACTCTGTGGGGGAGAGCGTCATCGCCCGCAGATGGCGTCTGGA	383
Db	151	TGTACCGAAGACGGGGCTACTCTGTGGGGGAGAGGTCATATGCCCCCAGATGGTCTCTGA	210
QY	384	CAGACGCCACATGCGCTCAAGCCCCGCTCATATAGTTACACTGGGGGACAGCAACCTCAGA	443
Db	211	CACACACCCACATGCCCTNNAAGCCCCGCTCATATAGTTACACTGGGGGACAGCAACCTCAGA	270
QY	444	AGAGGAGAGGGCTGTGTAGCAGACACCGGAGACGCCACTGATGCTCTTCCCCACCCGGGCTTCA	503
	271	AGGAGAGAGGGCTGTGTAGCAGACACCGGAGACGCCACTGATGCTCTTCCCCACCCGGGCTTCA	330

OY	504	ACAAAGCCTCCCAACAAAGACACCGCAATGACATCAATGCTGGTGAAGATGGATCGC	563
Db	331	ACAAAGCCTCCCAACAAAGACACCGCAATGACATCAATGCTGGTGAAGATGGATCGC	390
OY	564	CAGTCTCATCACTGGGGCTGTGCGACCCCTCAACCCCTCTCTCAAGCTGTGTACGCTG	623
Db	331	CAGTCTCATCACTGGGGCTGTGCGACCCCTCAACCCCTCTCTCAAGCTGTGTACGCTG	450
OY	624	GCACGAGTGCCTCATTTTCCGGCTGGGGCAGCAGCTCCAGCCCCAGTTACGCTCCCTC	683
Db	451	GCACGAGTGCCTCATTTTCCGGCTGGGGCAGCAGCTCCAGCCCCAGTTACGCTCCCTC	510
OY	684	ACACCTTGCAGTGGCCCAATCACCATTATTGAGCACCAGAAAGTGTGAAACGCTACCC	743
Db	511	ACACCTTGCAGTGGCCCAATCACCATTATTGAGCACCAGAAAGTGTGAAACGCTACCC	570
OY	744	CCGGCAACATCACACACACACATGCTGTGTGCCACGCTGACAGAAAGGGGGCAGGACTCCT	803
Db	571	CCGGCAACATCACACACACACATGCTGTGTGCCACGCTGACAGAAAGGGGGCAGGACTCCT	630
OY	804	GCCAGGTGACATCCGGGGGGCCCTCGTGTGTATAACAGTCTGTTCAAGGACATTATCTCC	863
Db	631	GCCAGGTGACATCCGGGGGGCCCTCGTGTGTATAACAGTCTGTTCAAGGACATTATCTCC	690
OY	864	GGGGCCAGGATCCGTGTGCGATCACCCGAAACCTGTGTCTACACGAAAGTCTGCAAAAT	923
Db	691	GGGGCCAGGATCCGTGTGCGATCACCCGAAACCTGTGTCTACACGAAAGTCTGCAAAAT	750
OY	924	ATGTGACTGTGATCCAGGAGACGATGAAGACAAATTGAACTGGAGC-----CAGCC	974
Db	751	ATGTGACTGTGATCCAGGAGACGATGAAGACAAATTGAACTGGAGC-----CAGCC	810
OY	975	ACCAAGCCCATCACCTCTCATTT	997
Db	811	CCCAAGCCCATCACCTCTCATTT	833

## RESULT 7

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US-09-386-642-10
: Sequence 10, Application US/09386642
: Patent No. 6420157
: GENERAL INFORMATION:
: APPLICANT: Darrow, Andrew
: APPLICANT: Qi, Jensen
: APPLICANT: Andrade-Gordon, Patricia
: TITLE OF INVENTION: Zymogen Activation System
: FILE REFERENCE: ORT-1028
: CURRENT APPLICATION NUMBER: US/09/386,642
: CURRENT FILING DATE: 1999-08-31
: NUMBER OF SEQ ID NOS: 60
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 10
: LENGTH: 1052
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
: OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-10

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Query Match	50.98;	Score 662.4;	DB 4	Length 1052;
Best Local Similarity	98.48;	Pred. No. 4.3e-158;		
Matches 669; Conservative	0;	Mismatches 11;	Indels 0;	Gaps 0

QY	DB	QY
293	CATCCCAACCCCTGGGAGGACACCCCTGTTCCAGAAAGACCGGCTACTCTGTGGGGCAGC	357
196	CATCCCAACCCCTGGGAGGACACCCCTGTTCCAGAAAGACCGGCTACTCTGTGGGGCAGC	255
359	CTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCTCTAAGCCCCGGCTACATAGATT	418
256	CTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCTCTAAGCCCCGGCTACATAGATT	315

OY 419 CACCTGGGGCAGCAACCTCCAGAGGAGGGCTGTGACGACACCCGGACAGCCACT 478  
DB 316 CACCTGGGGCAGCAACCTCCAGAGGAGGGCTGTGACGACACCCGGACAGCCACT 375  
OY 479 GAGTCTCTCCCGCCAGCCCGGCTTCAACAACAGCTCCCGCAACAAAGACCCGCAATGAC 538  
DB 376 GAGTCTCTCCCGCCAGCCCGGCTTCAACAACAGCTCCCGCAACAAAGACCCGCAATGAC 435  
OY 539 ATCATGCTGTGAAGAGTGCATTCGCCATGTCATCACCTGGGCTGTGCGAACCCCTCAC 598  
DB 436 ATCATGCTGTGAAGAGTGCATTCGCCATGTCATCACCTGGGCTGTGCGAACCCCTCAC 495  
OY 599 CTCACCTGAGGCTGTGACGCTGGGACGACGCTGCTCATTTCCGCTGGGGGACGACG 658  
DB 496 CTCACCTGAGGCTGTGACGCTGGGACGACGCTGCTCATTTCCGCTGGGGGACGACG 555  
OY 659 TCCAGACCCCGCAGTTACGCTGCTCACACCTTGGGATGCGCCAAACATCACCATTGAG 718  
DB 556 TCCAGACCCCGCAGTTACGCTGCTCACACCTTGGGATGCGCCAAACATCACCATTGAG 615  
OY 719 CACCAAGAAGTGTGAAGAGCTTACCCGCGCAACATCACAGACACCAGTGTGTGCCAGC 778  
DB 616 CACCAAGAAGTGTGAAGAGCTTACCCGCGCAACATCACAGACACCAGTGTGTGCCAGC 675  
OY 779 GTGCAGAGAGGGGCAAGGACTCCTGCGAGGGTGAATCCGGGGGCGCTCTGTCTGTAC 838  
DB 676 GTGCAGAGAGGGGCAAGGACTCCTGCGAGGGTGAATCCGGGGGCGCTCTGTCTGTAC 735  
OY 839 CAGTCTCTTCAAGGCATTATCTCTGCGGCGCAGAGATCCGTGTGCATCCCGAAAGCT 898  
DB 736 CAGTCTCTTCAAGGCATTATCTCTGCGGCGCAGAGATCCGTGTGCATCCCGAAAGCT 795  
OY 899 GGTGTCTACAGAAAGTGTGAATATGTGACTGTGATCCAGAGAGATGAAGAAAT 958  
DB 796 GGTGTCTACAGAAAGTGTGAATATGTGACTGTGATCCAGAGAGATGAAGAAAT 855  
OY 959 TAGACTGAGCCACCACCA 978  
DB 856 TCTAGACTGAGCCACCACCA 875

RESULT 8  
US-09-702-705-109  
: Sequence 109, Application US/09702705  
: Patent No. 6504010  
: GENERAL INFORMATION:  
: APPLICANT: Wang, Tongtong  
: APPLICANT: Bangur, Chaitanya S.  
: APPLICANT: Lodes, Michael A.  
: APPLICANT: Fanger, Gary  
: APPLICANT: Vedvick, Tom  
: APPLICANT: Carter, Darick  
: APPLICANT: Retter, Marc  
: APPLICANT: Mannion, Jane  
: APPLICANT: Fan, Liqun  
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
: TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
: FILE REFERENCE: 210121.478C14  
: CURRENT APPLICATION NUMBER: US/09/702,705  
: CURRENT FILING DATE: 2000-10-30  
: NUMBER OF SEQ ID NOS: 1833  
: SOFTWARE: FastSeq for Windows Version 3.0  
: SEQ ID NO 109  
: LENGTH: 662  
: TYPE: DNA  
: ORGANISM: Homo sapien  
US-09-702-705-109

Query Match 42.4%; Score 551.8; DB 4; Length 662;  
Best Local Similarity 99.5%; Pred. No. 3,2e-130;  
Matches 564; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 672 TAGCCCTGCTCACACCTTGTGATGCGCAACATCACCATCATTTGAGCACCAGAAAGTGTG 731

DB 14 TAGCCCTGCTCACACCTTGTGATGCGCAACATCACCATCATTTGAGCACCAGAAAGTGTG 73  
OY 732 AGAAGCGCTACCCCGGCAACATCACAGACACCATGATGTGTGCCAGGTGACGAGAGGG 791  
DB 74 AGAAGCGCTACCCCGGCAACATCACAGACACCATGATGTGTGCCAGGTGACGAGAGGG 133  
OY 792 GCAAGGACTCTGCCAGGGTACTCCGGGGGCGCTGTGCTGTAAACAGTCTTTCAAG 851  
DB 134 GCAAGGACTCTGCCAGGGTACTCCGGGGGCGCTGTGCTGTAAACAGTCTTTCAAG 193  
OY 852 GCATTATCTCTGGGGGCGAGATCGGTGTGATCCACCCGAAAGCGTGTCTACAGA 911  
DB 194 GCATTATCTCTGGGGGCGAGATCGGTGTGATCCACCCGAAAGCGTGTGTACAGA 253  
OY 912 AAGTGTCAATATGTGACTGTGATCCAGAGAGATGAAAGAAATTAAGTGAACCA 971  
DB 254 AAGTGTCAATATGTGACTGTGATCCAGAGAGATGAAAGAAATTAAGTGAACCA 313  
OY 972 CCCACACAGCCCATCACCTTCATTTCCACTTGTGTGTGTCTGTCTGTCTGTTA 1031  
DB 314 CCCACACAGCCCATCACCTTCATTTCCACTTGTGTGTGTCTGTCTGTCTGTTA 373  
OY 1032 ATAAAGAAACCTTAAGCCAAAGACCTCTACAGAAATCTTTGGGCTCTCTGAGTACAGA 1091  
DB 374 ATAAAGAAACCTTAAGCCAAAGACCTCTACAGAAATCTTTGGGCTCTCTGAGTACAGA 433  
OY 1092 GATGCTGTACTTAATATCAACCTGGGGTTCGAATTCAGTGAAGCTGTGAATTC 1151  
DB 434 GATGCTGTACTTAATATCAACCTGGGGTTCGAATTCAGTGAAGCTGTGAATTC 493  
OY 1152 TGCCCTTGAATATGTGACTGTGGGAATGACAAACCTGTTTCTCTGTATATCC 1211  
DB 494 TGCCCTTGAATATGTGACTGTGGGAATGACAAACCTGTTTCTCTGTATATCC 553  
OY 1212 CAGCCCC-AAAGACAGCTCTGGCCAT 1237  
DB 554 CAGCCCCAAAGACAGCTCTGGACCT 580

RESULT 9  
US-09-736-457-109  
: Sequence 109, Application US/09736457  
: Patent No. 6509448  
: GENERAL INFORMATION:  
: APPLICANT: Wang, Tongtong  
: APPLICANT: Bangur, Chaitanya S.  
: APPLICANT: Lodes, Michael A.  
: APPLICANT: Fanger, Gary  
: APPLICANT: Vedvick, Tom  
: APPLICANT: Carter, Darick  
: APPLICANT: Retter, Marc  
: APPLICANT: Mannion, Jane  
: APPLICANT: Fan, Liqun  
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
: TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
: FILE REFERENCE: 210121.478C15  
: CURRENT APPLICATION NUMBER: US/09/736,457  
: CURRENT FILING DATE: 2000-12-13  
: NUMBER OF SEQ ID NOS: 1864  
: SOFTWARE: FastSeq for Windows Version 3.0  
: SEQ ID NO 109  
: LENGTH: 662  
: TYPE: DNA  
: ORGANISM: Homo sapien  
US-09-736-457-109

Query Match 42.4%; Score 551.8; DB 4; Length 662;  
Best Local Similarity 99.5%; Pred. No. 3,2e-130;  
Matches 564; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 672 TAGCCCTGCTCACACCTTGTGATGCGCAACATCACCATCATTTGAGCACCAGAAAGTGTG 731

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Db 14 TAGGCTGCTTACACCTTGGGATGCGCCACATACCATCATTTAGACACCGAAGTGTG 73
QY 732 AGAAGCGCTTACCCCGGCAACATCACAGACACCATGATGTGTCCAGCGGTGAGGAAGGG 791
Db 74 AGAAGCGCTTACCCCGGCAACATCACAGACACCATGATGTGTCCAGCGGTGAGGAAGGG 133
QY 732 GCAAGGACTCTCTGCGAGGTGACTCGGGGGCCCTCTGTGTGTAAACAGTCTCTTCAAG 851
Db 134 GCAAGGACTCTCTGCGAGGTGACTCGGGGGCCCTCTGTGTGTAAACAGTCTCTTCAAG 193
QY 832 GATATATCTCTGCGGGCCAGGATCCGTGTGCGATACCCGAAAGCCTGTGTCTACAGA 911
Db 194 GATATATCTCTGCGGGCCAGGATCCGTGTGCGATACCCGAAAGCCTGTGTCTACAGA 253
QY 912 AAGTGTGCAATATGTGAGCTGATTCAGAGAGACAGTGAAGAACAATTAGATGTGACCCA 971
Db 254 AAGTGTGCAATATGTGAGCTGATTCAGAGAGACAGTGAAGAACAATTAGATGTGACCCA 313
QY 972 CCCACACAGCCCATCACCCCTCCATTTCCACTTGTGTGTCTCTGTCTACCTGTGTA 1031
Db 314 CCCACACAGCCCATCACCCCTCCATTTCCACTTGTGTGTCTCTGTCTACCTGTGTA 373
QY 1032 ATAAAGAAACCTTAAAGCAAGACCCCTCTACGAACATTTCTTGGCCCTCTGGACTACAGA 1091
Db 374 ATAAAGAAACCTTAAAGCAAGACCCCTCTACGAACATTTCTTGGCCCTCTGGACTACAGA 433
QY 1092 GATGCTGTACCTTAAATATCAACCTGTGGTTCGAATCAGTGAAGCTGATTTCAAAATTC 1151
Db 434 GATGCTGTACCTTAAATATCAACCTGTGGTTCGAATCAGTGAAGCTGATTTCAAAATTC 493
QY 1152 TGCCCTGAAATATTTGTGACTCTGGGAATGACAAACCTGTGTGTCTCTGTGTATCCC 1211
Db 494 TGCCCTGAAATATTTGTGACTCTGGGAATGACAAACCTGTGTGTCTCTGTGTATCCC 553
QY 1212 CAGCCCC-AAAGACAGCTCTGGCCAT 1237
Db 554 CAGCCCCAAAGACAGCTCTGGACCT 580
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RESULT 10
US-09-280-116-3
; Sequence 3, Application US/09280116A
; Patent No. 631427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-3
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Query Match 36.8%; Score 478.8; DB 4; Length 618;
Best Local Similarity 90.8%; Pred. No. 9,1e-112;
Matches 590; Conservative 0; Mismatches 22; Indels 38; Gaps 6;
Db 337 GCGGCTACTCTGTGGGGGAGCGTCATCGCCCGCAGATGGCTCTGACAGACAGCCACATG 396
1 GCGGCTACTCTGTGGGGGAGC-CTCATCG-CTTCAGATGGCTCTGACAGACAGCCACATG 58
QY 397 CCTCAAGCCCGCTCAATAGTTACCTGTGGGAGCAGCAACCTTCAGAAAGAGAGAGGCTG 456
Db 59 CCTCAAGCCCGCTCAATAGTTACCTGTGGGAGCAGCAACCTTCAGAAAGAGAGAGGCTG 118
QY 457 TGAGCAGACCCGGACAGCACTGAAGTCTTCCGCCACCCCGGCTTCAACACACAGCTCC 516
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Db 119 TGAGCAGACCCCGAGACGCCACTGAGTCTTCCCGCCCGGCTTCACACAGCTCC 178
QY 517 CAACAAAGACCAACCGCAATGACATCATGTGTGGAAGATGGATGGCCAGT-CTCAMPNA 575
Db 179 CAACAAAGACCAACCGCAATGACATCATGTGTGGAAGATGGATGGCCAGTCTCATNA 238
QY 576 CCTGGCTGTGGACCCCTCACCCCTCTCTCAAGCTGTGTCACTGTGTGACAGCTGAC 635
Db 239 CCTGGCTGTGGACCCCTCACCCCTCTCTCAAGCTGTGTGTGTGTGTGTGTGTGTGTGT 298
QY 636 TCATTTCCGGCTGTGGGAGCAGCAGTCCAGCCCGCAGTTACGCTGCTCTACACCTTGCAT 695
Db 299 TCATTTCCGGCTGTGGGAGCAGCAGTCCAGCCCGCAGTTACGCTGCTCTACACCTTGCAT 358
QY 696 GGGCCAAACATCAACCATTTGAGACCCACAGTGTGAGAAACCCCTTACCCCGGCAATCA 755
Db 359 GGGCCAAACATCAACCATTTGAGACCCACAGTGTGAGAAACCCCTTACCCCGGCAATCA 418
QY 756 CAGACACCATGTGTGTGTGCGACGCTGCAGAGAGGGGCAAGGACTCTGCGAGGTGACT 815
Db 419 CAGACACCATGTGTGTGTGCGACGCTGCAGAGAGGGGCAAGGACTCTGCGAGGTGACT 478
QY 816 CCGGGGGCCCTCTGTGTGTGTAACAGTCTTTCAGGCATTAATCTCTGGGG--CCAGGA 873
Db 479 C-----AAAGGCATTAATCTCTGGGGCCAGGAC 507
QY 874 TCCGTGTGATCACCCGAAAGCCTGTGTGTACACGAAAGCTGCAAAATATGTGTGACAG 933
Db 508 TCCGTGTGATCACCCGAAAGCCTGTGTGTGTACACGAAAGCTGCAAAATATGTGTGACAG 567
QY 934 GATCCAGGA--GACGATGAAGAACAATTAGACTGACCCACCCACACAG 981
Db 568 GATCCAGGAAGAAGCATTTGAAGAAACAATTAGACTGACCCACCCACACAAAG 617
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RESULT 11
US-09-280-116-136
; Sequence 136, Application US/09280116A
; Patent No. 631427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-136
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Query Match 34.0%; Score 441.8; DB 4; Length 472;
Best Local Similarity 99.1%; Pred. No. 1,8e-102;
Matches 465; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
Db 69 CAACAAAGCTGGAGAGAGA-GGAATCTGCGCTCGGGTTCGCGAGATGCA-GAGTTGAG 126
Db 4 CAACAAAGCTGGAGAGAGAGCAAGCAATCTCGGCTCGGGTTCGCGAGATGCAAGAGTTGAG 63
QY 127 GTGGCTGCGGACTGGAATCATTCGGGCGAGAGTCTCAACAGACAGCAAGAACTGGGCG 186
Db 64 GTGGCTGCGGACTGGAATCATTCGGGCGAGAGTCTCAACAGACAGCAAGAACTGGGCG 123
QY 187 CCGCTCTCCCGCTTCAGAGCCATGAGATTCTGCAAGTTAATCTGCTGTGGCAAC 246
Db 124 CCGCTCTCCCGCTTCAGAGCCATGAGATTCTGCAAGTTAATCTGCTGTGGCAAC 183
QY 247 AGGCTTGTAGGGGAGAGACAGAGATCATCAAGGGGTTGAGTCAAGCCTCACTCCA 306
```





APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLAAS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROUPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
TITLE OF INVENTION: OF THE PROSTATE  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-944-483-6

Query Match 28.3%; Score 368.4; DB 3; Length 406;  
Best Local Similarity 99.0%; Pred. No. 6,2e-84;  
Matches 402; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

QY 867 GCCAGATCCGTGTGCGATCAACCCGAAGCCGTGTCTACAGAAAGTCTCAATATG 926  
DB 406 GCCAGATCCGTGTGCGATCAACCCGAAGCCGTGTCTACAGAAAGTCTCAATATG 347  
QY 927 TGGACTGATCCAGAGACGATGAAGAACATTAAGTACAGCCACCCACAGCCCAT 986  
DB 346 TGGACTGATCCAGAGACGATGAAGAACATTAAGTACAGCCACCCACAGCCCAT 287  
QY 987 CACCTTCATTTCCACTGTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1046  
DB 286 CACCTTCATTTCCACTGTGTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 227  
QY 1047 CCAAGACCTCTACACATCTTTGGGCTCTCTGAGTACAGAGATGCTCTACTTAA 1106  
DB 226 CCAAGACCTCTGCGAATCTTTGGGCTCTCTGAGTACAGAGATGCTCTACTTAA 167  
QY 1107 TAATC-AACTGGGGTGTGAATC-AGTGAAGCTGATTCAAATTTGCTTGAATAT 1164  
DB 166 TAATCAGACTGGGGTGTGAATC-AGTGAAGCTGATTCAAATTTGCTTGAATAT 107  
QY 1165 TGTGCTCTGGGAATGACACACCGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1223

DB 106 TGTGACTGTGGGAATGACACACCGTGTGTGTCTCTCTCTCTCTCTCTCTCT 47  
QY 1224 CAGCTCTGGCCCATATATCAAGTTTCAATAATTTGCTAAATG 1269  
DB 46 CAGCTCTGGCCCATATATCAAGTTTCAATAATTTGCTAAATG 1

RESULT 15  
US-08-944-483-5  
Sequence 5, Application US/08944483  
Patent No. 6232456  
GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLAAS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROUPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
TITLE OF INVENTION: OF THE PROSTATE  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 262 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-944-483-5

Query Match 20.1%; Score 262; DB 3; Length 262;  
Best Local Similarity 100.0%; Pred. No. 4.1e-57;  
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 734 AACGCTACCCCGGGAACATCAACACACCATGATGTGCGAGGTCAGGAGGAGG 793  
DB 1 AACGCTACCCCGGGAACATCAACACACCATGATGTGCGAGGTCAGGAGGAGG 60  
QY 794 AAGGACTCTGCGAGGTCAGTCCGAGGCGCTCTGCTGTAAACAGTCTCTCAAGC 853  
DB 61 AAGGACTCTGCGAGGTCAGTCCGAGGCGCTCTGCTGTAAACAGTCTCTCAAGC 120  
QY 854 ATTATCTCTGGGCGAGGATCCGTGTGATCACCAGAAAGCTGTGTCTACACGAA 913

Db	121	ATTATCTCTGCTGGGCGCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAA	180
QY	914	GTCGCAAAATATGTGACTGTGATCCAGAGACGATGAAGACAATTAGACTGTGACCCACC	973
Db	181	GTCGCAAAATATGTGACTGTGATCCAGAGACGATGAAGACAATTAGACTGTGACCCACC	240
QY	974	CACGACAGCCGATCACCCCTCCA	995
Db	241	CACGACAGCCGATCACCCCTCCA	262

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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7688.371 Million cell updates/sec

Title: US-09-856-320A-1

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Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1301	100.0	1301	21	CDNA encoding huma
2	1283.4	98.6	1314	22	CDNA encoding huma
3	1271.4	97.7	1292	22	Human secreted pro
4	1223	94.0	1335	21	Nucleotide sequenc
5	1198	92.1	1304	21	Human PRO1279 (UNQ
6	1198	92.1	1204	22	Human CDNA sequenc
7	1198	92.1	1204	22	DNA encoding prote
8	1198	92.1	1204	24	Human angiotensin

9	1198	92.1	1204	24	ABL88175	Human PRO1279 CDNA
10	1198	92.1	1204	24	ABK3628	CDNA encoding huma
11	1198	92.1	1204	25	ACA03855	CDNA encoding huma
12	1198	92.1	1204	25	ACA04276	Human CDNA encodin
13	1198	92.1	1204	25	ABK93933	DNA encoding novel
14	1183	90.9	1186	24	ABK92131	Prostate cancer-as
15	1183	90.9	1186	25	ABK76468	Lung cancer-associ
16	1150	88.4	1158	20	AAK22639	CASB12 derived fro
17	1114.4	85.7	1192	22	AAK14842	Human PS13 gene c
18	1108.8	85.2	1191	22	AAK97777	Extended human sec
19	1106	85.0	1106	20	AAK22638	CASB12 nucleotide
20	1063	81.7	1166	22	AAK14841	Human PS13 consen
21	1039.4	79.9	1164	24	ABK51683	DNA encoding huma
22	1029.2	79.1	1146	20	AAV84589	Human secreted pro
23	1029.2	79.1	1146	20	AAV84589	Human secreted pro
24	758.6	58.3	934	21	AAK61765	CDNA encoding huma
25	673.2	51.7	833	19	AAV42925	DNA encoding huma
26	663.4	51.0	1323	21	AAK61764	CDNA encoding huma
27	662.4	50.9	1052	21	AAK87798	Activation constri
28	662.4	50.9	1052	22	AAK55270	Nucleotide sequenc
29	565.6	43.5	762	21	AAK31050	Human colon cancer
30	565.6	43.5	762	21	AAK31051	Human colon cancer
31	551.8	42.4	662	22	AAK68191	Human lung tumour
32	551.8	42.4	662	24	ABK38102	CDNA encoding clon
33	551.8	42.4	662	25	ACA10431	Human lung cancer-
34	551.8	42.4	662	25	ABK93932	Lung cancer therap
35	478.8	36.8	618	24	ABK30233	Human G-protein-co
36	456.2	35.1	502	24	ABK68664	Human ovarian canc
37	441.8	34.0	472	24	ABK30366	Human G-protein-co
38	409	31.4	409	24	ABK39071	Human lung cancer-
39	409	31.4	409	25	ACA11400	Human lung adenoca
40	409	31.4	409	25	ACA02586	Lung cancer therap
41	404.2	31.1	417	24	ABK80919	Human ovarian canc
42	369	28.4	391	24	ABK65887	Lung cancer relat
43	369	28.4	391	24	ABK67873	Ovary cancer relat
44	369	28.4	391	24	ABK69671	Prostate cancer re
45	369	28.4	391	24	ABK0912	Human ovarian canc

ALIGNMENTS

RESULT 1	AAA61763	AAA61763 standard; CDNA; 1301 BP.
ID	AAA61763	
XX	AAA61763;	
AC	23-OCT-2000 (first entry)	
XX		
DT	CDNA encoding human serine protease BSSP6 (hBSSP6) SEQ ID NO.1.	
XX		
DE		
XX	BSSP6; serine protease; human; hBSSP6; mouse; mBSSP6; brain;	
KW	diagnostic marker; antibody; transgenic animal; Alzheimer's disease;	
KW	epilepsy; cancer; inflammation; infertility; pancreatitis;	
KW	prostatic hypertrophy; ss.	
OS		
XX	Homo sapiens.	
OS		
PN	WO200031257-A1.	
PN		
PD	02-JUN-2000.	
XX		
PF	19-NOV-1999; 99WO-JP06476.	
XX		
PR	20-NOV-1998; 98JP-0347802.	
XX		
PA	(FUSO ) FUSO PHARM IND LTD.	
XX		
PI	Uemura H, Okui A, Komimami K, Yamaguchi N, Mitsui S;	
XX		
DR	WPI: 2000-400067/34.	
DR	P-PSDB: AAB11712.	

XX Serine protease BSSP6, useful in detecting homologs, mutants and  
PT polymorphic variants as markers for diagnosis of Alzheimer's disease,  
PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,  
PT using blood or other tissues

PS Claim 2; Page 67-69; 94pp; Japanese.

XX The invention relates to novel serine proteases designated BSSP6  
CC (AA61712-B11714), and to nucleic acids encoding them (AA61763-AA1765).  
CC The invention also relates to vectors and transformants comprising BSSP6  
CC nucleic acids; transgenic animals in which the expression level of BSSP6  
CC can be varied; and an MBSP6 knockout mouse. The invention additionally  
CC encompasses anti-BSSP6 antibodies and methods of production of such  
CC antibodies, methods of BSSP6 detection using the antibodies, and the  
CC use of BSSP6 proteins or fragments as diagnostic markers for certain  
CC medical conditions. Nucleotides encoding BSSP6 were initially  
CC isolated in a human brain cDNA library using degenerate PCR primers  
CC (AA61795-AA1796) based on conserved regions of serine proteases. The  
CC BSSP6 serine proteases and nucleotides encoding them are useful in  
CC detecting homologues, mutants and polymorphic variants in biological  
CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis  
CC and spleen) as diagnostic markers for conditions such as Alzheimer's  
CC disease, epilepsy, cancer, inflammation, infertility and prostatic  
CC hypertrophy. Sequences AA61763 and AA61765 represent cDNAs encoding  
CC human BSSP6 variants (hBSSP6), and sequence AA61764 represents cDNA  
CC encoding murine BSSP6 (mBSSP6).

XX Sequence 1301 BP: 332 A; 387 C; 330 G; 252 T; 0 other;

Query Match 100.0%; Score 1301; DB 21; Length 1301;  
Best Local Similarity 100.0%; Pred. No. 3e-229;  
Matches 1301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTTCTCTCACACCTGTCTCAGGGAGAGAGGAGAAAGCCAAAGGAGGAGCTA 60  
DB 1 CTGCTTCTCTCACACCTGTCTCAGGGAGAGAGGAGAAAGCCAAAGGAGGAGCTA 60  
QY 61 ACTGAAAAAACAAGCTGGGAGAGAGAGATCTGGCTGGGTTCCGAGATGACAGAG 120  
DB 61 ACTGAAAAAACAAGCTGGGAGAGAGAGATCTGGCTGGGTTCCGAGATGACAGAG 120  
QY 121 GTTAGAGGTGGTGGGAGAGAGATCTGGGAGAGAGTCTCAGAGAGCAAGAGAAC 180  
DB 121 GTTAGAGGTGGTGGGAGAGAGATCTGGGAGAGAGTCTCAGAGAGCAAGAGAAC 180  
QY 181 TGGGGCCCGCTCTCCCGCTCCAGGCCATGAGATCTGCAGTTAACTCTGTGTCT 240  
DB 181 TGGGGCCCGCTCTCCCGCTCCAGGCCATGAGATCTGCAGTTAACTCTGTGTCT 240  
QY 241 GGCACACAGGCTTTGAGGGAGAGAGACAGATCATCAAGGGGTTCCAGTCAAGCTCA 300  
DB 241 GGCACACAGGCTTTGAGGGAGAGAGACAGATCATCAAGGGGTTCCAGTCAAGCTCA 300  
QY 301 CTCCAGAGCCCTGGAGAGAGCCGTTGAGAAAGAGCGGCTCTGTGGGGAGAGCT 360  
DB 301 CTCCAGAGCCCTGGAGAGAGCCGTTGAGAAAGAGCGGCTCTGTGGGGAGAGCT 360  
QY 361 CATGCCCCCAGATGCTCTGACAGAGCCACTGCTCAAGCCCGGCTCATATGTTCA 420  
DB 361 CATGCCCCCAGATGCTCTGACAGAGCCACTGCTCAAGCCCGGCTCATATGTTCA 420  
QY 421 CTTGGGGAGAGACACTCCAGAAAGAGAGAGGCTGTGAGAGACAGCCGAGACCTGA 480  
DB 421 CTTGGGGAGAGACACTCCAGAAAGAGAGAGGCTGTGAGAGACAGCCGAGACCTGA 480  
QY 481 GTCTTCCCCACCGGCTTCAACAAGAGCTCCCAACAACAACACCGCATGACAT 540  
DB 481 GTCTTCCCCACCGGCTTCAACAAGAGCTCCCAACAACAACCGCATGACAT 540  
QY 541 CATGCTGTGAAAGATGAGATGACAGTCTCATCATCTGGGCTGTGGACCCCTCACCT 600  
DB 541 CATGCTGTGAAAGATGAGATGACAGTCTCATCATCTGGGCTGTGGACCCCTCACCT 600

QY 601 CTCTCAGAGCTGTGCTGCTGCTGACACAGCTGCTCATTTCCGGTGGGACAGCTC 660  
DB 601 CTCTCAGAGCTGTGCTGCTGCTGACACAGCTGCTCATTTCCGGTGGGACAGCTC 660  
QY 661 CAGCCCCAGTTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
DB 661 CAGCCCCAGTTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
QY 721 CCAGAGGTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
DB 721 CCAGAGGTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
QY 781 GCAGAGAGGGGGCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
DB 781 GCAGAGAGGGGGCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
QY 841 GTCTCTTCAAGCATTTATCTCTGAGGGGAGAGATCCGTTGATCAACCCGAAGCTGG 900  
DB 841 GTCTCTTCAAGCATTTATCTCTGAGGGGAGAGATCCGTTGATCAACCCGAAGCTGG 900  
QY 901 TGTCTACAGAAAGTCTGCAATATGAGAGTGTGATGATGATGATGATGATGATGAT 960  
DB 901 TGTCTACAGAAAGTCTGCAATATGAGAGTGTGATGATGATGATGATGATGATGAT 960  
QY 961 GACTGAGACCCACACACACAGCCATCACCCTCATTTCCAGTGGTGGTCTGT 1020  
DB 961 GACTGAGACCCACACACACAGCCATCACCCTCATTTCCAGTGGTGGTCTGT 1020  
QY 1021 TCTACTGTTTAAATGAAAGACCTTAAGCAAGCCTTACGAAATCTTTGGGCTCT 1080  
DB 1021 TCTACTGTTTAAATGAAAGACCTTAAGCAAGCCTTACGAAATCTTTGGGCTCT 1080  
QY 1081 GGACTACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
DB 1081 GGACTACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
QY 1141 GATTCAAAATTCGCTTGAATATGAGTCTGAGTCTGAGTCAACACCTGGTTGTCTC 1200  
DB 1141 GATTCAAAATTCGCTTGAATATGAGTCTGAGTCTGAGTCAACACCTGGTTGTCTC 1200  
QY 1201 TGTGTATCCCGACCCCAAGAGAGCTCCGCGCATATATCAAGGTTCAATTAAT 1260  
DB 1201 TGTGTATCCCGACCCCAAGAGAGCTCCGCGCATATATCAAGGTTCAATTAAT 1260  
QY 1261 TGTAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAA 1301  
DB 1261 TGTAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAA 1301

RESULT 2  
AAZ30222  
ID AAZ30222 standard; cDNA; 1314 BP.

XX AAZ30222;

DT 11-FEB-2000 (first entry)

DE cDNA encoding a human prostate-associated serum protease (PRASP).

XX Human; prostate-associated serum protease; PRASP; neuropsin; PSA;  
KW Inocyte clone 2733646; reproductive disorder; cancer;  
KW abnormal prolactin production; infertility; tubal disease;  
KW ovulatory defect; endometriosis; polycystic ovary syndrome;  
KW autoimmune disorder; ectopic pregnancy; breast cancer;  
KW abnormal spermatogenesis; testicular cancer; adenocarcinoma; leukemia;  
KW lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma; ss.

XX Homo sapiens.

XX Key location/Qualifiers

FT CDS 128..976

FT /\*tag= a





OY		961	GACTGGACCCACCACAGCAGGCCATCACTTTCGACTTGCGTTGTGCCTGT 	1020
Dd		959	GACTGGACCCACCACAGSCCATCACCTTCATTCCACTGGGTGTGCTGT 	1018
OY		1021	TCACTCTGTATAAAGAACCCCTAGACCCCTCTACGAACAATCTTTGGCCCTCT 	1080
Dd		1019	TCACTCTGTATAGAAGAAACCCCTTAGGCCAACCTCTAGACAATCTTTGGGCCCTCT 	1078
OY		1081	GGACTACAGGAGATGCTCTCACTTAATATCAACCTGGGTTTCGAATCACTGAGACCTG 	1140
Dd		1079	GGACTACAGGAGATGCTCTCACTTAATATCAACCTGGGTTTCGAATAACACTGAGACCTG 	1138
OY		1141	GATTCAAATTCCTGCCTTGAATATTTGTACTCTGGGAATGACAACACTGGTTGTCTCT 	1200
Dd		1139	GATTCAAATTCCTGCCTTGAATATTTGTACTCTGGGAATGACAACACTGGTTGTCTCT 	1198
OY		1201	TGTTGTATCCCAGCCCCCAAAGACAGCTCTGGCCATATATCAAGGTTTTCAATTAATAT 	1260
Dd		1199	TGTTGTATCCCAGCCCCCAAAGACAGCTCTGGCCATATATCAAGGTTTTCAATTAATAT 	1258
OY		1261	TGCTAAATGAAAAAAAAAAAAAAA 1289 	
Dd		1259	TGCTAAATGAAAAAAAAAAAAAAA 1287 	
<hr/>				
RESULT 4				
ID	AAZ45672			
XX	AAZ45672 standard; DNA; 1335 BP.			
XX	AAZ45672;			
DT	06-APR-2000 (first entry)			
DE	Nucleotide sequence of prostate specific gene clone 1863352.			
XX				
KW	Human; prostate specific gene; PSG; prostate tumour; prostate cancer; metastasis; prostate; ss.			
OS	Homo sapiens.			
PN	WO9960162-A1.			
PD	25-NOV-1999.			
Pf	12-MAY-1999; 99WO-US10548.			
PR	21-MAY-1998; 98US-0086265.			
PA	(DIAD-) DIADEXUS LLC.			
PI	All S, Salceda S, Sun Y, Caferkey R;			
PT	WPJ; 2000-126384/11.			
Diagnosing, monitoring, and staging prostate cancer -				
Example 1; Page 28; 30pp; English.				
The present sequence represents a human prostate specific gene (PSG) (gene ID 221558). The mRNA levels for PSG are about 20 fold higher in the prostate than in other tissues. The PSG mRNA was found to be overexpressed in prostate tumour samples. The specification describes a method for diagnosing the presence of, or metastatic potential of, prostate cancer in a patient. The method comprises measuring PSG levels in a cell, tissue or bodily fluid sample of the patient and a control (i.e., a normal human without cancer), where increased PSG levels in the patient compared to the control is associated with the presence of, or metastasis of prostate cancer. The method can also be used for staging prostate cancer in a patient. The methods are used to detect, monitor, stage and give a prognosis for prostate cancer.				
Sequence	1335 BP; 314 A; 405 C; 349 G; 266 T; 1 other;			

Query Match	94.0%;	Score 1223;	DB 21;	Length 1335;
Best Local Similarity	99.5%;	Pred. No.5;7e-215;		
Matches 1259;	Conservative	0;	Mismatches 0;	Indels 6;
Gaps				3
OY	1	CTGCCTTGTCACACACTGGTGTGAGGGGAGAGGGGAGCAAAAGCCAAAGGAAGGACCCTA	60	
Dd	71	CTGCCCTTGTCACACACTGGTGTGAGGGGAGAGGGGAGCAAAAGCCAAAGGAAGGACCCTA	130	
OY	61	ACTGAAAACAACAAAGCTGGGAGAAGCAGGAATCGCGTCGGGTTCCGACATGCAGAG	120	
Dd	131	ACTGAAAACAACAAAGCTGGGAGAAGCAGGAATCGCGTCGGGTTCCGACATGCAGAG	190	
OY	121	GTGGAGGTGGCGTGGCGGAGCTGGAATACTCGGGGAGAGGTCTCACAGCAGCCAAAGAAC	180	
Dd	191	GTGGAGGTGGCGTGGCGGAGCTGGAATACTCGGGGAGAGGTCTCACAGCAGCCAAAGAAC	250	
OY	181	TGGGGCCCCGCTCTCCCCCTCCAGGCCCATGAGATTGCGAGTTAAATCGCTTGACT	240	
Dd	251	TGGGGCCCCGCTCTCCCCCTCCAGGCCCATGAGATTGCGAGTTAAATCGCTTGACT	310	
OY	241	GGCAACAGGGCTTGTAGGGGGAGAGACCAGATCATCAAAGGGGTTCCAGTGCACACCTCA	300	
Dd	311	GGCAACAGGGCTTGTAGGGGGAGAGACCAGATCATCAAAGGGGTTCCAGTGCACACCTCA	370	
OY	301	CTCCCAGCCCTGGGAGGSCACCCCTGTGAGAAAGACGCGGCTACTCTGTGGGGCAGCGCT	360	
Dd	371	CTCCCAGCCCTGGGAGGSCACCCCTGTGAGAAAGACGCGGCTACTCTGTGGGGCAGCGCT	430	
OY	361	CATGCCCCCGCAGATGGCTCTGACAGCAGCCCATCTGGCTCAAGCC---CCGCTACATAG	416	
Dd	431	CATGCCCCCGCAGATGGCTCTGACAGCAGCCCATCTGGCTCAAGCCCGCTACATAG	490	
OY	417	TTCAACCTGGGGAGCAGCAACCTCCAGAGAGAGAGGCTGTAGAGACAGCCCGAGACGCA	476	
Dd	491	TTCAACCTGGGGAGCAGCAACCTCCAGAGAGAGAGGCTGTAGAGAGACCCCGAGACGCA	550	
OY	477	CTGAGTCTTCCCCCACCCCGGGCTTCAACAACAGCTCTCCCAACAAAGACCAACCGCAATG	536	
Dd	551	CTGAGTCTTCCCCCACCCCGGGCTTCAACAACAGCTCTCCCAACAAAGACCAACCGCAATG	610	
OY	537	AACATCATCTGGTAGAATGGCATGGCATGGCATGCTCATACCTGGGCTGTGGACCCCTCA	596	
Dd	611	AACATCATCTGGTAGAATGGCATGGCATGGCATGCTCATACCTGGGCTGTGGACCCCTCA	670	
OY	597	CCCTCTCCTCAGCGCGTGTCACTGCTGCGACACAGCTGCGCTAATTTCCGGCTGGGGACACA	656	
Dd	671	CCCTCTCCTCAGCGCGTGTCACTGCTGCGACACAGCTGCGCTAATTTCCGGCTGGGGACACA	730	
OY	657	CGTCCAGCCCCCAGTTACGCGCTGCCTCACACCTTGCGATGGCGCCAACTCACATCATTTG	716	
Dd	731	CGTCCAGCCCCCAGTTACGCGCTGCCTCACACCTTGCGATGGCGCCAACTCACATCATTTG	790	
OY	717	AGCACCAAAATGTGAGAAGCGCTTAACCCGGGCAACATACAGAACCAATGTTGTGTGCCA	776	
Dd	791	AGCACCAAAATGTGAGAAGCGCTTAACCCGGGCAACATACAGAACCAATGTTGTGTGCCA	850	
OY	777	GCATGACAGGAAGGGGGCAAGACCTGTCCAGGGGAGTCCGGGGGGCCCTGTGGTCTGTGA	836	
Dd	851	GCATGACAGGAAGGGGGCAAGACCTGTCTCCAGGGTACTCCGGGGGGCCCTGTGGTCTGTGA	910	
OY	837	ACCAAGTCTCTTCAAGGCAATTAATCTCTGGGGGCGAGATCCGCTGTGCATCAACCCGAAGC	896	
Dd	911	ACCAAGTCTCTTCAAGGCAATTAATCTCTGGGGGCGAGATCCGCTGTGCATCAACCCGAAGC	970	
OY	897	CTGGTGTCTAACAAGATCTGCAAAATATGTGGACTGATTCAGSAGACATGTAAGACA	956	
Dd	971	CTGGTGTCTAACAAGATCTGCAAAATATGTGGACTGATTCAGSAGACATGTAAGACA	1030	
OY	957	ATTAGACTGAGCCACCACCAACAGACCATACCTCCATTTCACTTGGGTTTGGTTTC	1016	
Dd	1031	ATTAGACTGAGCCACCACCAACAGACCATACCTCCATTTCACTTGGGTTTGGTTTC	1090	
OY	1017	CTGTTCACCTGTTAATAGAAACCCCTAAGCCAAAGCCCTCTACGAACATTTCTTTGGGCC	1076	



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Db      1091  CTGTTCACTCTGTTATTAAGAAACCTTAGCCAAACCTCTACGACATTCTTTGGCC 1150
QY      1077  TCCTGACATACAGAGATGCTGTCACCTTAATATCAACCTGGGGTTCGAAATCAGTGAGA 1136
Db      1151  TCCTGACATACAGAGATGCTGTCACCTTAATATCAACCTGGGGTTCGAAATCAGTGAGA 1210
QY      1137  CCTGATTCAAATTCCTGCTTGAATATGTGACTCTGGGATGACACACACCTGGTTGT 1196
Db      1211  CCTGATTCAAATTCCTGCTTGAATATGTGACTCTGGGATGACACACACCTGGTTGT 1270
QY      1197  TCTGTGTTGATCCCGCCCAAGACAGCTCCTGGCCATATATCAAGTTTCATTA 1256
Db      1271  TCTGTGTTGATCCCGCCCAAGACAGCTCCT-GCCATATATCA-GTTTCATTA 1328
QY      1257  TATTT 1261
Db      1329  TATTT 1333

RESULT 5
AAA37072
ID      AAA37072 standard; cDNA; 1204 BP.
XX
AC      AAA37072;
XX
DT      08-AUG-2000 (first entry)
XX
DE      Human PRO1279 (UNQ649) cDNA sequence SEQ ID NO:169.
XX
KW      Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW      transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
KW      ss.
XX
OS      Homo sapiens.
XX
PN      WO200012708-A2.
XX
PD      09-MAR-2000.
XX
PE      01-SEP-1999; 99WO-US20111.
XX
PR      01-SEP-1998; 98US-0098716.
PR      01-SEP-1998; 98US-0098749.
PR      01-SEP-1998; 98US-0098750.
PR      02-SEP-1998; 98US-0098803.
PR      02-SEP-1998; 98US-0098821.
PR      02-SEP-1998; 98US-0098843.
PR      09-SEP-1998; 98US-0099536.
PR      09-SEP-1998; 98US-0099596.
PR      09-SEP-1998; 98US-0099598.
PR      09-SEP-1998; 98US-0099602.
PR      09-SEP-1998; 98US-0099642.
PR      10-SEP-1998; 98US-0099741.
PR      10-SEP-1998; 98US-0099754.
PR      10-SEP-1998; 98US-0099763.
PR      10-SEP-1998; 98US-0099782.
PR      10-SEP-1998; 98US-0099808.
PR      10-SEP-1998; 98US-0099812.
PR      10-SEP-1998; 98US-0099815.
PR      10-SEP-1998; 98US-0099816.
PR      15-SEP-1998; 98US-0100385.
PR      15-SEP-1998; 98US-0100388.
PR      15-SEP-1998; 98US-0100584.
PR      16-SEP-1998; 98US-0100584.
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PR      16-SEP-1998; 98US-0100661.
PR      16-SEP-1998; 98US-0100662.
PR      16-SEP-1998; 98US-0100664.
PR      17-SEP-1998; 98US-0100663.
PR      17-SEP-1998; 98US-0100684.
PR      17-SEP-1998; 98US-0100710.
PR      17-SEP-1998; 98US-0100711.

PR      17-SEP-1998; 98US-0100919.
PR      17-SEP-1998; 98US-0100930.
PR      18-SEP-1998; 98US-0100848.
PR      18-SEP-1998; 98US-0100849.
PR      18-SEP-1998; 98US-0101014.
PR      18-SEP-1998; 98US-0101068.
PR      18-SEP-1998; 98US-0101071.
PR      22-SEP-1998; 98US-0101279.
PR      23-SEP-1998; 98US-0101471.
PR      23-SEP-1998; 98US-0101472.
PR      23-SEP-1998; 98US-0101474.
PR      23-SEP-1998; 98US-0101475.
PR      23-SEP-1998; 98US-0101476.
PR      23-SEP-1998; 98US-0101477.
PR      23-SEP-1998; 98US-0101479.
PR      24-SEP-1998; 98US-0101738.
PR      24-SEP-1998; 98US-0101741.
PR      24-SEP-1998; 98US-0101743.
PR      24-SEP-1998; 98US-0101743.
PR      24-SEP-1998; 98US-0101915.
PR      24-SEP-1998; 98US-0101916.
PR      29-SEP-1998; 98US-0102207.
PR      29-SEP-1998; 98US-0102240.
PR      29-SEP-1998; 98US-0102307.
PR      29-SEP-1998; 98US-0102330.
PR      29-SEP-1998; 98US-0102331.
PR      30-SEP-1998; 98US-0102484.
PR      30-SEP-1998; 98US-0102487.
PR      30-SEP-1998; 98US-0102571.
PR      30-SEP-1998; 98US-0102571.
PR      01-OCT-1998; 98US-0102684.
PR      01-OCT-1998; 98US-0102687.
PR      02-OCT-1998; 98US-0102965.
PR      06-OCT-1998; 98US-0103258.
PR      06-OCT-1998; 98US-0103449.
PR      07-OCT-1998; 98US-0103314.
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PR      07-OCT-1998; 98US-0103335.
PR      07-OCT-1998; 98US-0103396.
PR      07-OCT-1998; 98US-0103401.
PR      08-OCT-1998; 98US-0103633.
PR      08-OCT-1998; 98US-0103678.
PR      08-OCT-1998; 98US-0103679.
PR      08-OCT-1998; 98US-0103711.
PR      14-OCT-1998; 98US-0104257.
PR      20-OCT-1998; 98US-0104987.
PR      20-OCT-1998; 98US-0105000.
PR      21-OCT-1998; 98US-0105002.
PR      21-OCT-1998; 98US-0105104.
PR      22-OCT-1998; 98US-0105169.
PR      22-OCT-1998; 98US-0105266.
PR      26-OCT-1998; 98US-0105693.
PR      26-OCT-1998; 98US-0105694.
PR      27-OCT-1998; 98US-0105807.
PR      27-OCT-1998; 98US-0105881.
PR      27-OCT-1998; 98US-0105882.
PR      27-OCT-1998; 98US-0106062.
PR      28-OCT-1998; 98US-0106023.
PR      28-OCT-1998; 98US-0106029.
PR      28-OCT-1998; 98US-0106030.
PR      28-OCT-1998; 98US-0106032.
PR      28-OCT-1998; 98US-0106033.
PR      28-OCT-1998; 98US-0106178.
PR      29-OCT-1998; 98US-0106248.
PR      29-OCT-1998; 98US-0106384.
PR      29-OCT-1998; 98US-0106384.
PR      30-OCT-1998; 98US-0106500.
PR      30-OCT-1998; 98US-0106464.
PR      03-NOV-1998; 98US-0106856.
PR      03-NOV-1998; 98US-0106902.
PR      03-NOV-1998; 98US-0106905.
PR      03-NOV-1998; 98US-0106919.
PR      03-NOV-1998; 98US-0106932.
PR      03-NOV-1998; 98US-0106934.
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PR 10-NOV-1998: 98US-0107783.  
 PR 17-NOV-1998: 98US-0108775.  
 PR 17-NOV-1998: 98US-0108779.  
 PR 17-NOV-1998: 98US-0108787.  
 PR 17-NOV-1998: 98US-0108788.  
 PR 17-NOV-1998: 98US-0108801.  
 PR 17-NOV-1998: 98US-0108802.  
 PR 17-NOV-1998: 98US-0108806.  
 PR 17-NOV-1998: 98US-0108807.  
 PR 17-NOV-1998: 98US-0108867.  
 PR 17-NOV-1998: 98US-0108925.  
 PR 18-NOV-1998: 98US-0108848.  
 PR 18-NOV-1998: 98US-0108849.  
 PR 18-NOV-1998: 98US-0108850.  
 PR 18-NOV-1998: 98US-0108851.  
 PR 18-NOV-1998: 98US-0108852.  
 PR 18-NOV-1998: 98US-0108858.  
 PR 18-NOV-1998: 98US-0108904.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;  
 XX  
 DR MPI: 2000-237871/20.  
 XX P-PSDB: AAY99390.  
 PT New mammalian DNA sequences encoding transmembrane, receptor or  
 PT secreted PRO polypeptides, useful for screening of potential peptide or  
 PT small molecule inhibitors of the relevant receptor/ligand interactions  
 PS Claim 2, Fig 101; 773pp; English.  
 XX  
 XX AAA37022 to AAA37144 encode the new isolated human transmembrane,  
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The  
 CC transmembrane and receptor PRO proteins can be used for screening of  
 CC potential peptide or small molecule inhibitors of the relevant  
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
 CC encoding them have various industrial applications, including uses as  
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent  
 CC PCR primers and hybridisation probes used in the isolation of the PRO  
 CC polypeptides from the present invention.  
 XX  
 SO Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Query Match 92.1%; Score 1198; DB 21; Length 1204;  
 Best Local Similarity 100.0%; Pred. No. 2,1e-210;  
 Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 GTTCGCGAGATGCAAGGTTGAGTGGCTGCGGAGCTGGAAGTCAATCGGCGAGAGTCTC 163  
 DB 1 GTTCGCGAGATGCAAGGTTGAGTGGCTGCGGAGCTGGAAGTCAATCGGCGAGAGTCTC 60  
 QY 164 ACAGAGCCCAAGGAACCTGCGGCCGCTCTCCCTCCAGGCCATGAGATTCTGCAG 223  
 DB 61 ACAGAGCCCAAGGAACCTGCGGCCGCTCTCCCTCCAGGCCATGAGATTCTGCAG 120  
 QY 224 TTAATCTGCTGCTCTGCGCAACAGGCTTGTAGGGGAGAGACGAGATCAATCAAGGGG 283  
 DB 121 TTAATCTGCTGCTCTGCGCAACAGGCTTGTAGGGGAGAGACGAGATCAATCAAGGGG 180  
 QY 284 TTGCGAGTGAAGCCCTCATCCAGCCCTGCGAGAGAGCCCTGTTGAGAAAGAGCGGCTA 343  
 DB 181 TTGCGAGTGAAGCCCTCATCCAGCCCTGCGAGAGAGCCCTGTTGAGAAAGAGCGGCTA 240  
 QY 344 CTCTGTGGGGGAGCGCTCATCGCCCGCCAGATGAGCTCTGAGAGAGCCACAGCGCTCAAG 403  
 DB 241 CTCTGTGGGGGAGCGCTCATCGCCCGCCAGATGAGCTCTGAGAGAGCCACAGCGCTCAAG 300  
 QY 404 CCCCAGTACATAGTTACCTGCGGAGAGCAACAACCTCCAGAAAGAGAGGCTGTGACGAG 463  
 DB 301 CCCCAGTACATAGTTACCTGCGGAGAGCAACAACCTCCAGAAAGAGAGGCTGTGACGAG 360  
 QY 464 ACCGGAGACGACCTAGAGTCTTCCGCCACCCCGGCTTCAACACAGCCTCCCAACAAA 523

DB 361 ACCGGAGACGACCTAGAGTCTTCCGCCACCCCGGCTTCAACACAGCCTCCCAACAAA 420  
 QY 524 GACCAACCGCAATGACATCATGCTGGTGAAGATGAGCATGCGCACTCTCATACCTGGCT 583  
 DB 421 GACCAACCGCAATGACATCATGCTGGTGAAGATGAGCATGCGCACTCTCATACCTGGCT 480  
 QY 584 GTGCGACCCCTCAACCTCTCTCAAGCTGATGATGATGATGATGATGATGATGATGATGAT 643  
 DB 481 GTGCGACCCCTCAACCTCTCTCAAGCTGATGATGATGATGATGATGATGATGATGATGAT 540  
 QY 644 GGCTGGGGAGAGAGCTCAAGCCCGCCAGTTACGCTGCTCAACCTTGGATGCGCAAC 703  
 DB 541 GGCTGGGGAGAGAGCTCAAGCCCGCCAGTTACGCTGCTCAACCTTGGATGCGCAAC 600  
 QY 704 ATCACCACATGATGAGACACAGAAAGTGTGAAGACGCTACCCCGCAACATCAACAGACC 763  
 DB 601 ATCACCACATGATGAGACACAGAAAGTGTGAAGACGCTACCCCGCAACATCAACAGACC 660  
 QY 764 ATGATGTGTGCCAGGCTGAGAGAGGGGCAAGAGACTCTGCGAGAGTACTCCGGGGGC 823  
 DB 661 ATGATGTGTGCCAGGCTGAGAGAGGGGCAAGAGACTCTGCGAGAGTACTCCGGGGGC 720  
 QY 824 CCTGTGCTGTGTAACCACTCTCTCAAGGCAATATCTCTGCGGCGAGATCCTGTGCG 883  
 DB 721 CCTGTGCTGTGTAACCACTCTCTCAAGGCAATATCTCTGCGGCGAGATCCTGTGCG 780  
 QY 884 ATCACCACGAAACCTGGTGTCTCAACAGAAAGTGTGAAGACGCTACCTATGATGATGATGAT 943  
 DB 781 ATCACCACGAAACCTGGTGTCTCAACAGAAAGTGTGAAGACGCTACCTATGATGATGATGAT 840  
 QY 944 ACAGTGAAGAACATTTAGACTGAGACCCACCCAGAGCCATCCATTTCCACT 1003  
 DB 841 ACAGTGAAGAACATTTAGACTGAGACCCACCCAGAGCCATCCATTTCCACT 900  
 QY 1004 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1063  
 DB 901 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 QY 1064 CATTTTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123  
 DB 961 CATTTTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 QY 1124 GAATACAGTGAAGACCTGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1183  
 DB 1021 GAATACAGTGAAGACCTGATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 QY 1184 ACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243  
 DB 1081 ACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 QY 1244 AGGTTCAATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1301  
 DB 1141 AGGTTCAATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1198

RESULT 6  
 AAS21496  
 ID AAS21496 standard; CDNA; 1204 BP.  
 XX  
 AC AAS21496;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human cDNA sequence encoding for PRO1279 polypeptide.  
 XX  
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor- $\alpha$ ; TNF- $\alpha$ ;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIa; gene therapy; ss.  
 XX  
 XX Homo sapiens.

PN WO200140466-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000WO-US32678.  
 XX  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28694.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99US-0170262.  
 PR 20-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07373.  
 PR 17-MAR-2000; 2000WO-US08439.  
 PR 17-MAR-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 10-NOV-2000; 2000WO-US30873.  
 XX  
 PA (GENTH ) GEMENTECH INC.  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerlisen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart JA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2001-408281/43.  
 DR P-PSDB; AAU12424.  
 XX  
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT Lung, breast, prostate, cervical  
 XX  
 PS Claim 3; Fig 505; 813P; English.  
 PS  
 CC AA521244-AA521518 encode for novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, the release of a cytokine from peripheral blood  
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.  
 CC  
 XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Query Match 92.1%; Score 1198; DB 22; Length 1204;  
 Best Local Similarity 100.0%; Pred. No. 2,1e-210;  
 Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 104 GTTCGGAGATGACAGAGTTGAGGTGGCTGGGGAGTGGAGTATGATGGGAGAGTCTC 163  
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 Db 1 GTTCGGAGATGACAGAGTTGAGGTGGCTGGGGAGTGGAGTATGATGGGAGAGTCTC 60  
 Oy 164 ACAGAGCAAGGAAGAACTGGGGCCCGCTCTCCCTCCAGGCCATGAGATTCCTCAG 223  
 |||||||  
 Db 61 ACAGAGCAAGGAAGAACTGGGGCCCGCTCTCCCTCCAGGCCATGAGATTCCTCAG 120  
 Oy 224 TTAATCCTGCTTCTCTGGCAACAGGGCTTTAGGGGAGAGACCAAGATCATCAGGG 283  
 |||||||  
 Db 121 TTAATCCTGCTTCTCTGGCAACAGGGCTTTAGGGGAGAGACCAAGATCATCAGGG 180  
 Oy 284 TTGAGTGCAGACCTCATCTCCAGCCCGGAGAGCAGCCCTGTCGAGAGAGCGGCTA 343  
 |||||||  
 Db 181 TTGAGTGCAGACCTCATCTCCAGCCCTGTCGAGAGAGCGGCTA 240  
 Oy 344 CTCTGGGGGAGAGCTCATGCCCCAGATGCTCTGACAGAGCCCATGCTCTCAG 403  
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 Db 241 CTCTGGGGGAGAGCTCATGCCCCAGATGCTCTGACAGAGCCCATGCTCTCAG 300  
 Oy 404 CCCCCGTCATATGATTCACCTGGGGCAGACAACTCCAGAAAGAGAGGGCTGTGACAG 463  
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 Db 301 CCCCCGTCATATGATTCACCTGGGGCAGACAACTCCAGAAAGAGAGGGCTGTGACAG 360  
 Oy 464 ACCGGAGAGAGCTGAGTCTTCCCGCACCCCGCTTCACACAGAGCTCCCAAGAA 523  
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 Db 361 ACCGGAGAGAGCTGAGTCTTCCCGCACCCCGCTTCACACAGAGCTCCCAAGAA 420  
 Oy 524 GACCAGCGCAATGACATCATGCTGTGAAGATGAGATGCGCATGCTCATCTGCTG 583  
 |||||||  
 Db 421 GACCAGCGCAATGACATCATGCTGTGAAGATGAGATGCGCATGCTCATCTGCTG 480  
 Oy 584 GTGGGACCCCTCACCCCTCTCTACAGCTGTGTCTACTGTGGACACAGCTGCTATTTC 643  
 |||||||  
 Db 481 GTGGGACCCCTCACCCCTCTCTACAGCTGTGTCTACTGTGGACACAGCTGCTATTTC 540  
 Oy 644 GGCTGGGGCAGACAGTCTCAGGCCCGCAGTTCAGCTGCTCAGCTTGGAGTGGCCAG 703  
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 Db 541 GGCTGGGGCAGACAGTCTCAGGCCCGCAGTTCAGCTGCTCAGCTTGGAGTGGCCAG 600  
 Oy 704 ATCACCATCATTTAGACACACAGAAAGTGTGAGAACGCTACCCGGCAACATCACAGACC 763  
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 Db 601 ATCACCATCATTTAGACACACAGAAAGTGTGAGAACGCTACCCGGCAACATCACAGACC 660  
 Oy 764 ATGCTGTGGCCACAGCTGACAGGAAGGGGGCAAGAGACTCCGCGGCTGACTCCGGGGC 823  
 |||||||  
 Db 661 ATGCTGTGGCCACAGCTGACAGGAAGGGGGCAAGAGACTCCGCGGCTGACTCCGGGGC 720  
 Oy 824 CCTGTGTCGTGTAAACCAAGTCTCTTCAAGGCAATTCCTCTGGGGCCAGATTCGTCGC 883  
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 Db 721 CCTGTGTCGTGTAAACCAAGTCTCTTCAAGGCAATTCCTCTGGGGCCAGATTCGTCGC 780  
 Oy 884 ATCACCCGAAAGCCTGTGTCTACAGCAAGAGTGTCAATATGTGACTGATTCAGAG 943  
 |||||||  
 Db 781 ATCACCCGAAAGCCTGTGTCTACAGCAAGAGTGTCAATATGTGACTGATTCAGAG 840  
 Oy 944 ACGATGAAGAAATTTAGATGAGACCAACCCACAGAGCCCATTCATCTTCATCT 1003  
 |||||||  
 Db 841 ACGATGAAGAAATTTAGATGAGACCAACCCACAGAGCCCATTCATCTTCATCT 900  
 Oy 1004 TGGGTGTGGTTCCTGCTGCTGCTGTTAATGAAGAACCTTAAGCAAGACCTCTAGAA 1063  
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 Db 901 TGGGTGTGGTTCCTGCTGCTGCTGTTAATGAAGAACCTTAAGCAAGACCTCTAGAA 960  
 Oy 1064 CATTCCTTGGGCTCTCTGAGACTACAGAGATGCTGCTCAATTAATCAACCTGGGTTTC 1123  
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 Db 961 CATTCCTTGGGCTCTCTGAGACTACAGAGATGCTGCTCAATTAATCAACCTGGGTTTC 1020  
 Oy 1124 GAATATGATGAGACCTGATTCAAATTTCTGCTTGAATATTTGTGACTTGGGAATGACA 1183

Db 1021 GAATATGAGACCTGAGATCAATTCCTGGAATATGACTCTGGGAATGACA 1080  
|  
QY 1184 ACACGTGTTTCTCTCTGTATCCAGCCCAAGACAGCTCTGGCATATATCA 1243  
|  
Db 1081 ACACGTGTTTCTCTGTATCCAGCCCAAGACAGCTCTGGCATATATCA 1140  
|  
QY 1244 AGGTTCAATTAATATTCCTAAATGAAAAAATGAAAAAATGAAAAA 1301  
|  
Db 1141 AGGTTCAATTAATATTCCTAAATGAAAAAATGAAAAAATGAAAAA 1198  
|  
RESULT 7  
AAFS4320  
ID AAF54320 standard; DNA; 1204 BP.  
XX  
AC AAF54320;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE DNA encoding protein of the invention #51.  
XX  
KW Secreted; transmembrane; gene therapy; ss.  
XX  
OS Unidentified.  
XX  
PN WO200078961-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 18-FEB-2000; 2000WO-US04342.  
XX  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28513.  
PR 02-DEC-1999; 99WO-US28513.  
PR 16-DEC-1999; 99WO-US30095.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
XX  
PA (GENE ) GENENTECH INC.  
XX  
PI Baker KP, Bolstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
PI Pan Y, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;  
PI Watanabe CK, Williams PM, Wood WI;  
XX  
DR WPI: 2001-071395/08.  
XX  
PT Secreted and transmembrane proteins and nucleic acids designated PRO,  
PT useful as hybridization probes, in chromosome and gene mapping and gene  
PT therapy -  
XX  
PS Claim 2; Fig 101; 787pp; English.  
XX  
XX The present invention relates to secreted and transmembrane proteins.  
XX These proteins and the DNA encoding them may be used as hybridization  
XX probes, in chromosome and gene mapping and in the generation of  
XX anti-sense RNA and DNA. They may also be used to generate either  
XX transgenic animals or knockout animals which are in turn useful for  
XX development and screening of therapeutically useful reagents.  
XX The nucleic acids may also be used in gene therapy.  
XX  
SO Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;  
  
Query Match 92.1%; Score 1198; DB 22; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 2.1e-210;  
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 104 GTTCCGACAGTGCAGAGTTGAGTGGCTGCGGAGCTGGAATCATCGGAGAGGTCTC 163

Db 1 GTTCCGACAGTGCAGAGTTGAGTGGCTGCGGAGCTGGAATCATCGGAGAGGTCTC 60  
|  
QY 164 ACAGCGACCAAGAACCTGGGGCCCGCTCCCTCCAGGCAATGAGATTCGAC 223  
|  
Db 61 ACAGCGACCAAGAACCTGGGGCCCGCTCCCTCCAGGCAATGAGATTCGAC 120  
|  
QY 224 TTATATCTCTCTCTCTGCGCAACAGGGCTTGAAGGGGAGACAGAGATCATCAAGGG 283  
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Db 121 TTATATCTCTCTCTCTGCGCAACAGGGCTTGAAGGGGAGACAGAGATCATCAAGGG 180  
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QY 284 TTGAGTGCAGAGCTTACCTCCAGAGCCCTGGAGAGCCCTGTTCAGAAAGACGGGCTA 343  
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Db 181 TTGAGTGCAGAGCTTACCTCCAGAGCCCTGGAGAGCCCTGTTCAGAAAGACGGGCTA 240  
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QY 344 CTCTGTGGGGCGAGCTCATGCGCCCAAGATGAGCTCTGACAGACCCCACTGCTCAAG 403  
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Db 241 CTCTGTGGGGCGAGCTCATGCGCCCAAGATGAGCTCTGACAGACCCCACTGCTCAAG 300  
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QY 404 CCCCCTATAGTATGTTACCTGGGGGAGACAAACCTCCAGAGAGAGGGCTGTGAGCAG 463  
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Db 301 CCCCCTATAGTATGTTACCTGGGGGAGACAAACCTCCAGAGAGAGGGCTGTGAGCAG 360  
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QY 464 ACCCGGACAGCCACTGAGTCTTCCCGCACCCCGCTTAAACAACAGCTCCCAACAA 523  
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QY 524 GACCAACCGCAATGACATCATGCGGTGAAGATGGCATGCGCATGCTCCATCACTGGGCT 583  
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QY 584 GTGCGACCCCTGACCTCTCTCTACAGCTGTGTACAGTGTGAGACACAGCTGCTCATTTCC 643  
|  
Db 481 GTGCGACCCCTGACCTCTCTCTACAGCTGTGTACAGTGTGAGACACAGCTGCTCATTTCC 540  
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QY 644 GCGTGGGGGAGACAGTCTCCAGCCCGATTACGCTGCTCTACACCTTGGATGCGCAAC 703  
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Db 541 GCGTGGGGGAGACAGTCTCCAGCCCGATTACGCTGCTCTACACCTTGGATGCGCAAC 600  
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QY 704 ATCAACCATATTGAGACAGCAGAAAGTGTGAAGAGCTTACCCGGCAACATCAAGACAC 763  
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Db 601 ATCAACCATATTGAGACAGCAGAAAGTGTGAAGAGCTTACCCGGCAACATCAAGACAC 660  
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QY 764 ATGTGTGTGCCAGCGCTGACAGGAAGGGGGCAAGAGACTCTGCGAGGGTACCTCGGGGG 823  
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Db 661 ATGTGTGTGCCAGCGCTGACAGGAAGGGGGCAAGAGACTCTGCGAGGGTACCTCGGGGG 720  
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QY 824 CCTGTGTGTGTACAGCTCTCTCAAGGCAATTTATCTCTGGGGGCAAGATCCGTGTCCG 883  
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Db 721 CCTGTGTGTGTACAGCTCTCTCAAGGCAATTTATCTCTGGGGGCAAGATCCGTGTCCG 780  
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QY 884 ATCAACCGCAAGACCTGCTGTCTACAGAAAGTCTGCAATATGTGGATGATCCAGAG 943  
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Db 781 ATCAACCGCAAGACCTGCTGTCTACAGAAAGTCTGCAATATGTGGATGATCCAGAG 840  
|  
QY 944 ACAGTGAAGAACATTTAGACTGAGCCACCAACAGCCATCACTTCCTCACT 1003  
|  
Db 841 ACAGTGAAGAACATTTAGACTGAGCCACCAACAGCCATCACTTCCTCACT 900  
|  
QY 1004 TGGTGTGTGTGTCTGT 1063  
|  
Db 901 TGGTGTGTGTGTCTGT 960  
|  
QY 1064 CATTTTGTGGGCTCTGTGAGTACAGAGAGATGTGCAATTAATCAAACTGGGGTTC 1123  
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Db 961 CATTTTGTGGGCTCTGTGAGTACAGAGAGATGTGCAATTAATCAAACTGGGGTTC 1020  
|  
QY 1124 GAATTCAGTGAAGCTGTGATTAATTCGCTTGAATATGTGATCTGGGAATGACA 1183  
|  
Db 1021 GAATTCAGTGAAGCTGTGATTAATTCGCTTGAATATGTGATCTGGGAATGACA 1080  
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QY 1184 ACACCTGTTTGTCTCTGTATCCAGCCCAAGACAGCTCTGGCATATATCA 1243  
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481 GTGCGACCCCTCACCCTCTCCACGCGTGTGCTGCTGGCACCAGCTGCTCATTTCC 540
OY      644 GGCCTGGGACAGCAGCTCCAGCCCGCAGTTACGCTGCTCCACACCTTGATGCCAC 703
Db      541 GGCCTGGGACAGCAGCTCCAGCCCGCAGTTACGCTGCTCCACACCTTGATGCCAC 600
OY      704 ATCACCATTGTTGAGCAGCAGAGTGTGAGAACGCCCTACCCGGGACATCAGACACC 763
Db      601 ATCACCATTGTTGAGCAGCAGAGTGTGAGAACGCCCTACCCGGGACATCAGACACC 660
OY      764 ATGCTGTGTGCGCAGCTGCGAGAGAGGGGCAAGACTCTCTGCGAGGTGATCCGGGGC 823
Db      661 ATGCTGTGTGCGCAGCTGCGAGAGAGGGGCAAGACTCTCTGCGAGGTGATCCGGGGC 720
OY      824 CCTGCTGCTGTGAACGAGCTCTTCAAGGATTTCTCTGCGGGGCGAGAGTCCGTTGCG 883
Db      721 CCTGCTGCTGTGAACGAGCTCTTCAAGGATTTCTCTGCGGGGCGAGAGTCCGTTGCG 780
OY      884 ATCACCAGAAAGCCTGCTGTCTACAGAAAGTCTGCAATATATGTGACTGATCCAGAG 943
Db      781 ATCACCAGAAAGCCTGCTGTCTACAGAAAGTCTGCAATATATGTGACTGATCCAGAG 840
OY      944 ACGATGAAGAAACATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1003
Db      841 ACGATGAAGAAACATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
OY      1004 TGGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1063
Db      901 TGGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
OY      1064 CATCTTTTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123
Db      961 CATCTTTTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
OY      1124 GAAATCATGAGAGAGCTGATTCATATTTCTGCTTGAATATTTGTACTCTGGGAATGACA 1183
Db      1021 GAAATCATGAGAGAGCTGATTCATATTTCTGCTTGAATATTTGTACTCTGGGAATGACA 1080
OY      1184 ACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243
Db      1081 ACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
OY      1244 AGGTTCAATAAATAATTTGCTAATGAAAAAATTTGCTAATGAAAAAATTTGCTAAT 1301
Db      1141 AGGTTCAATAAATAATTTGCTAATGAAAAAATTTGCTAATGAAAAAATTTGCTAAT 1198

```

RESULT 9  
ID ABL88175 standard; cDNA, 1204 BP.  
AC ABL88175;

DT 16-MAY-2002 (first entry)

DE Human PRO1279 cDNA sequence SEQ ID NO:207.

XX Human; angiogenesis; cardiatic; cytoslastic; antiangiogenic; hypotensive;  
XX Human; arteriosclerosis; PRO agonist; PRO antagonist; trauma;  
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
XX age-related macular degeneration; arterial restenosis; angina;  
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
XX wound healing; chromosome mapping; gene mapping; gene; ss.

XX Homo sapiens.  
XX WO200200690-A2.  
XX PD 03-JAN-2002.

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PF      20-JUN-2001; 2001WO-US19692.
XX      23-JUN-2000; 2000US-213637P.
PR      20-JUL-2000; 2000US-219556P.
PR      25-JUL-2000; 2000US-220624P.
PR      25-JUL-2000; 2000US-220664P.
PR      28-JUL-2000; 2000WO-US20710.
PR      02-AUG-2000; 2000US-222655P.
PR      17-AUG-2000; 2000US-0643657.
PR      23-AUG-2000; 2000WO-US23522.
PR      24-AUG-2000; 2000WO-US23328.
PR      07-SEP-2000; 2000US-230978P.
PR      18-SEP-2000; 2000US-0664610.
PR      18-SEP-2000; 2000US-0665350.
PR      24-OCT-2000; 2000US-242922P.
PR      08-NOV-2000; 2000US-0709238.
PR      10-NOV-2000; 2000WO-US30873.
PR      01-DEC-2000; 2000WO-US32678.
PR      20-DEC-2000; 2000WO-US34956.
PR      22-JAN-2001; 2001US-0767609.
PR      28-FEB-2001; 2001US-0796498.
PR      28-FEB-2001; 2001WO-US06520.
PR      01-MAR-2001; 2001WO-US06666.
PR      09-MAR-2001; 2001US-0802706.
PR      14-MAR-2001; 2001US-0808689.
PR      22-MAR-2001; 2001US-0816744.
PR      05-APR-2001; 2001US-0828366.
PR      10-MAY-2001; 2001US-0834208.
PR      10-MAY-2001; 2001US-0854280.
PR      25-MAY-2001; 2001US-0866034.
PR      25-MAY-2001; 2001WO-US17092.
PR      30-MAY-2001; 2001US-0870574.
PR      30-MAY-2001; 2001WO-US17443.
PR      01-JUN-2001; 2001WO-US17800.

```

(GETH ) GENENTECH INC.

PA Baker KP, Ferrara N, Gerber H, Gertsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX WPI; 2002-090516/12.  
DR P-PSDB; ABB84920.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
XX infarction), endothelial or angiogenic disorders in a mammal -  
XX Claim 2; Fig 207; 565pp; English.

CC ABL88072 to ABL88258 encode the PRO proteins given in ABB8817 to  
CC ABB85003. The PRO proteins and polynucleotides have cardiatic, cytoslastic,  
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
CC carcinoma) and wound healing. The PRO polynucleotides have applications  
CC in molecular biology, including use as hybridisation probes, and in  
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
CC probes used in the exemplification of the present invention.

XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Query Match 92.1%; Score 1198; DB 24; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 2.1e-210;  
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 104 GTTCCGAGATGACAGAGTTAGGTGGCTGCGGACCTGGAAATCATGCGGGCAGAGTCTC 163
DB 1 GTTCCGAGATGACAGAGTTAGGTGGCTGCGGACCTGGAAATCATGCGGGCAGAGTCTC 60
OY 164 ACACGAGCAAGAAAGCTGGGGGCGGCTCCCGCCCGGCGGCGCATGAGGATTCGTGAG 223
DB 61 ACACGAGCAAGAAAGCTGGGGGCGGCTCCCGCCCGGCGGCGCATGAGGATTCGTGAG 120
OY 224 TTAATCTGCTTGTCTGGCAACAGGGCTTGTAGGGGGAGAGACAGGATCATCAAGGG 283
DB 121 TTAATCTGCTTGTCTGGCAACAGGGCTTGTAGGGGGAGAGACAGGATCATCAAGGG 180
OY 284 TTGAGAGCAAGCTTCACTCCACGCTTGGGAGGACAGCCCTGTTCCGAGAGACCGGCTA 343
DB 181 TTGAGAGCAAGCTTCACTCCACGCTTGGGAGGACAGCCCTGTTCCGAGAGACCGGCTA 240
OY 344 CTCTGTGGGCGAGCTCATATGCGCCGAGATGGCTCTGACAGGACGCAATGCTCAAG 403
DB 241 CTCTGTGGGCGAGCTCATATGCGCCGAGATGGCTCTGACAGGACGCAATGCTCAAG 300
OY 404 CCGCGTACATAGTTCACTGGGGCAGACAACTCCAGAGAGAGAGGGCTGTGACAG 463
DB 301 CCGCGTACATAGTTCACTGGGGCAGACAACTCCAGAGAGAGAGGGCTGTGACAG 360
OY 464 ACCCGGACAGCACTGAGTCTTCCCGACCCGCGCTTCAACAAACAGCTTCCCAAAA 523
DB 361 ACCCGGACAGCACTGAGTCTTCCCGACCCGCGCTTCAACAAACAGCTTCCCAAAA 420
OY 524 GACACCGCAATGACATATGCTGTGAAGATGGATGGCATGCGAGTCTCATACCTGGGCT 583
DB 421 GACACCGCAATGACATATGCTGTGAAGATGGATGGCATGCGAGTCTCATACCTGGGCT 480
OY 584 GTGCGACCCCTCACTCTCTCTACGCTGTGTCACTGCTGGACACAGCTGCTCATTTTC 643
DB 481 GTGCGACCCCTCACTCTCTCTACGCTGTGTCACTGCTGGACACAGCTGCTCATTTTC 540
OY 644 GGGCGGGGCGACAGTCCACCCCAATTAAGCTTACGCTTCAACACTTGGCGCCAAAC 703
DB 541 GGGCGGGGCGACAGTCCACCCCAATTAAGCTTACGCTTCAACACTTGGCGCCAAAC 600
OY 704 ATACCATCATATGAGCACAGAGTGTGAAGAGCTTACCCCGGCAATCACAGACAC 763
DB 601 ATACCATCATATGAGCACAGAGTGTGAAGAGCTTACCCCGGCAATCACAGACAC 660
OY 764 ATGGTGTGTCCAGAGCTGTGAGAGAGGGGCAAGAGCTCTGCCAGGGTGAATCCGGGGC 823
DB 661 ATGGTGTGTCCAGAGCTGTGAGAGAGGGGCAAGAGCTCTGCCAGGGTGAATCCGGGGC 720
OY 824 CCTCTGGTGTGAACAGTCTCTTCAAGGATATCTCCCTGGGGCCAGGATTCGTGCG 883
DB 721 CCTCTGGTGTGAACAGTCTCTTCAAGGATATCTCCCTGGGGCCAGGATTCGTGCG 780
OY 884 ATACCCGAAAGCGTGTGTCTACAGAAAGTGTCAAAATATGTGAGCTGATCCAGGAG 943
DB 781 ATACCCGAAAGCGTGTGTCTACAGAAAGTGTCAAAATATGTGAGCTGATCCAGGAG 840
OY 944 AGCATGAAGAAATTAAGACTGAGCCACCCACAGAGCCCATCACCCTTCATTTCCACT 1003
DB 841 AGCATGAAGAAATTAAGACTGAGCCACCCACAGAGCCCATCACCCTTCATTTCCACT 900
OY 1004 TGGTGTGGTGTCTCTTCACTCTGTAAATAGAAAACCTTAAGCCAAAGCCCTCAAGAA 1063
DB 901 TGGTGTGGTGTCTCTTCACTCTGTAAATAGAAAACCTTAAGCCAAAGCCCTCAAGAA 960
OY 1064 CATTTTGGGCGCTCTGAGCTACAGAGAGTGTGACTTAATTAATCAACCTGGGGTTC 1123
DB 961 CATTTTGGGCGCTCTGAGCTACAGAGAGTGTGACTTAATTAATCAACCTGGGGTTC 1020
OY 1124 GAAATCAGTGAAGCTGTGAATTCGCTTTGAATATTTGACTCTGGGAATGACA 1183
DB 1021 GAAATCAGTGAAGCTGTGAATTCGCTTTGAATATTTGACTCTGGGAATGACA 1080
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OY 1184 ACACCTGGTTGTCTCTGTGTATCCCGACGCCCAAGACAGCTCCTGGCCATATATCA 1243
DB 1081 ACACCTGGTTGTCTCTGTGTATCCCGACGCCCAAGACAGCTCCTGGCCATATATCA 1140
OY 1244 AGCTTCAATTAATTTGCTAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1301
DB 1141 AGCTTCAATTAATTTGCTAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198

RESULT 10
ABK33628
ID ABK33628 standard; cDNA; 1204 BP.
XX
AC ABK33628;
XX
DT 08-MAY-2002 (first entry)
XX
DE cDNA encoding human PRO protein, Seq ID No 185.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.
XX
OS Homo sapiens.
XX
PN M0200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US21066.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX
PA (GENTH ) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Gimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-112001/22.
DR P-PSDB; AA083684.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
XX
XX Claim 2; Figure 185; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
CC
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CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
CC liver tumour. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression, in pericyte cells, for stimulating  
CC the proliferation or differentiation of chondrocyte cells, for  
CC stimulating the release of tumour necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal  
CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes,  
CC and in chromosome and gene mapping. ABRK3536-ABR3657 represent human  
CC PRO protein coding sequences of the invention.  
XX

Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Query Match 92.1%; Score 1198; DB 24; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 2,1e-210;  
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 GTTCGACATGACAGGTTGAGTGGTCGCGGAGTGAAGTCAATGAGGAGTCTC 163  
DB 1 GTTCCGACATGACAGGTTGAGTGGTCGCGGAGTGAAGTCAATGAGGAGTCTC 60  
QY 164 ACAGCAGCCAGAGAACTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCTGCAG 223  
DB 61 ACAGCAGCCAGAGAACTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCTGCAG 120  
QY 224 TTAATCCTGCTGCTGCGCAACAGGGGCTTGTAGGGGGAGAGACAGATCAATCAAGGG 283  
DB 121 TTAATCCTGCTGCTGCGCAACAGGGGCTTGTAGGGGGAGAGACAGATCAATCAAGGG 180  
QY 284 TTCGAGTGCAGACCTCTACTCCAGCCCTGGCAGGCAAGCCCTGTGAGAGAGCGGGCTA 343  
DB 181 TTCGAGTGCAGACCTCTACTCCAGCCCTGGCAGGCAAGCCCTGTGAGAGAGCGGGCTA 240  
QY 344 CTCTGTGGGGGAGCGCTATGCGCCCAATAGTGGCTTCTACAGCAGCCCACTGCTCAAG 403  
DB 241 CTCTGTGGGGGAGCGCTATGCGCCCAATAGTGGCTTCTACAGCAGCCCACTGCTCAAG 300  
QY 404 CCCCCTACATAGTACCTGGGGGAGCACAACCTTCAGAGAGAGGGCTGTGAGCAG 463  
DB 301 CCCCCTACATAGTACCTGGGGGAGCACAACCTTCAGAGAGAGGGCTGTGAGCAG 360  
QY 464 ACCCGGACAGCCATGAGTGCCTTCCGCCACCCGGCTTCAACAAAGCTCCCAACAA 523  
DB 361 ACCCGGACAGCCATGAGTGCCTTCCGCCACCCGGCTTCAACAAAGCTCCCAACAA 420  
QY 524 GACACCGCAATGACATGCTGTGGTGAAGATGGATGCCAGTCCATCACTCGGGCT 583  
DB 421 GACACCGCAATGACATGCTGTGGTGAAGATGGATGCCAGTCCATCACTCGGGCT 480  
QY 584 GTGCGACCCCTCACCCTCTCTCAGCGTGTCTACTGTGCGACAGCTGCTCTATTTC 643  
DB 481 GTGCGACCCCTCACCCTCTCTCAGCGTGTCTACTGTGCGACAGCTGCTCTATTTC 540  
QY 644 GGCTGGGGAGCAGCTCCAGCCCCAGTTAGCGCTGCTCAGACCTTGGATGCCCAAC 703  
DB 541 GGCTGGGGAGCAGCTCCAGCCCCAGTTAGCGCTGCTCAGACCTTGGATGCCCAAC 600  
QY 704 ATCACCATCATTTGACACAGAGTGTGAAGCGCTACCCCGGAAATCAACAAACCC 763  
DB 601 ATCACCATCATTTGACACAGAGTGTGAAGCGCTACCCCGGAAATCAACAAACCC 660  
QY 764 ATGCTGTGTGCGAGCGTGCAGAGAAAGGGGCAAGAGACTCTGCGAGGGTACTCGGGGGC 823  
DB 661 ATGCTGTGTGCGAGCGTGCAGAGAAAGGGGCAAGAGACTCTGCGAGGGTACTCGGGGGC 720  
QY 824 CCTCTGTGTGTAAACAGTCTCTTAAAGGCAATATCTCTGCGGCGAGGATCGTGTGG 883  
DB 721 CCTCTGTGTGTAAACAGTCTCTTAAAGGCAATATCTCTGCGGCGAGGATCGTGTGG 780  
QY 884 ATCACCAGGAAAGCGGTGTCTACAGGAAAGTCTCAAAATGTGAGCTGAGTCCAGAG 943

DB 781 ATCACCAGGAAAGCGGTGTCTACAGGAAAGTCTCAAAATGTGAGCTGATCCAGAG 840  
QY 944 ACAGTGAAGAACATATAGACTGGAGCCACCCACACAGCCCATACCTTCATTTCCACT 1003  
DB 841 ACAGTGAAGAACATATAGACTGGAGCCACCCACACAGCCCATACCTTCATTTCCACT 900  
QY 1004 TGGTGTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1063  
DB 901 TGGTGTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
QY 1064 CATCTCTTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123  
DB 961 CATCTCTTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
QY 1124 GAAATCAGTGAAGACCTGATTCGAATTCGCTGAAATATTTGCTGCTGGAATGACA 1183  
DB 1021 GAAATCAGTGAAGACCTGATTCGAATTCGCTGAAATATTTGCTGCTGGAATGACA 1080  
QY 1184 ACACCTGTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243  
DB 1081 ACACCTGTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
QY 1244 AGTTTCATTAATATTTCTTAATGAAAAAATTTTCTTAATGAAAAAATTTTCTTAAT 1301  
DB 1141 AGTTTCATTAATATTTCTTAATGAAAAAATTTTCTTAATGAAAAAATTTTCTTAAT 1198

## RESULT 11

AC03855  
ID AC03855 standard; cDNA; 1204 BP.

XX ACA03855;

XX 23-MAY-2003 (first entry)

DE cDNA encoding human PRO polypeptide #253.

XX human; PRO polypeptide; secreted and transmembrane protein;

KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;

KW cytoskeletal; gene; ss.

XX Homo sapiens.

XX US2003036180-A1.

PD 20-FEB-2003.

PF 09-MAY-2002; 2002US-0143114.

XX 31-MAR-1997; 97WO-US05230.

PR 12-JUN-1998; 98WO-US12456.

PR 14-JUL-1998; 98WO-US14552.

PR 28-AUG-1998; 98WO-US17888.

PR 10-SEP-1998; 98WO-US18824.

PR 14-SEP-1998; 98WO-US19093.

PR 14-SEP-1998; 98WO-US19177.

PR 16-SEP-1998; 98WO-US19330.

PR 17-SEP-1998; 98WO-US19437.

PR 07-OCT-1998; 98WO-US21141.

PR 29-OCT-1998; 98WO-US22992.

PR 20-NOV-1998; 98WO-US24855.

PR 01-DEC-1998; 98WO-US25108.

PR 05-JAN-1999; 99WO-US00106.

PR 08-MAR-1999; 99WO-US05028.

PR 10-MAR-1999; 99WO-US05190.

PR 20-APR-1999; 99WO-US08615.

PR 14-MAY-1999; 99WO-US10733.

PR 02-JUN-1999; 99WO-US12252.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

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PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 10-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0862636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.

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PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
PA (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart JA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
DR WPI: 2003-332040/31.
XX P-PSDB; AB068822.
XX
PT New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in
PT tissue typing, and in chromosome identification
XX
PS Claim 2; Fig 505; 660pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists.
CC The PRO polypeptides are useful for stimulating the release of
CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating the
CC proliferation or differentiation of chondrocytes, and detecting the
CC presence of tumours. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and
CC gene mapping, in the generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptides, for generating transgenic animals or
CC knockout animals, for the genetic analysis of individuals with genetic
CC disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
CC encoding the human PRO polypeptides of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipdentry.html.
CC
XX
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

```

Query Match 92.1%; Score 1198; DB 25; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 2,1e-210;  
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 104 GTTCGCGAGATGCGAGGTGAGGTGCTCGGAGCTGGAAGTCATCGGCGAGAGCTCTC 163
DB 1 GTTCGCGAGATGCGAGAGGTGAGGTGCTCGGAGCTGGAAGTCATCGGCGAGAGCTCTC 60
QY 164 ACAGCAGCCAGAGAACTGGGGCCCGCTCTCCCTCCCTCGAGGCCATGAGATTCTGCAG 223
DB 61 ACAGCAGCCAGAGAACTGGGGCCCGCTCTCCCTCCCTCGAGGCCATGAGATTCTGCAG 120
QY 224 TTATCTCTGCTGTGCTGGCAACAGGCTGTGAGGGGGAAGACAGATCATCAAGGGG 283
DB 121 TTATCTCTGCTGTGCTGGCAACAGGCTGTGAGGGGGAAGACAGATCATCAAGGGG 180
QY 284 TTCGAGTGCAGAGCTCTCACTCCAGCCCTGGCAGGACAGCCCTGTTTCGAGAGAGCGGCTA 343
DB 181 TTGAGAGTGCAGAGCTCTCACTCCAGCCCTGGCAGGACAGCCCTGTTTCGAGAGAGCGGCTA 240
QY 344 CTCTGTGGGGCGAGAGCTCATGCGCCCGCAGATGGCTCTGTCAGACAGCCCATCTCTCAAG 403
DB 241 CTCTGTGGGGCGAGAGCTCATGCGCCCGCAGATGGCTCTGTCAGACAGCCCATCTCTCAAG 300
QY 404 CCGCGCTACATAGTTACCTCTGGGGCGAGACAACTCTCAGAGAGAGAGGGCTGTGACAG 463
DB 301 CCGCGCTACATAGTTACCTCTGGGGCGAGACAACTCTCAGAGAGAGAGGGCTGTGACAG 360
QY 464 ACCCGGACAGCACTGAGTCTCTCCCGACCGGGCTTCAACAAAGCCCTCCCAACAA 523
DB 361 ACCCGGACAGCACTGAGTCTCTCCCGACCGGGCTTCAACAAAGCCCTCCCAACAA 420

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QY 524 GACCAACCGCATGATCATGCTGTGAAGATGGCATCCGACATCCATCCATTCGGGCT 583  
DB 421 GACACACCGCAATGACATGCTGGTGAAGATGGCATCCGACATCCATCCATTCGGGCT 480  
QY 584 GTGCGACCCCTCACCCTTCCTCAGCTGTGTACAGTGGGACGACGCGCCCATTTCC 643  
DB 481 GTGCGACCCCTCACCCTTCCTCAGCTGTGTACAGTGGGACGACGCGCCCATTTCC 540  
QY 644 GGCCTGGGGAGCAGCTGCAGCCCCCAGTTACGCTGCTCCACACCTTGGGATGGCCAAC 703  
DB 541 GGCCTGGGGAGCAGCTGCAGCCCCCAGTTACGCTGCTCCACACCTTGGGATGGCCAAC 600  
QY 704 ATCACCATCATTTAGACACCAAGATGTGAAGGCTTACCCGGCAACATCACAGACCC 763  
DB 601 ATCACCATCATTTAGACACCAAGATGTGAAGGCTTACCCGGCAACATCACAGACCC 660  
QY 764 ATGCTGTGTGCGACGGGTGAGGAGGGGGGCAAGGATCTCTGCAAGGCTATCTCCGGGGC 823  
DB 661 ATGCTGTGTGCGACGGGTGAGGAGGGGGGCAAGGATCTCTGCAAGGCTATCTCCGGGGC 720  
QY 824 CCTGTGTGTGTACACGATCTCTCAAGCATTTATCTCTGGGGCCAGGATCCGTGTGC 883  
DB 721 CCTGTGTGTGTACACGATCTCTCAAGCATTTATCTCTGGGGCCAGGATCCGTGTGC 780  
QY 884 ATCACCAGCAAGCCGTGTGTGTACACGAAAGTGTGCAATATGTGATGTGATCCAGAG 943  
DB 781 ATCACCAGCAAGCCGTGTGTGTGTACACGAAAGTGTGCAATATGTGATGTGATCCAGAG 840  
QY 944 ACAGTGAAGACAAATTAAGACTGGACCCACCCACGACCCACCCCTCCATTCGACT 1003  
DB 841 ACAGTGAAGACAAATTAAGACTGGACCCACCCACGACCCACCCCTCCATTCGACT 900  
QY 1004 TGGTGTGTGTGTCTCTGTCTACTCTGTTAATAAGAAACCCTTAAGCCAGACCTCTACGA 1063  
DB 901 TGGTGTGTGTGTCTCTGTCTACTCTGTTAATAAGAAACCCTTAAGCCAGACCTCTACGA 960  
QY 1064 CATTTCTTTGGGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1123  
DB 961 CATTTCTTTGGGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020  
QY 1124 GAATACAGTGAAGACCTGTGATCAAAATTCGCTTGAATATGTGTGTGTGTGTGTGTGT 1183  
DB 1021 GAATACAGTGAAGACCTGTGATCAAAATTCGCTTGAATATGTGTGTGTGTGTGTGTGT 1080  
QY 1184 ACACCTGT 1243  
DB 1081 ACACCTGT 1140  
QY 1244 AGCTTTCAATTAATATTTGTCTAAATGAAAAAATTTGTGTGTGTGTGTGTGTGTGT 1301  
DB 1141 AGCTTTCAATTAATATTTGTCTAAATGAAAAAATTTGTGTGTGTGTGTGTGTGTGT 1198

RESULT 12  
ACA04276  
ID ACA04276 standard; cDNA: 1204 BP.  
XX  
AC ACA04276;  
XX  
DT 27-MAY-2003 (first entry)  
XX  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 505.  
XX  
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;  
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
KW infertility; birth defects; premature aging; AIDS; biosensor;  
KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
KW bioreactor; tumour.  
XX  
OS Homo sapiens.  
XX  
PN US2003032155-A1.

XX PD 13-FEB-2003.  
XX PF 03-MAY-2002; 2002US-0137865.  
XX  
PR 31-MAR-1997; 97WO-US05230.  
PR 12-JUN-1998; 98WO-US12456.  
PR 14-JUL-1998; 98WO-US14552.  
PR 28-AUG-1998; 98WO-US17888.  
PR 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19093.  
PR 14-SEP-1998; 98WO-US19094.  
PR 14-SEP-1998; 98WO-US19177.  
PR 16-SEP-1998; 98WO-US19330.  
PR 07-OCT-1998; 98WO-US21141.  
PR 29-OCT-1998; 98WO-US22991.  
PR 29-OCT-1998; 98WO-US22992.  
PR 20-NOV-1998; 98WO-US24855.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 10-MAR-1999; 99WO-US05190.  
PR 20-APR-1999; 99WO-US08615.  
PR 14-MAY-1999; 99WO-US10733.  
PR 02-JUN-1999; 99WO-US12252.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21947.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 22-DEC-1999; 99WO-US30720.  
PR 30-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 11-FEB-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05746.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.

PR 01-DEC-2000; 2000WO-US32678.  
 PR 28-DEC-2000; 2000WO-US34955.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 22-JUN-2001; 2001WO-US20116.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0806889.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 18-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 01-JUN-2001; 2001US-0866034.  
 PR 05-JUN-2001; 2001US-0872035.  
 PR 14-JUN-2001; 2001US-0874503.  
 PR 19-JUN-2001; 2001US-0882636.  
 PR 21-JUN-2001; 2001US-0886342.  
 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.

XX (GETH ) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerlesen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;  
 XX WPI: 2003-331925/31.  
 DR P-PSDB: AB067098.

XX New secreted and transmembrane nucleic acids and polypeptides,  
 PT designated as PRO, useful for treating inflammation, organ failure,  
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature  
 PT aging, AIDS, or cancer -

XX Claim 2; Fig 505; 659pp; English.

XX The invention relates to an isolated nucleic acid comprising, or which is  
 CC at least 80% identical to, or the full-length coding sequence of, any of  
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide  
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid  
 CC further comprises the full-length coding sequence of the DNA deposited  
 CC under American Type Culture Collection (ATCC) accession number in a list  
 CC given in the specification. Also included are vectors and host  
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO  
 CC antibodies, PRO extracellular domains and mature sequences, methods  
 CC of detecting PRO proteins, methods for stimulating the release of  
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,  
 CC and the proliferation of differentiation of chondrocyte cells, the  
 CC proliferation of, or gene expression in pericyte cells, the release or  
 CC proteoglycans from cartilage, proliferation of inner ear utricular  
 CC supporting cells, the proliferation of T-lymphocyte cells, the release  
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the  
 CC proliferation of endothelial cells), a method for modulating the uptake  
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,  
 CC a method for inhibiting the binding of A-peptide to factor VIIa,  
 CC or the differentiation of adipocyte cells, a method for detecting the  
 CC presence of a tumour in a mammal and an oligonucleotide probe derived  
 CC from any of the nucleotide sequences cited above. The nucleic acids and  
 CC polypeptides are useful for treating inflammatory diseases, organ  
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,  
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or

CC diabetic complications. The nucleic acids are useful as hybridisation  
 CC probes, in chromosome and gene mapping, and in generating antisense RNA  
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors. Both are useful in tissue typing.  
 CC The present sequence encodes a PRO protein of the invention.  
 XX

SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Query Match 92.1%; Score 1198; DB 25; Length 1204;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-210;  
 Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 GTTCCGAGATGCAGAGGTTAGGTGGTGGGAGCTGGAAGTATCGGACAGAGTCTC 163  
 DB 1 GTTCCGAGATGCAGAGGTTAGGTGGTGGGAGCTGGAAGTATCGGAGAGTCTC 60  
 OY 164 ACAGAGCCAGGAACCTGGGGCCGCTCCCTCCGAGGACATGAGGATTCCTCAG 223  
 DB 61 ACAGAGCCAGGAACCTGGGGCCGCTCCCTCCGAGGACATGAGGATTCCTCAG 120  
 OY 224 TTAATCCTGCTTGTGGCAACAGGCTTGAAGGGAGAGACAGGATCATCAAGGG 283  
 DB 121 TTAATCCTGCTTGTGGCAACAGGCTTGAAGGGAGAGACAGGATCATCAAGGG 180  
 OY 284 TTGCAAGTCAAGCCTCACTCCACGCTGGCAGCAGCCTGTTGAGAAAGCGGCTA 343  
 DB 181 TTGCAAGTCAAGCCTCACTCCACGCTGGCAGCAGCCTGTTGAGAAAGCGGCTA 240  
 OY 344 CTCTGTGGGGGAGCGCATGCGCCCAAGATGGTCTCGACAGGACCACTGCTCAAG 403  
 DB 241 CTCTGTGGGGGAGCGCATGCGCCCAAGATGGTCTCGACAGGACCACTGCTCAAG 300  
 OY 404 CCCCCTACATATGTTCACTGGGGCAGACACAACTCCAGAAAGAGAGGCTGTGACAG 463  
 DB 301 CCCCCTACATATGTTCACTGGGGCAGACACAACTCCAGAAAGAGAGGCTGTGACAG 360  
 OY 464 ACCCGAGAGCAGCTAGTCTTCCCAACCCGCGCTTCAACAACAGCCTCCCAACAA 523  
 DB 361 ACCCGAGAGCAGCTAGTCTTCCCAACCCGCGCTTCAACAACAGCCTCCCAACAA 420  
 OY 524 GACCAGCGAATGATCATGCTGTGTAAGTGTGATGCGACATGCTCATCACTGGGCT 583  
 DB 421 GACCAGCGAATGATCATGCTGTGTAAGTGTGATGCGACATGCTCATCACTGGGCT 480  
 OY 584 GTGGACCCCTCAACCTCTCTCTCAAGCTGTGTCACTCTGTGGACAGCCTGCTATTTC 643  
 DB 481 GTGGACCCCTCAACCTCTCTCTCTCAAGCTGTGTCACTCTGTGGACAGCCTGCTATTTC 540  
 OY 644 GCGTGGGGCAGACAGTCCAGCCCACTTACGCTGCTCTACACCTTGGATGCGCCAC 703  
 DB 541 GCGTGGGGCAGACAGTCCAGCCCACTTACGCTGCTCTACACCTTGGATGCGCCAC 600  
 OY 704 ATCACCAATCTTGGAGCAGCAAGAGTGTGAGAAAGCTTACCCGGCAACATCACAGAC 763  
 DB 601 ATCACCAATCTTGGAGCAGCAAGAGTGTGAGAAAGCTTACCCGGCAACATCACAGAC 660  
 OY 764 ATGGTGTGTCCAGCTGTGAGAAAGGGGGCAAGAGACTCTGCAAGGGTGACTCCGGGGG 823  
 DB 661 ATGGTGTGTCCAGCTGTGAGAAAGGGGGCAAGAGACTCTGCAAGGGTGACTCCGGGGG 720  
 OY 824 CTTCTGTGTGTGAACAGCTCTCTTCAAGAGCATATCTCTGCGGCCAGAGATCGGTGCG 883  
 DB 721 CTTCTGTGTGTGAACAGCTCTCTTCAAGAGCATATCTCTGCGGCCAGAGATCGGTGCG 780  
 OY 884 ATCACCGGAAGGCTGTGTCTCTACAGAAAGTGTGCAAAATATGTGGATGATCCAGGAG 943  
 DB 781 ATCACCGGAAGGCTGTGTCTCTCTACAGAAAGTGTGCAAAATATGTGGATGATCCAGGAG 840  
 OY 944 ACGATGAAGAACAATTAGATGAGACCCACACAGCCATACCTTCATTTCCACT 1003  
 DB 841 ACGATGAAGAACAATTAGATGAGACCCACACAGCCATACCTTCATTTCCACT 900  
 OY 1004 TGGTGTTTGGTCTCTGTTCACTCTGTTAATGAAGAACCTTAAGCAAGACCTCTAGCA 1063



16-AUG-2001; 2001US-0931836.  
 19-DEC-2001; 2001US-0028072.  
 (GETH ) GENENTECH INC.  
 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,  
 Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,  
 Smith V, Stewart JA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 WPI: 2003-148238/14.  
 P-PSDB: ABUS95903.  
 Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 are therapeutically useful for enhancing immune response and in cancer  
 treatments.  
 Claim 2; Fig 505; 659pp; English.  
 The invention describes an isolated human PRO polypeptide. The PRO  
 polypeptides are useful in detecting PRO polypeptides in a sample, in  
 linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 in modulating at least one biological activity of a cell expressing a PRO  
 polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
 stimulate adrenal cortical capillary endothelial growth and PRO536,  
 PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 useful for treating conditions or disorders where angiogenesis would be  
 beneficial, e.g. wound healing and antagonist of this polypeptide are  
 useful for treating cancerous tumours. PRO812 inhibits vascular  
 endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 cells and is thus useful for inhibiting endothelial cell growth in  
 mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 stimulated T-lymphocytes and are therapeutically useful for enhancing  
 immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of  
 retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 rod photoreceptor cells) and therefore are useful for treating retinal  
 disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 and therefore are useful for treating kidney disorders associated with  
 decreased mesangial cell function such as Berger disease or other  
 nephropathies associated with dermatitis, herpeticiformis or Crohn's  
 disease. PRO1310, PRO844, PRO1312 and PRO1387 induce the  
 proliferation and/or redifferentiation of chondrocytes in culture and  
 are thus useful for treating sports injuries, and arthritis. This  
 sequence encodes a novel human PRO protein.  
 Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;  
 Query Match 92.1%; Score 1198; DB 25; Length 1204;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-110;  
 Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 104 GTTCCGAGATGACAGAGTGTGAGTGGCTGCGGACTGGAATGATCGGCGAGAGTCTC 163  
 1 GTTCCGAGATGACAGAGTGTGAGTGGCTGCGGACTGGAATGATCGGCGAGAGTCTC 60  
 164 ACAGCAGCCCAAGAACCTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCTGCAG 223  
 61 ACAGCAGCCCAAGAACCTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCTGCAG 120  
 224 TTAATCTGCTTCTCTGCGACACAGGGCTTGTAGGGGGAGACACAGATCATCAAGGG 283  
 121 TTAATCTGCTTCTCTGCGACACAGGGCTTGTAGGGGGAGACACAGATCATCAAGGG 180  
 284 TTGGAGTGAAGCTCACTCCAGCCCTGGCAGGACCCCTGTTGGAAGAGCGGCTA 343  
 181 TTGGAGTGAAGCTCACTCCAGCCCTGGCAGGACCCCTGTTGGAAGAGCGGCTA 240  
 344 CTCTGTGGGGGAGCGCTCATCGCCCGAGATGGCTCTGTACACAGCCCTGCTGCTCAAG 403

241 CTGTGTGGGGGAGCGCTCATCGCCCGACAGATGAGCTCTGTACAGCAGCCCACTGCTCAAG 300  
 404 CCCCCTACATAGTTCACCTGGGGCAGACAACTCCAGAAAGAGAGGGCTGTGACAG 463  
 301 CCCCCTACATAGTTCACCTGGGGCAGACAACTCCAGAAAGAGAGGGCTGTGACAG 360  
 464 ACCCGAGACGCACTGAGTCTTCCCGACCCCGCTTCAACAAACAGCCTCCCAACAA 523  
 361 ACCCGAGACGCACTGAGTCTTCCCGACCCCGCTTCAACAAACAGCCTCCCAACAA 420  
 524 GACACCGCAATGACATCATCTGTTGTAAGATGGCAATCCGCAATGCTCATCTGGGCT 583  
 421 GACACCGCAATGACATCATCTGTTGTAAGATGGCAATCCGCAATGCTCATCTGGGCT 480  
 584 GTGGACCCCTTACCTCTCTCAAGCTGTGTCTGCTGCTGACACAGCTGCTCATTTCC 643  
 481 GTGGACCCCTTACCTCTCTCAAGCTGTGTCTGCTGCTGACACAGCTGCTCATTTCC 540  
 644 GGTGGGGGAGCAGCTCCAGCCCGCTTACGCTGCTTCAACCTTGGATGGCGCAAC 703  
 541 GGTGGGGGAGCAGCTCCAGCCCGCTTACGCTGCTTCAACCTTGGATGGCGCAAC 600  
 704 ATCAGCATATTGACACAGAAAGTGTAGAAAGCCCTTACCCCGCAATCATCAGAAC 763  
 601 ATCAGCATATTGACACAGAAAGTGTAGAAAGCCCTTACCCCGCAATCATCAGAAC 660  
 764 ATGATGTGTGACAGCTGTGACAGAAAGGGGCAAGACTCTGCGAGGGTGAATCCGGGG 823  
 661 ATGATGTGTGACAGCTGTGACAGAAAGGGGCAAGACTCTGCGAGGGTGAATCCGGGG 720  
 824 CCTGTGTGTGTACAGCTGTCTTCAAGGCAATATCTCTGCGGGCCAGATCCGTGTGCG 883  
 721 CCTGTGTGTGTACAGCTGTCTTCAAGGCAATATCTCTGCGGGCCAGATCCGTGTGCG 780  
 884 ATCAGCGAAAGCTGTGTGTACAGAAAGTGTGCAATATGAGTGTGATGATCCAGAG 943  
 781 ATCAGCGAAAGCTGTGTGTGTACAGAAAGTGTGCAATATGAGTGTGATGATCCAGAG 840  
 944 ACAGTGAAGAACATTAATGACTGACCCAGCCACAGCCCATCCCTCATTTCCACT 1003  
 841 ACAGTGAAGAACATTAATGACTGACCCAGCCACAGCCCATCCCTCATTTCCACT 900  
 1004 TGGGT 1063  
 901 TGGGT 960  
 1064 CATCTTTGGGCTCTGCTGACTACAGAGATGCTGCTTAATTAATCACTGGGGTTC 1123  
 961 CATCTTTGGGCTCTGCTGACTACAGAGATGCTGCTTAATTAATCACTGGGGTTC 1020  
 1124 GAATTCAGTACAGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1183  
 1021 GAATTCAGTACAGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1080  
 1184 ACACCTGGT 1243  
 1081 ACACCTGGT 1140  
 1244 AGGTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1301  
 1141 AGGTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1198  
 RESULT 14  
 ABR92131  
 ID ABR92131 standard; DNA: 1186 BP.  
 XX ABR92131;  
 AC ABR92131;  
 DX 15-AUG-2002 (first entry)  
 XX  
 DE Prostate cancer-associated DNA sequence #17.  
 XX

KW prostate cancer; prostate tumour tissue; human; mammal; cytostatic;  
KM gene therapy; gene; ds.  
XX  
OS Mammalia.  
XX  
PN WO200230268-A2.  
XX  
PD 18-APR-2002.  
XX  
PF 12-OCT-2001; 2001WO-US32045.  
XX  
PR 13-OCT-2000; 2000US-0687576.  
PR 08-DEC-2000; 2000US-0733288.  
PR 08-DEC-2000; 2000US-0733742.  
PR 24-JAN-2001; 2001US-263957P.  
PR 16-MAR-2001; 2001US-276791P.  
PR 16-MAR-2001; 2001US-276888P.  
PR 06-APR-2001; 2001US-281922P.  
PR 24-APR-2001; 2001US-286214P.  
PR 30-APR-2001; 2001US-0847046.  
PR 04-MAY-2001; 2001US-288589P.  
XX  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
PI Gish KC, Mack DH, Wilson KE, Afar D, Hervezi P;  
XX  
DR WPI: 2002-471335/50.  
XX P-PSDB; AB661816.  
XX  
PT Detecting a prostate cancer-associated transcript in a cell in a  
PT patient, useful for diagnosing prostate cancer (PC) or screening  
PT modulators of PC, by determining if prostate cancer-associated genes  
PT are expressed in a prostate tissue  
XX  
PS Claim 22; Page 313; 436pp; English.  
XX  
CC The present invention relates to methods of detecting a prostate  
CC cancer-associated transcript in a cell from a patient. The method  
CC comprises contacting a biological sample from the patient with  
CC prostate cancer-associated polynucleotides (designated PC genes) that  
CC selectively hybridise to a sequence that is at least 80% identical  
CC to them. The prostate cancer-associated polynucleotide sequences  
CC are differentially expressed in prostate tumour tissue or in  
CC prostate cancer and are derived from the tissues of various  
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).  
CC The methods of the invention are useful for diagnosing and treating  
CC prostate cancer in mammals. The prostate cancer-associated genes are  
CC useful for diagnosing or treating prostate cancer, as well as for  
CC identifying modulators of prostate cancer or agents that inhibit  
CC prostate cancer. The nucleic acid sequences are particularly useful  
CC in gene therapy, as a vaccine or in antisense applications.  
CC ABK2115-ABK92263 represent prostate cancer-associated polynucleotide  
CC sequences.  
XX  
SQ Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 other;

Query Match 90.9%; Score 1183; DB 24; Length 1186;  
Best Local Similarity 100.0%; Pred. No. 1.2e-207;  
Matches 1183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 AGGAATTCGCGCTCGGTTCCGACATGCAGAGTTGAGGTGGCTGCGGAGCTGGAATC 147  
DB 1 AGGAATTCGCGCTCGGTTCCGACATGCAGAGTTGAGGTGGCTGCGGAGCTGGAATC 60  
QY 148 ATCGGGCAGAGGTCACAGCAGCAAGGAACCTGGGGCCGCTCTCCCTCCAGGC 207  
DB 61 ATCGGGCAGAGGTCCTCACAGCAGCAAGGAACCTGGGGCCGCTCTCCCTCCAGGC 120  
QY 208 CATGAGATTCGTGCAATTATCTCTGCTCTGGCAACAGAGGCTGTAGGGGAGAGAC 267  
DB 121 CATGAGATTCGTGCAATTATCTCTGCTCTGGCAACAGAGGCTGTAGGGGAGAGAC 180  
QY 268 CAGGATCATCAAGGGGTTGAGTGCAGAGCCTCATCCAGCCCTTGACAGGACGCCCTGTT 327

DB 181 CAGGATCATCAAGGGGTTGAGTGCAGAGCCTCATCCAGCCCTTGACAGGACGCCCTGTT 240  
QY 328 CGAGAAGACGCGCTACTCTGTGGGGGAGACGGCTCATGCCCCAGATGGCTCTGCACG 387  
DB 241 CGAGAAGACGCGGCTACTCTGTGGGGGAGACGGCTCATGCCCCAGATGGCTCTGCACG 300  
QY 388 AGCCCACTGCTCAAGCCCGGCTACATAGTTGACCTGGGGGAGACACAACTCCAGAGA 447  
DB 301 AGCCCACTGCTCAAGCCCGGCTACATAGTTGACCTGGGGGAGACACAACTCCAGAGA 360  
QY 448 GGAGGGCTGTGAGCAGACCCGAGACCCACTGAGTCTTCCCCACCCCGCTTCAACA 507  
DB 361 GGAGGGCTGTGAGCAGACCCGAGACCCACTGAGTCTTCCCCACCCCGCTTCAACA 420  
QY 508 CAGCCTCCCAACAAAGACACCGCAATGATCATGCTGGGGAAGATGGCATTCGCAAT 567  
DB 421 CAGCCTCCCAACAAAGACACCGCAATGATCATGCTGGGGAAGATGGCATTCGCAAT 480  
QY 568 CTCATATCACTGGGCTGTGCGACCCCTCACCTCTCTCAGCCTGTGTCAGTGTGCAC 627  
DB 481 CTCATATCACTGGGCTGTGCGACCCCTCACCTCTCTCAGCCTGTGTCAGTGTGCAC 540  
QY 628 CAGCTGCTCATTTCCGGCTGGGGGAGACAGCTTCAGACCCCAAGTTACGCTCTCAC 687  
DB 541 CAGCTGCTCATTTCCGGCTGGGGGAGACAGCTTCAGACCCCAAGTTACGCTCTCAC 600  
QY 688 CTTGGATCGGCAACATCATCATATGAGGACCCAGAGTGGAGAAAGCCCTACCCGG 747  
DB 601 CTTGGATCGGCAACATCATCATATGAGGACCCAGAGTGGAGAAAGCCCTACCCGG 660  
QY 748 CAACATCACAGACACCAGTGTGTGCCAGCGTGCAGGAAGGGGGCAAGACTCTGCCA 807  
DB 661 CAACATCACAGACACCAGTGTGTGCCAGCGTGCAGGAAGGGGGCAAGACTCTGCCA 720  
QY 808 GGGTACATCCGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 867  
DB 721 GGGTACATCCGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780  
QY 868 CCAGATCCGTTGGGATCACCCGAAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 927  
DB 781 CCAGATCCGTTGGGATCACCCGAAAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 840  
QY 928 GGACTGTATCCAGAGACGATGAAGAACATTAAGACTGAGCCACACACAGCCCATC 987  
DB 841 GGACTGTATCCAGAGACGATGAAGAACATTAAGACTGAGCCACACACAGCCCATC 900  
QY 988 ACCCTCATTTCCACTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1047  
DB 901 ACCCTCATTTCCACTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960  
QY 1048 CAAGACCCCTTCAAGAACATCTTTGGGCTCCTGTGACATGAGAGATGCTGCATTAT 1107  
DB 961 CAAGACCCCTTCAAGAACATCTTTGGGCTCCTGTGACATGAGAGATGCTGCATTAT 1020  
QY 1108 AATCAACCTGGGGTTCGAATCAGTGAACCTGATTCGAATTCCTGCTTGAATATTGT 1167  
DB 1021 AATCAACCTGGGGTTCGAATCAGTGAACCTGATTCGAATTCCTGCTTGAATATTGT 1080  
QY 1168 GACTCTGGGAATGACAAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1227  
DB 1081 GACTCTGGGAATGACAAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140  
QY 1228 TCCCTGGCAATATCAAGGTTTCATTAATATTTCTTAATGA 1270  
DB 1141 TCCCTGGCAATATCAAGGTTTCATTAATATTTCTTAATGA 1183

RESULT 15  
ABX76468  
ID ABX76468 standard; DNA: 1186 BP.  
XX  
AC ABX76468;



XX 02-APR-2003 (first entry)  
 XX Lung cancer-associated polynucleotide #332.  
 DE  
 XX  
 KW Lung cancer-associated polynucleotide; gene: ds; cytostatic; emphysema;  
 KW antiinflammatory; antileukemic; non-small cell lung cancer; atelectasis;  
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
 XX  
 OS Unidentified.  
 XX  
 PN W0200286443-A2.  
 PD 31-OCT-2002.  
 XX  
 PF 18-APR-2002; 2002WO-US12476.  
 XX  
 PR 18-APR-2001; 2001US-284770P.  
 PR 10-MAY-2001; 2001US-290492P.  
 PR 09-NOV-2001; 2001US-339245P.  
 PR 13-NOV-2001; 2001US-350666P.  
 PR 29-NOV-2001; 2001US-334370P.  
 PR 12-APR-2002; 2002US-372246P.  
 PA (BOSB-) BOS BIOTECHNOLOGY INC.  
 PI Aziz N, Murray R;  
 XX WPI: 2003-093161/08.  
 DR P-PSDB; ABUS6739.  
 XX  
 PT Detecting a lung cancer-associated transcript in a cell from a patient  
 PT for treating lung cancer, by contacting a biological sample from the  
 PT patient with a polynucleotide that exhibits increased or decreased  
 PT expression in lung cancer -  
 PS  
 PS Claim 22; Page 443; 453pp; English.  
 XX  
 CC The invention relates to a method for detecting a lung cancer-associated  
 CC transcript in a cell from a patient, comprising contacting a biological  
 CC sample from the patient with a polynucleotide that selectively hybridises  
 CC to a sequence that is at least 80 % identical to a gene that exhibits  
 CC increased or decreased expression in lung cancer samples. Lung  
 CC cancer-associated polynucleotides and polypeptides are used for  
 CC identifying a compound that modulates a lung cancer-associated  
 CC polypeptide, for inhibiting proliferation of a lung cancer-associated  
 CC cell to treat lung cancer in a patient and for treating a mammal having  
 CC lung cancer by administering a modulatory compound identified. The  
 CC methods are useful for treating lung cancer, such as small cell lung  
 CC cancer, non-small cell lung cancer or other benign or precancerous  
 CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive  
 CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial  
 CC and polypeptides are useful for diagnostic purposes and as targets for  
 CC screening for therapeutic compounds that modulate lung cancer, such as  
 CC antiproliferatives. Sequences ABX76124-ABX76474 represent lung cancer-associated  
 CC polynucleotides of the invention.  
 CC  
 SO Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 other;  
 Query Match 90.9%; Score 1183; DB 25; Length 1186;  
 Best local similarity 100.0%; Pred. No. 1.2e-207;  
 Matches 1183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 88 AGGAATCTGGCTCGGCTTCCGAGATGCGAGGTGAGTGGCTGCGGAGCTGGAATC 147  
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Thu Oct 16 09:48:33 2003

us-09-856-320a-1.rmg

Page 21

Search completed: October 15, 2003, 13:18:30  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 15, 2003, 11:00:23 ; Search time 6360.37 Seconds

(without alignments)  
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Perfect score: 1301

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Searched: 288871 segs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

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Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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2	1301	100.0	1301	6	AB041036
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4	1283.4	98.6	1314	6	BD130920
5	1198	92.1	1204	6	AX358932
6	1198	92.1	1204	6	AX362425
7	1198	92.1	1204	6	AX454622
8	1198	92.1	1204	6	AX464372
9	1198	92.1	1204	6	AX491100
10	1198	92.1	1204	6	AX697101
11	1181.4	90.8	1186	6	AB012917
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13	1150	88.4	1158	6	BD137020
14	1114.4	85.7	1192	6	AR152174
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16	1108.8	85.2	1191	6	BD139483
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## ALIGNMENTS

RESULT 1	BD091587	1301 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD091587				
DEFINITION	Novel serine protease BSSP.				
ACCESSION	BD091587				
VERSION	BD091587.1	GI:22637198			
KEYWORDS	WO 0031257-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	Uemura,H., Okui,A., Komianml,K., Yamaguchi,N. and Mitsui,S.				
JOURNAL	Novel serine protease BSSP				
	Patent: WO 0031257-A 1 02-JUN-2000;				



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BASE COUNT 332 a 387 c 330 g 252 t

ORIGIN

Query Match 100.0%; Score 1301; DB 9; Length 1301;  
Best Local Similarity 100.0%; Pred. No. 1.6e-301;  
Matches 1301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

AR098430 1314 bp DNA linear PAT 14-FEB-2001

LOCUS AR098430

DEFINITION Sequence 2 from patent US 6075136.

ACCESSION AR098430

VERSION AR098430.1 GI:12807687

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1314)

AUTHORS Tang, Y. Tom., Corley, N.C. and Guegler, K.J.

TITLE Prostate-associated serine protease

JOURNAL Patent: US 6075136-A 2 13-JUN-2000;

FEATURES

Location/Qualifiers

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BASE COUNT 320 a 400 c 337 g 257 t

ORIGIN

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DB 76 ACTGAAACAAACAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 135

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DEFINITION	Serine protease relating to human prostate.				
ACCESSION	BD130920				
VERSION	BD130920.1	GI:23225865			
KEYWORDS	JP 2002503471-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	Tang,T.Y., Corley,N.C. and Guegler,R.J.				
TITLE	Serine protease relating to human prostate				
JOURNAL	Patent: JP 2002503471-A 1, 05-FEB-2002;				
COMMENT	INCYTE PHARMACEUTICALS INC				
	OS Homo sapiens (human)				
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	PF 17-FEB-1998 US 09/025059				
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QY 721 CCAGAAAGTGTGAAGAGCCCTACCCCGGCAACATCATCATCATTTAGTGTGCGACGCT 780  
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LOCUS Sequence 185 from Patent WO0193983.  
DEFINITION AX358932  
ACCESSION AX358932  
VERSION AX358932.1 GI:18675367  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homilidae; Homo.  
REFERENCE  
1 Baker, K.P., Desnoyers, L., Gerltsen, M.E., Goddard, A.,  
AUTHORS

Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
Watanabe, C.K. and Wood, W.I.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0193983-A 185 13-DEC-2001;  
Genentech Inc. (US)  
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Location/Qualifiers  
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BASE COUNT 306 a 364 c 294 g 240 t  
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Query Match 92.1%; Score 1198; DB 6; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 8.9e-277; Mismatches 0; Indels 0; Gaps 0;  
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LOCUS Sequence 185 from Patent WO0208288.  
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ACCESSION AX362425  
VERSION AX362425.1 GI:18694670  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
Godowski, P., U., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
Watanabe, C.K., and Wood, W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0208288-A 185 31-JAN-2002;  
Genentech, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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BASE COUNT 306 a 364 c 294 g 240 t  
ORIGIN

Query Match 92.1%; Score 1198; DB 6; Length 1204;  
Best Local Similarity 100.0%; Pred. No. 8.9e-277;  
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 GTTCCGCAATGACAGAGTTGAGTGGCTCGCGGACTGGAATGATCGGGCAGAGTCTC 163  
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LOCUS Sequence 207 from Patent WO0208288.  
DEFINITION AX454622  
ACCESSION AX454622  
VERSION AX454622.1 GI:21713935  
KEYWORDS  
SOURCE Homo sapiens (human)

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ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
Baker, R.P., Ferrara, N., Gerber, H., Gerlitsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE          Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL        Patent: WO 0208284-A 207 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerlitsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
FEATURES       Location/Qualifiers
source         1..1204
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BASE COUNT     306 a 364 c 294 g 240 t
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Query Match    92.1%; Score 1198; DB 6; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.9e-277;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
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LOCUS      AX464372
DEFINITION Sequence 505 from Patent WO0140466.
ACCESSION AX464372
VERSION    AX464372.1 GI:21899202
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
1
Baker, R.P., Beresini, M., DeForge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.O., Gerlitsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tamas, D., Watanabe, C.K.,
Wood, W.I. and Zhang, Z.
TITLE       Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL     Patent: WO 0140466-A 505 07-JUN-2001;
Genentech Inc. (US)
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source      1..1204
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BASE COUNT  306 a 364 c 294 g 240 t
ORIGIN
Query Match    92.1%; Score 1198; DB 6; Length 1204;
Best Local Similarity 100.0%; Pred. No. 8.9e-277;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 GTTCCGAGATGCAAGGTTGAGTGCTGCGGAGCTGAGATCATCGGGCAGAGTCTC 163
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LOCUS Sequence 207 from Patent WO0200690.  
DEFINITION AX491100  
ACCESSION AX491100  
VERSION AX491100.1 GI:22323887  
KEYWORDS  
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ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
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AUTHORS Baker K.P., Ferrara N., Gerber H., Gertlisen M.E., Goddard A.,  
Godowski P.J., Gurney A.L., Hillan K.J., Marsters S.A., Pan J.,  
Pohl N.F., Stephan J.P., Watanabe C.K., Williams P.M., Wood W.I.  
and Ye W.  
TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
JOURNAL Patent: WO 0200690-A 207 03-JAN-2002;  
Genentech, Inc. (US)  
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VERSION AX697101.1 GI:29498066  
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REFERENCE  
AUTHORS Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,  
Eaton, D.L., Gao, W.O., Pan, J., Botstein, D., Fong, S., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Smith, V., Tumas, D., Wood, R.I.,  
Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A. and Watanabe, C.K.  
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ACCESSION ABO12917.1 GI:3649790  
VERSION ABO12917.1 GI:3649790  
KEYWORDS TLSP, serine protease (TLSP).  
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REFERENCE 1  
AUTHORS Yoshida,S., Taniguchi,M., Suemoto,T., Oka,T., He,X. and Shiosaka,S.  
TITLE CDNA cloning and expression of a novel serine protease, TLSP  
JOURNAL Biochim. Biophys. Acta 1399 (2-3), 225-228 (1998)  
MEDLINE 98438738  
PUBMED 9765601  
REFERENCE 2 (bases 1 to 1186)  
AUTHORS Yoshida,S.  
TITLE Direct Submission  
SUBMITTED (10-APR-1998) Shigetaka Yoshida, Department of Anatomy 1,  
Aashikawa Medical College, Midorigaoka Higashi 2-1-1, Aashikawa,  
Hokkaido 078-8510, Japan (E-mail: syoshida@aashikawa-med.ac.jp,  
Tel:81-166-2300, Fax:81-166-68-2309)  
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AUTHORS	1 (bases 1 to 1213)		
TITLE	Strausberg,R.		
JOURNAL	Direct Submission		
REMARK	Submitted (22-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
COMMENT	NIH-MGC Project URL: http://mgc.ncl.nih.gov		
	Contact: MGC help desk		
	Email: cgapsb-re@mail.nih.gov		
	Tissue Procurement: Miklos Palkovits, M.D., Ph.D.		
	cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shitaki Toshituki and Piero Carninci (RIKEN)		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		

DNA Sequencing by: Institute for Systems Biology  
http://www.systemsbio.org  
contact: amadan@systemsbiology.org  
Anup Madan, Jessica Fahey, Erin Heltan, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 46 Row: m Column: 6  
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Db 638 TTGAGCACACAGAGTGTGAGAACGCTACCCGGCAACATCACAGACACATGGTGTG 697
QY 774 CCACGTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 833
Db 698 CCACGTCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 757
QY 834 GTACCCAGTCTCTCAAGCATTTATCTGCTGGGGCCAGATCCGTGTGATCAACCCGA 893
Db 758 GTACCCAGTCTCTCAAGCATTTATCTGCTGGGGCCAGATCCGTGTGATCAACCCGA 817
QY 894 AGCCTGTGTCTACAGCAAAAGTGTCAAAATGTGACTGTGATCCAGAGAGATGAAGA 953
Db 818 AGCCTGTGTCTACAGCAAAAGTGTCAAAATGTGACTGTGATCCAGAGAGATGAAGA 877
QY 954 ACAATTAGACTGTGACCCACACACACACACACACACACACACACACACACACACAC 1013
Db 878 ACAATTAGACTGTGACCCACACACACACACACACACACACACACACACACACACAC 937
QY 1014 TTCTGTCTCACTGTTAATAAAGAAACCTTAAGCCAGACCCCTACAGAACATCTTGG 1073
Db 938 TTCTGTCTCACTGTTAATAAAGAAACCTTAAGCCAGACCCCTACAGAACATCTTGG 997
QY 1074 GCTCTCTGACTACAGAGATGTGTCACTTAATAATCAACCTGGGTTGMAATCAAGTG 1133
Db 998 GCTCTCTGACTACAGAGATGTGTCACTTAATAATCAACCTGGGTTGMAATCAAGTG 1057
QY 1134 AGACCTGGATTCAAAATCTGCTGAATATGTGACTCTGGGAATGACACACACTGGTT 1193
Db 1058 AGACCTGGATTCAAAATCTGCTGAATATGTGACTCTGGGAATGACACACACTGGTT 1117
QY 1194 TGTCTCTGTGTATPCCCAAGCCCAAGACAGCTCTGGCCATATATCAAGTTCAAT 1253
Db 1118 TGTCTCTGTGTATPCCCAAGCCCAAGACAGCTCTGGCCATATATCAAGTTCAAT 1177
QY 1254 AAATATTGCTAAATGAAAAAAAAAAAAAAAAAAAA 1289
Db 1178 AAATATTGCTAAATGAAAAAAAAAAAAAAAAAAAA 1213
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Search completed: October 15, 2003, 16:00:41  
Job time : 6365.87 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 15, 2003, 20:25:46 ; Search time 169.824 Seconds  
(without alignments)  
2468.773 Million cell updates/sec

Title: US-09-856-320A-1  
Perfect score: 2370  
Sequence: 1 cgcctctgcacacacctg.....aaaaaaaaaaaaaaaaaa 1301

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 1201306

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -DEV-x1p  
-MODE=frame+np.model -DEV-x1p  
-Q/cgcn2.1/USPTO.spool.p/US09856320/rnat.15102003.105642.8657/app.query.fasta.1.2318  
-DB=Published Applications AA -QMT=fastan -SUPER=rapb -MINMATCH=0.1  
-LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bl0sum62  
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR=SCORE=pcr -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09856320.@CGN.1.1.23 @rnat.15102003.105642.8657  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FEAPOP=6 -FEAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications-AA:\*

- 1: /cgcn2.6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgcn2.6/ptodata/1/pubpaa/PTI\_NEW\_PUB.pep.\*
- 3: /cgcn2.6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgcn2.6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgcn2.6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgcn2.6/ptodata/1/pubpaa/PTUS\_PUBCOMB.pep.\*
- 7: /cgcn2.6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgcn2.6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgcn2.6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgcn2.6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgcn2.6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgcn2.6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgcn2.6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 14: /cgcn2.6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgcn2.6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgcn2.6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgcn2.6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgcn2.6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	1355	57.2	250	11	US-09-946-374-170	Sequence 170, App
2	1355	57.2	250	12	US-10-015-387A-170	Sequence 170, App
3	1355	57.2	250	12	US-10-137-870-506	Sequence 506, App
4	1355	57.2	250	12	US-10-140-018-506	Sequence 506, App
5	1355	57.2	250	12	US-10-140-021-506	Sequence 506, App
6	1355	57.2	250	12	US-10-140-274-506	Sequence 506, App
7	1355	57.2	250	12	US-10-140-471-506	Sequence 506, App
8	1355	57.2	250	12	US-10-140-807-506	Sequence 506, App
9	1355	57.2	250	12	US-10-140-922-506	Sequence 506, App
10	1355	57.2	250	12	US-10-140-924-506	Sequence 506, App
11	1355	57.2	250	12	US-10-140-926-506	Sequence 506, App
12	1355	57.2	250	12	US-10-141-698-506	Sequence 506, App
13	1355	57.2	250	12	US-10-141-702-506	Sequence 506, App
14	1355	57.2	250	12	US-10-141-704-506	Sequence 506, App
15	1355	57.2	250	12	US-10-142-421-506	Sequence 506, App
16	1355	57.2	250	12	US-10-142-432-506	Sequence 506, App
17	1355	57.2	250	12	US-10-142-433-506	Sequence 506, App
18	1355	57.2	250	12	US-10-143-033-506	Sequence 506, App
19	1355	57.2	250	12	US-10-144-994-506	Sequence 506, App
20	1355	57.2	250	12	US-10-145-628-506	Sequence 506, App
21	1355	57.2	250	12	US-10-145-631-506	Sequence 506, App
22	1355	57.2	250	12	US-10-145-633-506	Sequence 506, App
23	1355	57.2	250	12	US-10-145-746-506	Sequence 506, App
24	1355	57.2	250	12	US-10-145-748-506	Sequence 506, App
25	1355	57.2	250	12	US-10-145-823-506	Sequence 506, App
26	1355	57.2	250	12	US-10-145-826-506	Sequence 506, App
27	1355	57.2	250	12	US-10-145-870-506	Sequence 506, App
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33	1355	57.2	250	12	US-10-147-495-506	Sequence 506, App
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35	1355	57.2	250	12	US-10-147-504-506	Sequence 506, App
36	1355	57.2	250	12	US-10-147-508-506	Sequence 506, App
37	1355	57.2	250	12	US-10-147-509-506	Sequence 506, App
38	1355	57.2	250	12	US-10-147-511-506	Sequence 506, App
39	1355	57.2	250	12	US-10-147-511-506	Sequence 506, App
40	1355	57.2	250	12	US-10-147-529-506	Sequence 506, App
41	1355	57.2	250	12	US-10-153-397-506	Sequence 506, App
42	1355	57.2	250	12	US-10-153-586-506	Sequence 506, App
43	1355	57.2	250	12	US-10-158-783-506	Sequence 506, App
44	1355	57.2	250	12	US-10-158-786-506	Sequence 506, App
45	1355	57.2	250	12	US-10-006-130A-170	Sequence 170, App

ALIGNMENTS

RESULT 1  
US-09-946-374-170  
; Sequence 170, Application US/09946374  
; Publication No. US20030073129A1  
GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillen, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumans, Daniel  
; APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830PICI  
CURRENT APPLICATION NUMBER: US/09/946,374  
PRIOR FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
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PRIOR FILING DATE: 1998-09-29  
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PRIOR APPLICATION NUMBER: 60/102484  
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PRIOR APPLICATION NUMBER: 60/102487  
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PRIOR APPLICATION NUMBER: 60/102684  
PRIOR FILING DATE: 1998-10-01  
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PRIOR FILING DATE: 1998-10-02  
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PRIOR APPLICATION NUMBER: 60/103314  
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PRIOR APPLICATION NUMBER: 60/103395  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103396

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; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
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; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
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; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

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## Alignment Scores:

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Pred. No.: 1.85e-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 11 Gaps: 0

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US-09-856-320A-1 (1-1301) x US-09-946-374-170 (1-250)

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QY 209 ATGAGGATTCGTGACGTTAATCTGCTGCTGGCAACAGGGCTGTAGGGGAGAGACC 268
DB 1 MetArgileLeuGlnleuileuLeuAlaLeuAlaThrglyLeuValglyglutrr 20
QY 269 AGGATCATCAAGGGGTTCAGTGCAGCAAGCTCACTCCGCGGAGGACGCCCTGTTC 328
DB 21 ArgilelleuysglyPheglucyslySPronHisSerGlnProtrpGlnAlaLeuPhe 40
QY 329 GAGAAAGCGGGCTACTGTGTGGGGGAGCTATCGCCCGCCAGATGGCTCCTGACAGCA 388
DB 41 GlulysThrArgleuLeucysglyAlaThrleuileAlaProArgtrpLeuThrAla 60
QY 389 GCGCCACTGGCTCAAGCGCCGCTACATAGTTCACCTGGGGCAGACAACTCCAGAGAG 448
DB 61 AlaHisCysleuIlyProArgtrpIlyValHisleuGlyGlnHisasnleuGlnIlyGlu 80
QY 449 GAGGGCTGTGACAGACCGGACAGCAAGCTGAGTCTCCCGACCGCGGCTTCAACAC 508
DB 81 GlulysCysgluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheasnAn 100
QY 509 AGCCTCCCCCAACAAAGACCCGCAATGACATCATGCTGGTGAAGATGGCATCGCCAGTC 568
DB 101 SerleuProasnIlyAspHisArgasnAspIleMetleuValIlyMetAlaSerProVal 120
QY 569 TCCATTCACCTGGGTGTGGGACCCCTCACCTCTCTCTCAAGCTGTGTCACTGCTGGAC 628
DB 121 SerIleThrTrpAlaValArgProleuThrleuSerSerArgCysValThrAlaGlyThr 140
QY 629 AACTGCTTCATTTCCGGCTGGGGGAGACAGCTACGCCCCCAATGAGCTGCTGACACAC 688

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DB 141 SerCysleuIleSerlyTrpIlySerThrSerSerProGlnleuArgleuProHisThr 160
QY 689 TTGCGATGGCCCAATACATCACCATTCATGAGCACCAGAGTGTGAGAACGCTACCCGGC 748
DB 161 LeuArgCysAlaasnIleThrIleIleGlnHisGlnIlyCysGlnAsnAlaIlyProGly 180
QY 749 AACATCAGACACACATGCTGTGTGCACGCTGACAGGAAGGGGCAAGCACTCTCCAG 808
DB 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlyIlyAspSerCysGln 200
QY 809 GGTGATCCGGGGGCGCCCTGTGCTGTATACCATCTCTTCAGAGCATTCCTCTGGGC 868
DB 201 GlyAspSerGlyIlyProleuValCysasnGlnSerleuGlnIlyIleSerIlyGly 220
QY 869 CAGATCCGTGTGCGATCACCCGAAAGCCTGTGTGTACAGCAAGTCTGCAATATGTG 928
DB 221 GlnAspProCysAlaIleThrArgIlySPronGlyValIlyThrIlyValCysIlySTryVal 240
QY 929 GACTGATCCAGAGACGATGAAGAACAT 958
DB 241 AspTrpIleGlnGlnThrMetIlyAsnAn 250

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## RESULT 2

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US-10-015-387A-170
; Sequence 170, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoli, Nicholas F.

```

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 170
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-387A-170

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## Alignment Scores:

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Pred. No.: 1.85e-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 12 Gaps: 0

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US-09-856-320A-1 (1-1301) x US-10-015-387A-170 (1-250)

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DB 1 MetArgileLeuGlnleuileuLeuAlaLeuAlaThrglyLeuValglyglutrr 20
QY 269 AGGATCATCAAGGGGTTCAGTGCAGCAAGCTCACTCCGCGGAGGACGCCCTGTTC 328
DB 21 ArgilelleuysglyPheglucyslySPronHisSerGlnProtrpGlnAlaLeuPhe 40
QY 329 GAGAAAGCGGGCTACTGTGTGGGGGAGACGCTATCGCCCGCCAGATGGCTCCTGACAGCA 388

```

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Db 41 GlnuylstrArgrleuLeuCysGlyAlaThrIleuIleAlaProArgrTrpleuLeuThrAla 60
OY 389 GCCCACTGCTCAAGCCCCGCTACATAGTCACTGGGGAGACACCTCCAGAAAGAG 448
Db 61 AlaHtScylsleuLysProArgrTrIleValHtIsleuGlyGlnHtAsnIleuGlnLysGlu 80
OY 449 GAGGGCTGTGAGCAGACCCGGACAGACCACTAGTCTTCCGCCACCCGGCTTCAACAC 508
Db 81 GluGlyCysGluGlnThrArgThrAlaThrGlnSerPheProHtIsProGlyPheAsnAsn 100
OY 509 AGCTTCCCAACAAAGACCCCAATGACATGCTGCGTGAAGATGGCATCGCCATC 568
Db 101 SerIeuProAsnLysAspHtIsArgAsnAspIleMetIleuValLysMetAlaSerProVal 120
OY 569 TCCATACACTGGGTGTGCGACCCCTCACCTTCCTCAGCTGTCAGTGTGCGAC 628
Db 121 SerIleThrTrpAlaValArgProIeuThrIeuSerSerArgCysValThrAlaGlyThr 140
OY 629 AGCTGCTCATTTCCGGCTGGGGGACAGACGTCACAGCCCCAGTTACGCTTCCACAC 688
Db 141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnIleuArgLeuProHtIsThr 160
OY 689 TTGGCATCGCCCAACATCACCATCATTTGAGCAGCAGAAAGTGTGAAGAGCCGACCCGCG 748
Db 161 LeuArgCysAlaAsnIleThrIleIleGlnHtIsGlnLysCysGlnAsnAlaTrpProGly 180
OY 749 AACATCAGACAGACCCATGTTGTGTGCCAGCTGACAGAAAGGGGACAGATCTGCGAC 808
Db 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnLysGlyLysAspSerCysGln 200
OY 809 GGTGACTCCGGGGGCGCTGTGTCTGTACACAGTCTCTTCAAGCATTAATCTCGGGGCG 868
Db 201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerIeuGlnGlyIleIleSerTrpGly 220
OY 869 CAGATCCGTTGGGATCACCAGCCGGAAGGCTGTGTCTTCAAGAAAGTGTGCAAAATATG 928
Db 221 GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpVal 240
OY 929 GACTGATCCAGAGACGATGAAGACAAT 958
Db 241 AspTrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 3
US-10-137-870-506
; Sequence 506, Application US/10137870
; Publication No. US20030138883A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P33081C15
; CURRENT APPLICATION NUMBER: US/10/137,870
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
```

```
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-870-506

Alignment Scores:
Pred. No.: 1,85e-87
Score: 1355.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 57.17%
Db: 12 Gaps: 0

US-09-856-320a-1 (1-1301) x US-10-137-870-506 (1-250)

OY 209 ATGAGGATTCGACAGTTAATCTGCTGTGCAACAGGGGCTTGAAGGGGAGAGACC 268
Db 1 MetArgIleLeuGlnIleuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyThr 20
OY 269 AGGATCATCAAGGGGTTTCAGTGCAGACCTTCACAGCCCTGCGAGGACGCGCTTTC 328
Db 21 ArgIleIleLysGlyPheGlnCysLysLysProHtIsSerGlnProTrpGlnAlaLeuPhe 40
OY 329 GAGAAGACGGGCTACCTGTGTGGGGGCGACGTCATCGCCCAATGGCTTCTACAGCA 388
Db 41 GlnuylstrArgrleuLeuCysGlyAlaThrIleuIleAlaProArgrTrpleuLeuThrAla 60
OY 389 GCCCACTGCTCAAGCCCCGCTACATAGTCACTGGGGAGACACCTCCAGAAAGAG 448
Db 61 AlaHtScylsleuLysProArgrTrIleValHtIsleuGlyGlnHtAsnIleuGlnLysGlu 80
OY 449 GAGGGCTGTGAGCAGACCCGGACAGACCACTAGTCTTCCGCCACCCGGCTTCAACAC 508
Db 81 GluGlyCysGluGlnThrArgThrAlaThrGlnSerPheProHtIsProGlyPheAsnAsn 100
OY 509 AGCTTCCCAACAAAGACCCCAATGACATGCTGCGTGAAGATGGCATCGCCATC 568
Db 101 SerIeuProAsnLysAspHtIsArgAsnAspIleMetIleuValLysMetAlaSerProVal 120
OY 569 TCCATACACTGGGTGTGCGACCCCTCACCTTCCTCAGCTGTCAGTGTGCGAC 628
Db 121 SerIleThrTrpAlaValArgProIeuThrIeuSerSerArgCysValThrAlaGlyThr 140
OY 629 AGCTGCTCATTTCCGGCTGGGGGACAGACGTCACAGCCCCAGTTACGCTTCCACAC 688
Db 141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnIleuArgLeuProHtIsThr 160
OY 689 TTGGCATCGCCCAACATCACCATCATTTGAGCAGCAGAAAGTGTGAAGAGCCGACCCGCG 748
Db 161 LeuArgCysAlaAsnIleThrIleIleGlnHtIsGlnLysCysGlnAsnAlaTrpProGly 180
OY 749 AACATCAGACAGACCCATGTTGTGTGCCAGCTGACAGAAAGGGGACAGATCTGCGAC 808
Db 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnLysGlyLysAspSerCysGln 200
OY 809 GGTGACTCCGGGGGCGCTGTGTCTGTACACAGTCTCTTCAAGCATTAATCTCGGGGCG 868
Db 201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerIeuGlnGlyIleIleSerTrpGly 220
OY 869 CAGATCCGTTGGGATCACCAGCCGGAAGGCTGTGTCTTCAAGAAAGTGTGCAAAATATG 928
Db 221 GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpVal 240
OY 929 GACTGATCCAGAGACGATGAAGACAAT 958
Db 241 AspTrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 4
US-10-140-018-506
; Sequence 506, Application US/10140018
; Publication No. US20030138885A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
```



```

APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C158
CURRENT APPLICATION NUMBER: US/10/140,018
PRIORITY FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-018-506

```

```

Alignment Scores:
Pred. No.: 1,856-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 12 Gaps: 0

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US-09-856-320A-1 (1-1301) x US-10-140-018-506 (1-250)

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209 ATGAGGATTCCTGACATTAATCTGCTGCTGCGCAACAGGGCTTGTAGGGGAGAGACC 268
1 MetArgIleLeuGlnLeuIleuLeuAlaLeuAlaThrGlyLeuValGlyGlnThr 20
269 AGGATCATCAAGGGTTGAGTGCAGAGCTCACTCCAGCCCTGGCAGGACCCCTGTTG 328
21 ArgIleIleLeuGlyPheGlnCysIysProHisSerGlnProTyrGlnAlaIleuPhe 40
329 GAGAGAGCGGGCTACTGTGTGGGGGAGCGCTCATCGCCCCAGATGGCTCTGACAGCA 388
41 GlnLysThrArgLeuIleuLeuGlyAlaThrLeuIleAlaProLysTyrLeuIleuThrAla 60
389 GCGCCACTGCTCAAGCCCGCTACATAGTTCACTGGGGCAGACACCTCCAGAGAGAG 448
61 AlaHisCysLeuLeuLysProLysTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGln 80
449 GAGGCTGTGAGCAGACCCGGAGACAGCCAGTCAAGTCTCCCGCCAGCCCGGCTTCAACAAC 508
81 GlnGlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 100
509 AGCCTCCCAACAAGACACCCGCAATGACATCATGCTGGTAAAGTGGCATCCGCGAGTC 568
101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
569 TCCATACACCTGGGCTGTGCGAGCCCTCAAGCTCTGTCAGCGTGTGTCAGCTGTGACAC 628
121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaLysThr 140
629 AGCTGCTCATATTCGGGCTGGGGGAGCAGCTCCAGCCCGCCAGTACGCGCTGCTCAGAC 688
141 SerCysLeuIleSerGlyTyrPheLysThrSerSerProGlnLeuArgLeuProHisThr 160
689 TTGGCATGGCCAAATCATCATCATATGAGACACGAGAGTGTGANAAGCCCTACCCCGGC 748

```

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DB 161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGly 180
QY 749 AACATCAGACACACATGTTGTGTGTCAGCTGCAGAGGGGAGGAGACTCTCCAG 808
DB 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGln 200
QY 809 GGTGACTCCGGGGGCGCTGTGTGTAAACAGTCTTCAAGCAATTAATCTCTGGGGC 868
DB 201 GlyAspSerGlyCysProLeuValCysAsnGlnSerLeuGlnIleIleSerTrpGly 220
QY 869 CAGGATCCGTGCGCATCAACCCGGAAGCCGTGTTGTAAACGAAATGTGCAATATGTCG 928
DB 221 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 240
QY 929 GACTGATCCAGACAGATGAAGAACAT 958
DB 241 AspTrpIleGlnGlnThrMetLysAsnAsn 250

```

RESULT 5  
US-10-140-021-506  
Sequence 506, Application US/10140021  
Publication No. US20030138886A1

```

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C167
CURRENT APPLICATION NUMBER: US/10/140,021
PRIORITY FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-021-506

```

```

Alignment Scores:
Pred. No.: 1,856-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 12 Gaps: 0

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US-09-856-320A-1 (1-1301) x US-10-140-021-506 (1-250)

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209 ATGAGGATTCCTGACATTAATCTGCTGCTGCGCAACAGGGCTTGTAGGGGAGAGACC 268
1 MetArgIleLeuGlnLeuIleuLeuAlaLeuAlaThrGlyLeuValGlyGlnThr 20
269 AGGATCATCAAGGGTTGAGTGCAGAGCTCACTCCAGCCCTGGCAGGACCCCTGTTG 328
21 ArgIleIleLeuGlyPheGlnCysIysProHisSerGlnProTyrGlnAlaIleuPhe 40
329 GAGAGAGCGGGCTACTGTGTGGGGGAGCGCTCATCGCCCCAGATGGCTCTGACAGCA 388

```

```
Db 41 GILVSTHTRARGLEULEUCYSGLYALATHRLEULEALAPROLYGTTPRLEUTHRALA 60
QY 389 GCCCATGCTCTCAAGCCCCGCTACATAGTTCACCTGGGGGAGCAGCAACCTCCAGAAAGAG 448
Db 61 ALAHISCYSLLEULSPROARGTYRILEVALHISLEUGLYGINHISASNLLEUGLNLGSLU 80
QY 449 GAGGGCTGTGAGCAGACCCGAGCAGCCTAGTCCCTTCCCCCAGCCCGGCTTCACACAC 508
Db 81 GILVLYCSGLUGINTHTRARGTHRALATHRGISERPHROHISPROGLYPHASNASHN 100
QY 509 AGCTCCCAACAAGACACCCAGCAATGACATCATGCTGAGATGGCATGCGCACTC 568
Db 101 SERLEUPROASNLYSAPHISARGASNAPRIEMETLEUVALLYSMETALISERPROVAL 120
QY 569 TCCATCACTGGGCTGTGCGACCCCTCAGCCCTCTCAGCTGTGCTACTGTGGCACC 628
Db 121 SERLEUTHTRPALAVALARGPROLEUTHRLEUSERSERARGCYVALTHRALAGLYTHR 140
QY 629 AGCTGCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCGGTTACGCTGCTCCACAC 688
Db 141 SERCYSLEULISERGLYTPRGLYSERTHSERSEPROGLINLEUARGLEUPROHISTHR 160
QY 689 TTGGGATGCGCCACATCACCATCATGATGAGCAGCAGAAAGTGTGAAGCGCTACCGCAGC 748
Db 161 LEUARGCYSAALAHANLIEHTRILLELIEGLINHISGLINLYSCYSLUASNALATYRPROGLY 180
QY 749 AACATCACAGACACCATAGTGTGTGCCAGCGTGCAGAGAGGGGCGCAAGACTCCTCCAG 808
Db 181 ASNLIEHTRAPRTHMETVALCYSAALASERVALGINGLYGLYLSASPSERCYSGLN 200
QY 809 GGTGACTCCGGGGGCGCTGTGCTGTAAACAGTCTCTCAAGCATTAATCTCGGGGC 868
Db 201 GLYSPSERGLYGLYPROLEUVALCYSSASNLISERLEUNGILYLIETLIESERTIPGLY 220
QY 869 CAGGATCCGTGTGGGATCACCCGAAAGCTGTGTCTACAGAAAGTCTGCAAAATATGTG 928
Db 221 GLINSPROCYSAALAIETHTRARGLYSPROGLYVALTYRTHLYSVALCYLSYTYRVAL 240
QY 929 GACTGATCCAGGAGACGATGAAGAACAT 958
Db 241 ASPTRPLEGGLINGLUTRHMETLYSASNASHN 250

RESULT 6
US-10-140-274-506
; Sequence 506, Application US/10140274
; Publication No. US20030143674A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria A.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P333081C161
; CURRENT APPLICATION NUMBER: US/10/140,274
; PRIORITY FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
```

```
; TYPE: PRF
; ORGANISM: Homo Sapien
; US-10-140-274-506

Alignment Scores:
Pred. No.: 1,856-87
Score: 1355.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 57.17%
DB: 12 Gaps: 0

US-09-856-320a-1 (1-1301) x US-10-140-274-506 (1-250)

QY 209 ATGAGGATTTGCAAGTAACTCTGCTTGTGCAACAGAGGCTTGTAGGGGAGAGACC 268
Db 1 METARGILEUGLNLLEULIELEULEVALATHRGILEUVALIGLYGLUTHR 20
QY 269 AGGATCATCAAGGGGTTGAGTGCAGAGCTTCTCCAGCCCTGGCAGGAGCCCTGTTC 328
Db 21 ARGILEIYSGLYPNEGILUCYLYSPROHISSEGINPROTGRGINALALAEUPHE 40
QY 329 GAGAAGAGCGGCTACTGTGGGGGAGCGCTCATGCCGCCAGATGGCTCTGACAGCA 388
Db 41 GILVSTHTRARGLEULEUCYSGLYALATHRLEULEALAPROLYGTTPRLEUTHRALA 60
QY 389 GCCCATGCTCTCAAGCCCCGCTACATAGTTCACCTGGGGGAGCAGCAACCTCCAGAAAGAG 448
Db 61 ALAHISCYSLLEULSPROARGTYRILEVALHISLEUGLYGINHISASNLLEUGLNLGSLU 80
QY 449 GAGGGCTGTGAGCAGACCCGAGCAGCCTAGTCCCTTCCCCCAGCCCGGCTTCACACAC 508
Db 81 GILVLYCSGLUGINTHTRARGTHRALATHRGISERPHROHISPROGLYPHASNASHN 100
QY 509 AGCTCCCAACAAGACACCCAGCAATGACATCATGCTGAGATGGCATGCGCACTC 568
Db 101 SERLEUPROASNLYSAPHISARGASNAPRIEMETLEUVALLYSMETALISERPROVAL 120
QY 101 SERLEUPROASNLYSAPHISARGASNAPRIEMETLEUVALLYSMETALISERPROVAL 120
QY 569 TCCATCACTGGGCTGTGCGACCCCTCAGCCCTCTCAGCTGTGCTACTGTGGCACC 628
Db 121 SERLEUTHTRPALAVALARGPROLEUTHRLEUSERSERARGCYVALTHRALAGLYTHR 140
QY 629 AGCTGCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCGGTTACGCTGCTCCACAC 688
Db 141 SERCYSLEULISERGLYTPRGLYSERTHSERSEPROGLINLEUARGLEUPROHISTHR 160
QY 689 TTGGGATGCGCCACATCACCATCATGATGAGCAGCAGAAAGTGTGAAGCGCTACCGCAGC 748
Db 161 LEUARGCYSAALAHANLIEHTRILLELIEGLINHISGLINLYSCYSLUASNALATYRPROGLY 180
QY 749 AACATCACAGACACCATAGTGTGTGCCAGCGTGCAGAGAGGGGCGCAAGACTCCTCCAG 808
Db 181 ASNLIEHTRAPRTHMETVALCYSAALASERVALGINGLYGLYLSASPSERCYSGLN 200
QY 809 GGTGACTCCGGGGGCGCTGTGCTGTAAACAGTCTCTCAAGCATTAATCTCGGGGC 868
Db 201 GLYSPSERGLYGLYPROLEUVALCYSSASNLISERLEUNGILYLIETLIESERTIPGLY 220
QY 869 CAGGATCCGTGTGGGATCACCCGAAAGCTGTGTCTACAGAAAGTCTGCAAAATATGTG 928
Db 221 GLINSPROCYSAALAIETHTRARGLYSPROGLYVALTYRTHLYSVALCYLSYTYRVAL 240
QY 929 GACTGATCCAGGAGACGATGAAGAACAT 958
Db 241 ASPTRPLEGGLINGLUTRHMETLYSASNASHN 250

RESULT 7
US-10-140-471-506
; Sequence 506, Application US/10140471
; Publication No. US20030138887A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
```

```

APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P33081C163
CURRENT APPLICATION NUMBER: US/10/140,471
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRP
ORGANISM: Homo Sapien
US-10-140-471-506

```

Alignment Scores:	
Pred. No.:	1,856-87
Score:	1355.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	57.17%
DB:	12
	Gaps:
	250
	Matches:
	250
	Conservative:
	0
	Mismatch:
	0
	Indels:
	0
	Gaps:
	0

[illegible]

QY	749	MAATACAGAGACACCATGGTGTGTGTCACAGCGTCGAGAAAGGAGGCAAGATCCTGTCAG	808
Db	181	AsnIleIleHisAspIleMetValCysAlaSerValGlnGlnIuIyGlyLysAspSerCysGln	2007
QY	809	GGHACATCCGAGGGGCCCTCTGGTGTGTACACAGTCTCTTCAAGGCATATATCTCCGTGGGC	868
Db	201	GlyAspSerGlyGlyProIeuValLysAsnGlnSerIeuGlnGlyIleIleIleSerTyrGly	2207
QY	869	CACGATCCGTGTGCATCACCCGAAAGCCGTGGTGTCTACACGAAAGTCTGCAGAAATATGTG	928
Db	221	GlnAspProCysAlaIleIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal	2407
QY	929	GACTGGATCCAGAGACGATGAAGAAACAT	958
Db	241	AspTyrIleGlnGlnIuIleThrMetLysAsnGln	250

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RESULT 8
US-10-140-807-506
; Sequence 506, Application US/10140807
; Publication No. US2003013435A1
; GENERAL INFORMATION:

```

```

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C174
CURRENT APPLICATION NUMBER: US/10/140,807
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien

```

Alignment Scores:			
Pred. No.:	1,85e-87	Length:	250
Score:	1355.00	Matches:	250
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	57.17%	Indels:	0
DB:	12	Gaps:	0
US-09-856-320A-1 (1-1301) x US-10-140-807-506 (1-250)			
QY	209	ATGAGATTCCTGCACTTAATCCTCGTTCCTGGCAACAGGAGCTTGTAGGGGAGAGACC	268
Db	1	MeArgIleLeuGlnLeuIleLeuLeuAlaLeuAlaTrpGlyLeuValGlyGlyGlnTrp	20
QY	269	AGGATATCAAGGGGTTGAGTGCAGACGCTACTCCAGCCCTGGCAGGAGCCCTGTTC	328
Db	21	ArgIleIleIleGlyGlyPheGlnCysLysTrpHisSerGlnProTrpGlnAlaIleLeuPhe	40
QY	329	GAGAGACGGCGCTACTCTGTGGGGCGACGCTCATGCCCCAGATGGCTCTGTGACAGA	388
Db	41	GlnLysTrpArgLeuLeuLeuCysGlyAlaThrLeuIleIleAlaProAlaGlyTrpLeuLeuTrpAla	60



```

: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerlitsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P330R1C177
: CURRENT APPLICATION NUMBER: US/10/140,924
: PRIOR APPLICATION removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 506
: LENGTH: 250
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-140-924-506

Alignment Scores:
Pred. No.: 1,85e-87      Length: 250
Score: 1355.00          Matches: 250
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 57.17%      Indels: 0
Gaps: 12      Gaps: 0

US-09-856-320a-1 (1-1301) x US-10-140-924-506 (1-250)

QY 209 ATGAGAGATTCTGCACTTAATCTGCTGCTGCTGCGCAACAGGCGCTGTAGGGGAGAGACC 268
DB 1 MetArgIleLeuGlnLeuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyIthr 20
QY 269 AGCATCATCAAGGGGTGGAGTGCAGAGCTCACTCCAGCCCTGGAGGAGGAGCCCTGTC 328
DB 21 ArgIleIleGlyGlyPheGlnCysGlyProHisSerGlnProTrpGlnAlaLeuPhe 40
QY 329 GAGAAGACGGCGCTACTGTGTGGGGGAGCGCTCATCGCCCGAGATGGCTCTGCACAGA 388
DB 41 GluIysThrArgLeuLeuCysGlyAlaThrIleuIleAlaProArgTrpLeuIthrAla 60
QY 389 GCGCACTGCTCAAGCCCCGCTACATAGTTCACCTGGGGGAGACACACCTCCAGAGAGAG 448
DB 61 AlaHisCysLeuIlyProArgTrpGlyIleValHisLeuGlyGlnHisAsnLeuGlnIlysgln 80
QY 449 GAGGGGCTGAGCAGACCCGAGACGCACTGATGCTCCGCCACCCCGGCTTCAACAGAC 508
DB 81 GluGlyCysGlnGlnThrArgThrAlaTrpGlnPheProHisTrpGlyPheAsnAsn 100
QY 509 AGCCTCCCGCAACAAAGACCCGACCATGATCATCTGGTGGTGAAGATGGCATCGCGAGTC 568
DB 101 SerLeuProAsnIlyAspHisArgAsnAspIleMetLeuValIlyMetAlaSerProVal 120
QY 569 TCCATCATCCTGGGCTGTGGGAGCCCTCACCTCTCCCTCAGCTGTGTCACTGCTGGACCC 628
DB 121 SerIleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
QY 629 ACCTGCTCATTTGCGGGTGGGGGAGACAGCTCAGACCCCGCATTCAGCGCTGCTCAGAC 688
DB 141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY 689 TTGCGATGGCGCCACATCATCATGATGAGCAGACAGAGTGTGAGAACGCTTACCCGCGGC 748
DB 161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnIlyCysGlnAsnAlaIlyTrpGly 180

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QY 749 AACATCAGACACCATGGTGTGTGCCAGCTGCAGGAAGGGGCAAGACTCTCCAG 808
DB 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlyIlyAspSerCysGln 200
QY 809 GGTGATCCGGGGGCGCCCTGTGCTGTATACCAATCTCTTCAGAGCATTTATCTCTGGGC 868
DB 201 GlyAspSerGlyCylProLeuValCysAsnGlnSerLeuGlnIlyIleIleSerTrpGly 220
QY 869 CAGATCCGTGTGCATCACCCGAAAGCCTGTGTCTACACGAAAGTGTGCAATATGTG 928
DB 221 GlnAspProCysAlaIleThrArgIlyProGlyValIlyThrIlyValCysIlyTrpVal 240
QY 929 GACTGATCCAGGAGACGATGAAGAACAAT 958
DB 241 AspTrpIleGlnGlnIthrMetIlyAsnAsn 250

RESULT 11
US-10-140-926-506
: Sequence 506, Application US/10140926
: Publication No. US20030134356A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerlitsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P330R1C187
: CURRENT APPLICATION NUMBER: US/10/140,926
: PRIOR APPLICATION removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 506
: LENGTH: 250
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-140-926-506

Alignment Scores:
Pred. No.: 1,85e-87      Length: 250
Score: 1355.00          Matches: 250
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 57.17%      Indels: 0
Gaps: 12      Gaps: 0

US-09-856-320a-1 (1-1301) x US-10-140-926-506 (1-250)

QY 209 ATGAGAGATTCTGCACTTAATCTGCTGCTGCTGCGCAACAGGCGCTGTAGGGGAGAGACC 268
DB 1 MetArgIleLeuGlnLeuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyIthr 20
QY 269 AGCATCATCAAGGGGTGCAGTGCAGAGCTCACTCCAGCCCTGGAGGAGGAGCCCTGTC 328
DB 21 ArgIleIleGlyGlyPheGlnCysGlyProHisSerGlnProTrpGlnAlaLeuPhe 40
QY 329 GAGAAGACGGCGCTACTGTGTGGGGGAGCGCTCATCGCCCGAGATGGCTCTGCACAGA 388
DB 41 GluIysThrArgLeuLeuCysGlyAlaThrIleuIleAlaProArgTrpLeuIthrAla 60

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389 GCCCAGCTGCTCAAGCCCCGGTACATAGTTCACCTGGGGGAGCAGACACCTTCAGAGAG 448  
|||||  
Db 61 AlaHisCysLeuLysProArgTyrTlleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 80  
449 GAGGGCTGTGAGCAGACCCGGAGCAGCCACTGAGTCTTCCGCCACCCCGGGCTTCAACAC 508  
|||||  
Db 81 GluGlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsn 100  
509 AGCTCCCCAACAAGACCCAGCCAGATGATCATGCTGGTGAAGATGGCATGGCCAGTC 568  
101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetalSerProVal 120  
569 TCCATCACCTGGGGCTGGGAGCCCTCAGCCCTCTCCAGCTGGTGTACTGCTGGCACC 628  
|||||  
Db 121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140  
629 AGCTGCTCATTTCCGGCTGGGGGAGCAGCAGTCCAGCCCGAGTTTACGCTGCTCAGACC 688  
|||||  
Db 141 SerCysLeuIleSerGlyTrrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160  
689 TTGGGATGCGCCAAACATCACCATTGAGACACGAAAGTGTAGAACGCTTACCCCGGC 748  
161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGly 180  
749 AACATCAGACAGACCATGCTGTGTGCCAGGTGAGGAGGGGGGAGGAGACTCCGTCAG 808  
181 AsnIleThrAspTrpMetValCysAlaSerValGlnGlnLysGlyLysAspSerCysGln 200  
809 GGTGACTCCGGGGCCCTGTGCTGTAAACAGTCTTTCAGAGCATTAATTCCTGGGGC 868  
201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220  
869 CAGATCCGTGTGGGATACCCGAAAGCCTGTGCTTACAGAAAGTGTCAAAATATGTG 928  
221 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 240  
929 GACTGATCCAGAGAGCATGAGAACAAAT 958  
241 AspTrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 12  
US-10-141-698-506  
; Sequence 506, Application US/10141698  
; Publication No. US20030134357A1  
GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Matanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C206  
CURRENT APPLICATION NUMBER: US/10/141,698  
CURRENT FILING DATE: 2002-05-08  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien

US-10-141-698-506  
Alignment Scores:  
Pred. No.: 1,856-87 Length: 250  
Score: 1355.00 Matches: 250  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 57.17% Indels: 0  
DB: 12 Gaps: 0  
US-09-856-320A-1 (1-1301) x US-10-141-698-506 (1-250)  
QY 209 ATGAGAGATTCTGCACATTAATCTGCTCTCTGGCAGACGGGCTTGAAGGGAGAGACC 268  
|||||  
Db 1 MetArgIleLeuGlnLeuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyThr 20  
269 AGATATCATCAAGGGGTTGAGTGAAGCTCACTCCGAGCCCTGGAGGCGGCTGTTC 328  
|||||  
Db 21 ArgIleIleLysGlyPheGlnCysLysProHisSerGlnProTrrpGlnAlaAlaLeuPhe 40  
329 GAGAAGACGCGCTACTCTGTGGGGGAGCAGCTCATCGCCCGCCAGATGGCTCTGACAGCA 388  
41 GluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 60  
389 GCCCAGCTGCTCAAGCCCCGCTACATAGTTCACCTGGGGGAGCAGACACCTCCAGAGAG 448  
61 AlaHisCysLeuLysProArgTyrTlleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 80  
449 GAGGGCTGTGAGCAGACCCGGAGCAGCCACTGAGTCTTCCGCCACCCCGGGCTTCAACAC 508  
81 GluGlyCysGlnGlnThrArgThrAlaThrIleSerPheProHisProGlyPheAsnAsn 100  
509 AGCTCCCCAACAAGACCCAGCCAGATGATCATGCTGTGAAGATGGCATGGCCAGTC 568  
101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetalSerProVal 120  
569 TCCATCACCTGGGGCTGGGAGCCCTCAGCCCTCTCCAGCTGTGCTGCTGCTGGCACC 628  
121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140  
629 AGCTGCTCATTTCCGGCTGGGGGAGCAGCAGTCCAGCCCGAGTTTACGCTGCTCAGACC 688  
141 SerCysLeuIleSerGlyTrrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160  
689 TTGGGATGCGCCAAACATCACCATTGAGACACGAAAGTGTGAAAGCCCTTACCCCGGC 748  
161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGly 180  
749 AACATCAGACAGACCATGCTGTGTGCCAGGTGAGGAGGGGGGAGGAGACTCCGTCAG 808  
181 AsnIleThrAspTrpMetValCysAlaSerValGlnGlnLysGlyLysAspSerCysGln 200  
809 GGTGACTCCGGGGCCCTGTGCTGTAAACAGTCTTTCAGAGCATTAATTCCTGGGGC 868  
201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220  
869 CAGATCCGTGTGGGATACCCGAAAGCCTGTGCTTACAGAAAGTGTCAAAATATGTG 928  
221 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 240  
929 GACTGATCCAGAGAGCATGAGAACAAAT 958  
241 AspTrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 13  
US-10-141-702-506  
; Sequence 506, Application US/10141702  
; Publication No. US20030134358A1  
GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc





```

Db      61  AlahiscysleuLysProArgTyrIleValHisIleuGlyGlnHisAsnIleuGlnLysGlu 80
QY      449  GAGGGCTGTGAGCAGACCCGGAGACGCACTAGTCTTCCCAACCCGGCTTCAACAC 508
Db      81  GluGlycysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsn 100
QY      509  AGCTCCCAACAAAGACACCGGCAATGATCATGTGTGAGATGGATGGCATGGCAGTC 568
Db      101  SerLeuProAsnLysAspHisAlaArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY      569  TCCATCAGCTGGGCTGTCGACCCCTCACCTTCCTCAGCTGTGTGACATGCTGGCACC 628
Db      121  SerIleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
QY      629  AGTGGCTCATTTCCGGCTGGGGGAGCAGCTCACGCCCCAGTTACGCTGCTCACACC 688
Db      141  SerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY      689  TTGGGATGGCCCAACATCACATCATTTGACACCAAGAGTGTGAGAACCCCTACCCGGC 748
Db      161  LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGly 180
QY      749  AACATCAGACAGACCATGATGTGTGTCGACGCGAGAGAAAGGGGCAAGGACTCCGGCCAG 808
Db      181  AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGln 200
QY      809  GGTGACTCGGGGGCCCTGTGCTGTACCAAGTCTCTTCAAGGCAATTATCTCTGGGGC 868
Db      201  GlyAspSerGlyGlyProLeuValCysAsnGlnSerIleuGlnGlyIleIleSerTyrPly 220
QY      869  CAGATCCGCTGTGGGATACCCGGAAGCCGTGTGTCTACAGAAAGTGTGCAATATATGTG 928
Db      221  GlnAspProCysAlaIleThrAlaArgLysProGlyValTyrThrLysValCysLysTyrVal 240
QY      929  GACTGCATCCAGAGACGATGAGAACAAT 958
Db      241  AspTrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 15
US-10-142-421-506
; Sequence 506, Application US/10142421
; Publication No. US20030134360A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C218
; CURRENT APPLICATION NUMBER: US/10/142,421
; PRIORITY FILING DATE: 2002-05-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-421-506

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Alignment Scores:
Pred. No.: 1,856-87 Length: 250
Score: 1355.00 Matches: 250
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.17% Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-1 (1-1301) x US-10-142-421-506 (1-250)

QY      209  ATGAGGATTCGAGAGTTAAATCTCTCTCTGCGCAACAGGCTTTGAGGGAGAGACC 268
Db      1  MetArgIleLeuGlnLeuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyThr 20
QY      269  AGGATCATCAAGGGTTGAGTGCAGGCTCAGTCCAGCCCTGGAGGAGGAGCCCTGTC 328
Db      21  ArgIleIleLysGlyPheGluCysAlaLysProHisSerGlnProTrpGlnAlaAlaLeuPhe 40
QY      329  GAGAAAGACGCGCTACTCTGTGGGGGAGAGCTCATCGCCCAAGATGAGCTCTGACAGCA 388
Db      41  GluLysThrArgLeuLeuLysGlyAlaThrLeuIleAlaProLysTrpLeuLeuThrAla 60
QY      389  GCCCACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGCAAACTTCCAAAGAGAG 448
Db      61  AlahiscysleuLysProArgTyrIleValHisIleuGlyGlnHisAsnIleuGlnLysGlu 80
QY      449  GAGGGCTGTGAGCAGACCCGGAGACGCACTAGTCTTCCCAACCCGGCTTCAACAC 508
Db      81  GluGlycysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsn 100
QY      509  AGCTCCCAACAAAGACACCGGCAATGATCATGTGTGAGATGGATGGCATGGCAGTC 568
Db      101  SerLeuProAsnLysAspHisAlaArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY      569  TCCATCAGCTGGGCTGTCGACCCCTCACCTTCCTCAGCTGTGTGACATGCTGGCACC 628
Db      121  SerIleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
QY      629  AGTGGCTCATTTCCGGCTGGGGGAGCAGCTCACGCCCCAGTTACGCTGCTCACACC 688
Db      141  SerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY      689  TTGGGATGGCCCAACATCACATCATTTGACACCAAGAGTGTGAGAACCCCTACCCGGC 748
Db      161  LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaTyrProGly 180
QY      749  AACATCAGACAGACCATGATGTGTGTCGACGCGAGAGAAAGGGGCAAGGACTCCGGCCAG 808
Db      181  AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGln 200
QY      809  GGTGACTCGGGGGCCCTGTGCTGTACCAAGTCTCTTCAAGGCAATTATCTCTGGGGC 868
Db      201  GlyAspSerGlyGlyProLeuValCysAsnGlnSerIleuGlnGlyIleIleSerTyrPly 220
QY      869  CAGATCCGCTGTGGGATACCCGGAAGCCGTGTGTCTACAGAAAGTGTGCAATATATGTG 928
Db      221  GlnAspProCysAlaIleThrAlaArgLysProGlyValTyrThrLysValCysLysTyrVal 240
QY      929  GACTGCATCCAGAGACGATGAGAACAAT 958
Db      241  AspTrpIleGlnGlnThrMetLysAsnAsn 250

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Search completed: October 15, 2003, 20:55:02  
 Job time : 174.824 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

# OM nucleic - protein search, using frame\_plus\_n2p model

Run on: October 15, 2003, 17:31:30 ; Search time 61.1869 Seconds  
(without alignments)  
6749.699 Million cell updates/sec

Title: US-09-856-320A-1  
Perfect score: 2370  
Sequence: 1 cgccttgcctccacacctg.....aaaaaaaaaaaaaaaa 1301

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 2215726

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+n2p.model -DEV=xlp  
-O=/cgn2.1/USPRO.spool.P/US09856320/runat.15102003.105638.8500/app.query.fasta.1.2318  
-DB-A.Geneseq.19Jun03 -QEXT=fastan -SUPPLY=rag -MINMATCH=0.1 -IOOCL=0  
-IOOEXT=0 -NITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdl  
-LIST=45 -DOCALIGN=200 -THR=SCORE=500 -THR=MAX=100 -THR=MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09856320-ECGN.1.1.140.etrnat.15102003.105638.8500 -NCPU=6 -ICPU=3  
-NO\_MAP -LARGEOBJECTY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONCLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
A.Geneseq.19Jun03: \*  
1: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA1980.DAT: \*  
2: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA1981.DAT: \*  
3: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA1982.DAT: \*  
4: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA1983.DAT: \*  
5: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA1984.DAT: \*  
6: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA1985.DAT: \*  
7: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA1986.DAT: \*  
8: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA1987.DAT: \*  
9: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA1988.DAT: \*  
10: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA1989.DAT: \*  
11: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA1990.DAT: \*  
12: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA1991.DAT: \*  
13: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA1992.DAT: \*  
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19: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA1998.DAT: \*  
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22: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA2001.DAT: \*  
23: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA2002.DAT: \*  
24: /SIDSI/gcgdata/geneseq/geneseqp.embl/AA2003.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1523	64.3	282	AAV42439	CASB12 amino acid
2	1523	64.3	282	AA11712	Human serine protease
3	1523	64.3	282	AAV43636	A human prostatic a
4	1517	64.0	281	AAV42440	CASB12 polypeptide
5	1355	57.2	250	AA12325	Human TLSP. Homo
6	1355	57.2	250	AAV93930	Human PRO1279 (UMO
7	1355	57.2	250	AB50479	Human secreted pro
8	1355	57.2	250	AAU12424	Human PRO1279 poly
9	1355	57.2	250	AA12424	Protein of the inv
10	1355	57.2	250	AB61816	Prostate cancer-as
11	1355	57.2	250	AB61816	Human angiotensin
12	1355	57.2	250	AB84420	Human PRO1279 prot
13	1355	57.2	250	AA083684	Human PRO protein,
14	1355	57.2	250	AB066822	Human PRO polypept
15	1355	57.2	250	ABU67098	Human secreted/tra
16	1355	57.2	250	ABU59903	Novel secreted and
17	1355	57.2	250	ABU56739	Lung cancer-associ
18	1332.5	56.2	275	AA11714	Human serine prote
19	1325	55.9	250	AAV36093	Extended human sec
20	1324	55.9	248	AAE08017	Human PS133 consen
21	1279.5	54.0	247	ABG70276	Human Serine prote
22	1279	54.0	246	AAW89041	Polypeptide fragme
23	1279	54.0	246	AB51196	Human secreted pro
24	1252	52.8	228	AA121312	Human TLSP. Homo
25	1232	52.0	289	AA121312	Fusion gene with h
26	1232	52.0	289	AA121312	Amino acid sequenc
27	1197	50.5	228	AAW89042	Polypeptide fragme
28	1197	50.5	228	AAW89042	Human secreted pro
29	1187	50.1	276	AA11713	Mouse serine prote
30	758	32.0	251	AA16971	Human novel secret
31	756	31.9	250	AA121298	Human KLF-13 prote
32	754	31.8	247	AA121298	Human protein seq
33	754	31.8	247	AA121298	Human protein seq
34	745.5	31.5	296	AA121297	Human human enzyme
35	736	31.1	247	AAU86677	Human KLF-13 prote
36	736	31.1	247	AAU86677	Novel human connec
37	736	31.1	247	AAU86677	Novel human enzyme
38	698.5	29.5	260	AAU17043	Human novel secret
39	698.5	29.5	260	AAU17043	Human novel secret
40	698.5	29.5	260	AAU17043	Human novel secret
41	698.5	29.5	260	AAU17043	Human novel secret
42	698.5	29.5	260	AAU17043	Human novel secret
43	698.5	29.5	260	AAU17043	Human novel secret
44	698.5	29.5	260	AAU17043	Human novel secret
45	698.5	29.5	260	AAU17043	Human novel secret

## ALIGNMENTS

RESULT 1	ID	AAV42439	standard; Protein; 282 AA.
AC	AAV42439;		
XX			
XX			
DT	08-DEC-1999	(first entry)	
XX			
DE	CASB12 amino acid sequence.		
XX			
KW	neutropsin; cancer; assay; inhibitor; serine protease; immunogenic;		
KW	autoimmune disease.		
XX			
OS	Homo sapiens.		
PN	MO9949055-AL.		
XX			
PD	30-SEP-1999.		

XX 17-MAR-1999; 99WO-EP01894.  
 XX 20-MAR-1998; 98GB-0006095.  
 XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX Bruck CEM, Cassart J, Coche T, Vinals-bassols C;  
 DR WPI; 1999-580450/49.  
 DR N-PSDB; AA222638.  
 PT New human serine protease CASB12, for treatment, prevention and  
 PT diagnosis of cancer and autoimmune diseases  
 PS Claim 3; Page 48; 58pp; English.

XX This is the amino acid sequence of the CASB12 protein. The nucleotide  
 CC sequence of AA222638 shows homology with neuropsin and the encoded  
 CC protein AA142439 is structurally related to other proteins of the  
 CC serine protease family, having homology and/or structural similarity  
 CC with neuropsin. It is expected that as well as similar structure, these  
 CC proteins will also share similar biological functions and properties.  
 CC The CASB12 polypeptide and polynucleotides can be used to develop  
 CC methods for identifying agonists and antagonists/inhibitors of these  
 CC molecules, and thereby treating conditions associated with CASB12  
 CC polypeptide imbalance. The invention also provides for diagnostic assays  
 CC for detecting diseases associated with inappropriate CASB12 polypeptide  
 CC activity or levels.  
 CC Since CASB12 is either specifically expressed or highly over-expressed  
 CC in tumors compared to normal cells, the polypeptides and polynucleotides  
 CC of the invention are believed to be important immunogens for specific  
 CC prophylactic or therapeutic immunization against tumors. The  
 CC polypeptides and polynucleotides can therefore be targeted by antigen  
 CC specific immune reactions (which result in the destruction of the tumor  
 CC cell) or they can be used to diagnose the occurrence of tumor cells  
 XX Sequence 282 AA:

Alignment Scores:  
 Pred. No.: 2,24e-110 Length: 282  
 Score: 1523.00 Matches: 282  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 64.26% Indels: 0  
 DB: Gaps: 0

US-09-856-320A-1 (1-1301) x AA142439 (1-282)

QY 113 ATGCAGAGGTTGAGGTGGCTGCGGAGTGCATGTCAGAGGTCTCAGACGACCC 172  
 DB 1 MetGlnArgLeuAlaGlyTrpLeuAlaGlyAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20  
 QY 173 AAGGACCTGGGGCGGCTGCTGCTCCCTCCAGGCGCATGAGATTGCAATTAATCTG 232  
 DB 21 LysGlnProGlyAlaArgSerProLeuGlnAlaMetAlaGlyLeuGlnLeuLeu 40  
 QY 233 CTTCCTGTGGCAGACGGCTGTGAGGGGAGAGACGACGATCATCAAGGGCTTGAGTGC 292  
 DB 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleGlyGlyPheGlnLucy 60  
 QY 293 AAGCCTCACTCCAGCCCTGGCAGGACGCTGTTCGAGAAAGACGGGCTACTGTGGG 352  
 DB 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuGlyGly 80  
 QY 353 GCGACGCTCATGCGCCCAAGATGGCTCTGCACAGACGACCCATGCTCAACCCGGCTAC 412  
 DB 81 AlaThrLeuIleAlaProAlaGlyTrpLeuThrAlaAlaHisCysLeuLysProArgTyr 100  
 QY 413 ATAGTTCACCTGGGGCAGACACCTCCAGAAAGAGAGGGCTGTGAGCAGACCCGGACA 472  
 DB 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCysGlnGlnThrArgThr 120

QY 473 GCCACGAGTCTTCCGCCACCGGCTTCACAGACGCTCCCAACAAAGACACCGC 532  
 DB 121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140  
 QY 533 AATGACATCATGCTGGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 592  
 DB 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160  
 QY 593 CTCACCCCTCTCCTACAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 652  
 DB 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrPhe 180  
 QY 653 AGCAGCTCCACCCCGCAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712  
 DB 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200  
 QY 713 ATTGAGCCACCAAGTGTGAGAACGCCATACCCCGGCAACATCAGACACCATGCTGTGT 772  
 DB 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlnAsnIleThrAspThrMetValCys 220  
 QY 773 GCCAGCGTCAGAGAGGGGCGCAGAGCTCTGCGCAGGCTGACCTCGGGGCGCTCTGCTG 832  
 DB 221 AlaSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240  
 QY 833 TGTAACAGTCTCTTCAAGGCAATTAATCTCTGCGGCGCAGATCCGCTGCGATACCCGA 892  
 DB 241 CysAsnGlnSerLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 260  
 QY 893 AAGCCTGTCTCTACAGCAAGTCTGCAATATGATGATGATGATGATGATGATGATGATG 952  
 DB 261 LysProGlyValIleThrLysValCysLysIleThrAlaAspTrpIleGlnGlnThrMetLys 280  
 QY 953 AACCAAT 958  
 DB 281 AsnAsn 282

RESULT 2

AB11712  
 ID AB11712 standard; Protein: 282 AA.

AC AB11712;

DT 23-OCT-2000 (first entry)

DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO:2.

XX BSSP6: serine protease; human; hBSSP6; mouse; MBSSP6; brain;

XX diagnostic marker; antibody; transgenic animal; Alzheimer's disease;

XX epilepsy; cancer; inflammation; infertility; pancreatitis;

XX prostatic hypertrophy.

OS Homo sapiens.

XX WO200031257-A1.

PD 02-JUN-2000.

PF 19-NOV-1999; 99WO-JP06476.

PR 20-NOV-1998; 98JP-0347802.

PA (FUSO ) FUSO PHARM IND LTD.

PI Uemura H, Okui A, Komitani K, Yamaguchi N, Mitsui S;

DR WPI: 2000-400067/34.

DR N-PSDB; AAA61763.

PT Serine protease BSSP6, useful in detecting homologs, mutants and  
 PT polymorphic variants as markers for diagnosis of Alzheimer's disease,  
 PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,  
 PT using blood or other tissues

PS Claim 1; Page 69-70; 94pp; Japanese.

XX The invention relates to novel serine proteases designated BSSP6  
CC (AA611712-B11714), and to nucleic acids encoding them (AA611763-A61765).  
CC The invention also relates to vectors and transformants comprising BSSP6  
CC nucleic acids; transgenic animals in which the expression level of BSSP6  
CC can be varied; and an mBSSP6 knockout mouse. The invention additionally  
CC encompasses anti-BSSP6 antibodies and methods of production of such  
CC antibodies, methods of BSSP6 detection using the antibodies, and the  
CC use of BSSP6 proteins or fragments as diagnostic markers for certain  
CC medical conditions. Nucleotides encoding BSSP6 were initially  
CC isolated in a human brain cDNA library using degenerate PCR primers  
CC (AA61795-A61796) based on conserved regions of serine proteases. The  
CC BSSP6 serine proteases and nucleotides encoding them are useful in  
CC detecting homologues, mutants and polymorphic variants in biological  
CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis  
CC and spleen) as diagnostic markers for conditions such as Alzheimer's  
CC disease, epilepsy, cancer, inflammation, infertility and prostatic  
CC hypertrophy. Sequences AA611712 and AA611714 represent human BSSP6  
CC variants (mBSSP6), and sequence AA611713 represents murine BSSP6  
CC (mBSSP6).

CC  
XX  
SQ Sequence 282 AA:

Alignment Scores:  
Pred. No.: 2,24e-110 Length: 282  
Score: 1523.00 Matches: 282  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 64.26% Indels: 0  
DB: 21 Gaps: 0

US-09-856-320A-1 (1-1301) x AA611712 (1-282)

QY 113 ATGACAGAGTTAGAGTGGCTGGCGGAGTGCAGATCGGGGAGAGTCTCAGACAGCC 172  
DB 1 MetGlnArgLeuArgTyrLeuArgAspTyrPylSerSerGlyArgGlyLeuThrAla 20  
QY 173 AAGGACCTGGGGCGCCGCTCTCCGCCCTCCAGGCCATGAGATTCTGCAGTTAACTCTG 232  
DB 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40  
QY 223 CTGTGCTGGCAACGAGGCTGTAGGGAGAGACAGATCATCAAGGGGTTCAGATGTC 292  
DB 41 LeuAlaLeuAlaThrGlyLeuValIleGlyLeuThrArgIleIleGlySerIleGlyLeuGly 60  
QY 293 AAGCTCACTCCAGCCCTGGCAGGAGCCCTGTCGAGAGAGACCGGGTACTCTGTGGG 352  
DB 61 LysProHisSerGlnProTyrPheIleAlaLeuPheGluIleGlyThrArgLeuLeuGly 80  
QY 353 GCGACGCTCAGCCGCCAGATGCTCTGACAGCAGCCACTGCTCAAGCCCGCTAC 412  
DB 81 AlaThrLeuIleAlaProArgTyrLeuLeuThrAlaIleHisCysLeuYsProArgTyr 100  
QY 413 ATAGTTCACTGGGGCAGACAACTCCAGAAAGAGAGGGGTGTGAGCAGACCCGGACA 472  
DB 101 IleValHisLeuGlyGlnHisAsnLeuGlnIleGlyGlyGlyGlyGlnThrArgTyr 120  
QY 473 GCCACTGAGTCTCTCCCGCCAGCCCGGCTTCAACAACAGCCCTCCCAAAAGACACCGC 532  
DB 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnIleAspHisArg 140  
QY 533 AATGACATCAGCTGGTGAAGATGCGATCGCCAGTCTCCATCAGCTGGGCTGTGGACCC 592  
DB 141 AsnAspIleMetLeuValIleGlyMetAlaSerProValSerIleThrTrpAlaValArgPro 160  
QY 593 CTCACCTCTCTCTACAGGTGTGTACTGTGTGACACAGCTGCTCATTTCCGGCTGGGGC 652  
DB 161 LeuThrIleLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180  
QY 653 AGCAGCTCAGCCCGCCAGTACAGCTGCTGCTCAGACCTTGCAGTGGCGGCAATCAGCATC 712  
DB 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200

QY 713 ATGAGCACCAGAAAGTGTGAGAACCGCTACCCCGGACATCAGACACCATGTGTGT 772  
DB 201 IleGlnHisGlnIleGlyCysIleAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220  
QY 773 GCCAGCTGCAGAAAGGGGGCAGAGACTCTCCAGAGGTGATCCGGGGCCCTTGCTC 832  
DB 221 AlaSerValGlnGlnGlyGlyLeuLysAspSerCysGlnGlnIleAspSerGlyGlyProLeuVal 240  
QY 833 TGTAACTGCTCTTCAAGCATTTATCTCTGGGGCAGAGATCCGTCGATCCACCGCA 892  
DB 241 CysAsnGlnSerLeuGlnIleIleSerThrPylGlnAspProCysAlaIleThrArg 260  
QY 893 AAGCTGTGTCTACACGAAAGTTCGAAATGTGTGACTGATCCAGAGACGATGAG 952  
DB 261 LysProGlyValIleThrIleValCysIleValAspTyrIleGlnIleThrMetCys 280  
QY 953 AACCAT 958  
DB 281 AsnAsn 282

RESULT 3  
AA43636  
ID AA43636 standard; Protein; 282 AA.  
XX  
XX  
AC AA43636;  
XX  
DT 11-FEB-2000 (first entry)  
XX  
DE A human prostate-associated serum protease (PRASP).  
XX  
KW Human; prostate-associated serum protease; PRASP; neuropsin; PSA;  
KW Incyte clone 2723646; reproductive disorder; cancer;  
KW abnormal prolactin production; infertility; tubal disease;  
KW ovulatory defect; endometriosis; polycystic ovary syndrome;  
KW autoimmune disorder; ectopic pregnancy; breast cancer;  
KW abnormal spermatogenesis; testicular cancer; adenocarcinoma; leukaemia;  
KW lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma.  
XX  
XX Homo sapiens.  
FH  
FT Key Location/Qualifiers  
FT Peptide 1..50  
FT Modified-site /note= "signal sequence"  
FT Disulfide-bond 13  
FT /note= "potential protein kinase C phosphorylation site"  
FT /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"  
FT Disulfide-bond 79  
FT /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"  
FT Active-site 90..95  
FT /note= "serine protease trypsin family active site motif"  
FT Misc-difference 94  
FT /note= "this forms the active site catalytic triad with Asp142 and Ser235"  
FT Disulfide-bond 95  
FT /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"  
FT Modified-site 120  
FT /note= "potential casein kinase II phosphorylation site"  
FT Modified-site 131  
FT /note= "potential N-glycosylation site"  
FT Misc-difference 142  
FT /note= "this forms the active site catalytic triad with His94 and Ser235"  
FT Modified-site 164  
FT /note= "potential protein kinase C phosphorylation site"  
FT Disulfide-bond 174

FT	/note=	"this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
FT	Modified-site	192
FT	/note=	"potential protein kinase C phosphorylation site"
FT	Disulfide-bond	195
FT	/note=	"this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
FT	Modified-site	197
FT	/note=	"potential N-glycosylation site"
FT	Modified-site	199
FT	/note=	"potential casein kinase II phosphorylation site"
FT	Disulfide-bond	206
FT	/note=	"this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
FT	Modified-site	213
FT	/note=	"potential N-glycosylation site"
FT	Disulfide-bond	220
FT	/note=	"this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
FT	Modified-site	222
FT	/note=	"potential casein kinase II phosphorylation site"
FT	Active-site	229..240
FT	/note=	"serine protease trypsin family active site motif"
FT	Misc-difference	229
FT	/note=	"the corresponding residue (together with Ser235, Gly252 and Gly263) in neuropsin forms a oxyanion hole"
FT	Disulfide-bond	231
FT	/note=	"this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
FT	Misc-difference	235
FT	/note=	"the corresponding residue (together with Asp229, Gly252 and Gly263) in neuropsin forms a oxyanion hole"
FT	Misc-difference	235
FT	/note=	"this forms the active site catalytic triad with His94 and Asp142"
FT	Disulfide-bond	241
FT	/note=	"this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
FT	Modified-site	242
FT	/note=	"potential N-glycosylation site"
FT	Misc-difference	252
FT	/note=	"the corresponding residue (together with Asp229, Ser235 and Gly263) in neuropsin forms a oxyanion hole"
FT	Disulfide-bond	256
FT	/note=	"this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
FT	Modified-site	259
FT	/note=	"potential protein kinase C phosphorylation site"
FT	Misc-difference	263
FT	/note=	"the corresponding residue (together with Asp229, Ser235 and Gly263) in neuropsin forms a oxyanion hole"
FT	Modified-site	278
FT	/note=	"potential protein kinase C phosphorylation site"
XX	MO99A1387-A2.	
XX	PD	
XX	19-AUG-1999.	
XX	05-FEB-1999;	99WC-USO2571.
XX	17-FEB-1998;	98US-0025059.

PA	(INCY-)	INCYTE PHARM INC.
PI	Tang YT,	Corley NC, Guejler KJ;
PI	WP1; 2000-012993/01.	
DR	N-PSDB: AA230222.	
XX		
PT	New prostate-associated serum protease and polynucleotides which	
PT	identify and encode PRASP, useful for treating reproductive disorders	
PI	and cancer	
XX		
PS	Claim 1; Fig 1A-D; 67pp; English.	
XX		
CC	The present sequence represents human prostate-associated serum protease	
CC	(PRASP). The protein shows homology to neuropsin, a brain-specific	
CC	protease in mice, and PSA, a prostate-specific protease in humans.	
CC	Nucleic acids encoding PRASP were first identified in Incyte clone	
CC	273646 from the lung tumour cDNA library. Pharmaceutical compositions	
CC	containing PRASP, or antibodies to PRASP, and mimetics, agonists,	
CC	antagonists or inhibitors of PRASP, are used for treating or preventing	
CC	a reproductive disorder or cancer. Examples of reproductive disorder	
CC	include, abnormal prolactin production, infertility, tubal disease,	
CC	ovulatory defects, endometriosis, polycystic ovary syndrome, autoimmune	
CC	disorders, ectopic pregnancy, breast cancer, abnormal spermatogenesis	
CC	and testicular cancer. Examples of cancers which may be treated or	
CC	prevented include adenocarcinoma, leukemia, lymphoma, melanoma, myeloma,	
CC	sarcoma, teratocarcinoma, and cancers of the adrenal gland, bladder,	
CC	bone, bone marrow, brain, breast, cervix, penis, prostate, salivary	
CC	glands, skin, spleen, testis, thymus, thyroid and uterus. A vector	
CC	capable of expressing PRASP or an agonist which modulates the activity of	
CC	PRASP may be administered to treat or prevent a reproductive disorder or	
CC	cancer.	
XX		
XX		
SQ	Sequence	282 AA;
Alignment Scores:		
Pred. No.:	2,24e-110	Length: 282
Score:	1523.00	Matches: 282
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	64.26%	Indels: 0
DB:	21	Gaps: 0
US-09-856-320A-1 (1-1301) x AAIV43636 (1-282)		
QY	113 ATGCAGAGGTTAGGATGGCTGGCGGAGATGCATGCGGCGAGAGTTCACAGCAGCC	172
DB	1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla	20
QY	173 AAGGAACCTGGGGCCCGGCTCTCCGCCCTCCAGGCCATGAGGATTCGTCACTAATCTG	233
DB	21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu	40
QY	233 CTTCGCTCTGGCAACAGGCTTATAGGGGAGAGACAGGATCATCAACAGGGTGTGAGTGC	292
DB	41 LeuAlaLeuAlaIleThrIleValGlyGlyIleuThrArgIleIleIleYsglyPheGlyIcys	60
QY	293 AAGCCTCACTCCAGCCCTGGCGAGCGAGCCCTGTTGCAAAAGACGGGCTACTGTGGG	352
DB	61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyIleThrArgLeuIcysGly	80
QY	353 GCGAGCGCTATGCGCCCGCAGATGGGCTCGACAGAGCCCACTGCTCAAGCCCGGTAC	412
DB	81 AlaThrIleuLeuAlaProArgTrpLeuLeuThrAlaAlaIcysLeuLysProAlaGlyr	1000
QY	413 ATATGTTACCTGGGCGCAGACAACCTCCAGAAGAGAGAGGCTGTGACAGACCCGGACA	472
DB	101 IleValHisLeuGlyIleHisIleAsnLeuGlnIcysGlyIleuIleThrArgThr	1200
QY	473 GCCACTGAGTCTTCCCCCAGCCCGGCTTCAACAACAGCCTCCCAACAAAGACACCGC	5322
DB	121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg	1400

OY	553	AATGCAATCAATGCTGTGTGAAGATGGCATATGCCACATGCTCCATCATACCTGGGCTGTGGACCC	592		
Db	141	AsnAspIleMetLeuValIysMetAlaSerProValSerIleThrTrpAlaValArgPro	160		
OY	593	CTCACCCCTCCTCAAGCGTGTCACTGCTGGACACAGCTGGCTCATTTCCGGGTGGGGC	652		
Db	161	LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly	180		
OY	653	AGCAGCTCCAGCCCCAGTTTACGCGCTTCACCTTCACACCTTCGATGCGCAATCACCATC	712		
Db	181	SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaHisIleThrIle	200		
OY	713	ATTGAGCACCCAGAAATGTGTAGACAGCCCTACCCCCGACATCATACAGACACCATGTGTGT	772		
Db	201	IleGluHisGlnIysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys	220		
OY	773	GCCACGCTGCAGGAAGGGGGCAAGACACTCTCCACAGGAGACATCCGGGGGGCCCTGTGGTC	832		
Db	221	AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyAspSerIleGlyProLeuVal	240		
OY	833	TGTAAACGATCTCTTCAAGGCGATTTATCTCCTGGGGCAGAGATCCGTTGCGATCACCCGA	892		
Db	241	CysAsnGlnSerLeuGlnGlyIleIleIleSerTrpGlnAspProCysAlaIleThrArg	260		
OY	893	AAGCTGTGTCTACACGAAAGTCTGCAAAATATGTGTAGCTGATCCAGACAGACAGATGAAG	952		
Db	261	LysProGlyValTyrThrLysValCysIleSyrValAspTrpIleGlnGlnThrMetLys	280		
OY	953	AACAAAT 958			
Db	281	AsnAsn 282			
RESULT 4					
ID	AA42440	AA42440 standard; Protein; 281 AA.			
AC	AA42440;				
DT	08-DEC-1999	(first entry)			
DE	CASB12	polypeptide derived from Expressed Sequence Tag products.			
XX	neutropin; cancer; assay; inhibitor; serine protease; immunogenic;				
KW	autoimmune disease.				
XX	Homo sapiens.				
OS					
XX	MO9949055-A1.				
PN	30-SEP-1999.				
PD	17-MAR-1999;	99MO-EP01894.			
PF	20-MAR-1998;	98GB-0006095.			
PR	(SMIK )	SMITHKLINE BEECHAM BIOLOGICALS.			
XX	Bruck CEM, Cassart J, Coche T, Vinals-bassols C;				
PI	WPI; 1999-580450/49.				
DR	N-PSDB; AA222639.				
XX	New human serine protease CASB12, for treatment, prevention and	diagnosis of cancer and autoimmune diseases _			
PT	diagnosis of cancer and autoimmune diseases				
XX	Claim 27; Page 49-50; 58pp; English.				
PS	This is the amino acid sequence of CASB12 protein, derived from an				
CC	Expressed Sequence Tag (EST) search for tumor-specific and				
CC	tumor-associated antigens. The nucleotide sequence of AA222638 shows				
CC	homology with neutropin and the encoded protein AA42439 is structurally				
CC	related to other proteins of the serine protease family, having homology				
CC	and/or structural similarity with neutropin. It is expected that as well				

CC	as similar structure, these proteins will also share similar biological
CC	functions and properties.
CC	The CASB12 polypeptides and polynucleotides can be used to develop
CC	methods for identifying agonists and antagonists/inhibitors of these
CC	molecules, and thereby treating conditions associated with CASB12
CC	polypeptide imbalance. The invention also provides for diagnostic assays
CC	for detecting diseases associated with inappropriate CASB12 polypeptide
CC	activity or levels.
CC	Since CASB12 is either specifically expressed or highly over-expressed
CC	in tumors compared to normal cells, the polypeptides and polynucleotides
CC	of the invention are believed to be important immunogens for specific
CC	prophylactic or therapeutic immunization against tumors. The
CC	polypeptides and polynucleotides can therefore be targeted by antigen
CC	specific immune reactions (which result in the destruction of the tumor
CC	cell) or they can be used to diagnose the occurrence of tumor cells
xx	
xx	Sequence 281 AA:
SO	
Alignment Scores:	
Pred. No.:	6,57e-110 Length: 281
Score:	1517.00 Matches: 281
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	64.01% Indels: 0
DB:	Gaps: 0
US-09-856-320A-1 (1-1301) x AAAY42440 (1-281)	
QY	113 ATGCAGAGGTTGAGGTGGCTGGCGGACCTGGAAAGTCATGGGCGACAGGTCTCAGACAGCC 177
Db	1 MetcIntrgLeuArtrgTrpLeuArGAsprTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
QY	173 AAGGAACCTGGGGCCGGCTCTCCGCCCCACAGGGCCATGAGGATTCCTGCACTATATCTG 233
Db	21 LysGIuProeLylArtrgSerSerProLeuGlnAlaMetArGlyLeuGlnLeu 40
QY	233 CTTGCTCTGGCAACAGAGGCTTGAGGGGAGAGACAGATCAGATCAGAGGGCTGAGTGC 292
Db	41 LeuAlaLeuAlaThrGlyLeuValAGlyGlyGluThrArgIleIleIleGlyPheGluCys 60
QY	293 AAGCTCTACTCCAGCCCTGGGAGGAGCCCTGTTCGAAAGACGGCGGCTACTGTGGG 352
Db	61 LysProHIsSerGlnProTrpGlnAlaAlaLeuPheGluGlyThrArgLeuLeuCysGly 80
QY	353 GCGAGCGTCAATCGCCGCCAAGTGGCTCTCGACAGAGCCCACTGGCTCAAGCCCGCTAC 412
Db	81 AlaThrLeuIleAlaProArGlyTrpLeuLeuThrAlaAlaHisCysLeuLysProArGlyTr 100
QY	413 ATAGTTCACCTGGGGGAGACAAACCTCCAGAAAGAGAGGGCTGTGAGCAACCCGACA 472
Db	101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThr 120
QY	473 GCCACGTAGTCTTCCCCACCCCGGCTTCAACAAGACGCTCCCAACAAAGACCCGC 532
Db	121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
QY	533 AATGACATCATGGTGGTGAAGATGGAGATCGGACGTCATCACTGGCGTGGTCGACCC 592
Db	141 AsnAspLleMetLeuValLysMetAlaSerProValSerIleThrAlaValAlaArgPro 160
QY	593 CTCACCTCTCCACAGCTGTCTCACTGCTGGACACACTGCTCATTTCCGGCTGGGGC 652
Db	161 LeuThrLeuSerSerArgCysValIleThrAlaGlyThrSerCysLeuIleIleSerGlyTyrGly 180
QY	653 AGACAGTCCAGCCCCAGTTACGGCTGGCTCAACACTTGGATGGCCACATCACCATC 712
Db	181 SerThrSerSerProGlnLeuArGlyLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
QY	713 AATGAGACACAGAAAGTGAGAAAGCCTTACCCCGGCAACATCAGACACCAAGTGTGT 772
Db	201 IleGlnHisGlnLysCysGlnAsnAlaLayTrpGlnAlaIleThrAspTrpMetValCys 220
QY	773 GCCAGGCTGACAGAAAGGGGCAAGAGACTCTCCAGGTGTGACTCCGGGGGCGCTTGGTC 832

```

Db      221  ALaSerValGInGluGlyLysAspSerCysGInGlyAspSerGlyProLeuVal 240
QY      833  TGIACACGATCTCTCAAGGATATATCTCGGGCCAGGATCCGTGGCATCCGCCA 892
Db      241  CysAsnGInSerLeuGInGlyIleIleSerTrpGlyGInAspProCysAlaIleThrArg 260
QY      893  AAGCCTGTGTCTACACCAAGATCTGCAAAATATGTGACGTGATCCAGAGACGATGAAG 952
Db      261  LysProGlyValIleThrLysValCysLysTrpValAspTrpIleGInGluThrMetLys 280
QY      953  AAC 955
Db      281  Asn 281

```

RESULT 5  
AAB21325  
ID AAB21325 standard; Protein: 250 AA.

AC AAB21325;  
DT 02-FEB-2001 (first entry)

DE Human TLSP.

KM Human, KIK-L1; KIK-L2; KIK-L3; KIK-L4; KIK-L5; KIK-L6; TLSP;  
KW trypsin-like serine protease; kallikrein-like protein; serine protease;  
KM cytosolic; cancer; prostate cancer.

OS Homo sapiens.

PN WO200053776-A2.

PD 14-SEP-2000.

PF 09-MAR-2000; 2000WO-CA00258.

PR 11-MAR-1999; 99US-0124260.

PR 01-APR-1999; 99US-0127386.

PR 21-JUL-1999; 99US-0144919.

PA (MOON ) MOUNT SINAI HOSPITAL.

PI Yousef GM, Diamandis EP;

DR WPI: 2000-587440/55.

PT New kallikrein-like (KIK-L) proteins for diagnosing and treating KIK-L

PT protein mediated disorders, especially cancer.

PS Example 5; Fig 27; 184pp; English.

CC The present sequence is human trypsin-like serine protease (TLSP), a  
CC member of the serine protease family. Kallikreins and  
CC kallikrein-like proteins are a subgroup of the serine protease enzyme  
CC family. They catalyze the selective cleavage of specific polypeptide  
CC precursors to release peptides with potent biological activity. Nucleic  
CC acids encoding kallikrein-like proteins KIK-L1, KIK-L2, KIK-L3, KIK-L4,  
CC KIK-L5 and KIK-L6 have been isolated. The proteins are useful in the  
CC treatment, monitoring and diagnosis of cancers, especially prostate  
CC cancer. They can also be used to identify a substance that can associate  
CC with or mediate the biological activity of the proteins. Antibodies can  
CC be used to treat conditions mediated by the kallikrein-like proteins.

SO Sequence 250 AA;

Alignment Scores:

Pred. No.: 2.68e-97 Length: 250  
Score: 1355.00 Matches: 250  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 57.17% Indels: 0  
DB: 21 Gaps: 0

US-09-856-320A-1 (1-1301) x AAB21325 (1-250)

```

QY      209  ATGAGGATTCGACAGTTAATCTCTGCTGGCAACAGGGCTTGTAGGGGGAGAGACC 268
Db      1  MetArgIleLeuGInLeuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyIleThr 20
QY      269  AGATATCATCAAGGGGTTCTGACTGCAGGCTTCATCCAGCCCTGGCAGGCGCTTTC 328
Db      21  ArgIleIleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaIleLeuPhe 40
QY      329  GAGAAGACGGCGCTACTCTGTGGGGCGACGCTCATCCGCCAGATGGCTCTGACAGCA 388
Db      41  GluLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAla 60
QY      389  GCCCAGCTGCTCAAGCCCCGCTACATAGTTACCTGGGGGAGCAGCAACCTCCAGAGAG 448
Db      61  AlaHisCysLeuLysProArgTrpIleValHisLeuGlnHisAsnLeuGlnLysGlu 80
QY      449  GAGGCGTGTGAGCAGACCCGGAGACCCAGCTGAGTCTTCCGCCACCCGCGCTTCACAGAC 508
Db      81  GluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsn 100
QY      509  AGCCTCCCGCACAAGACCCAGCCAGATGACATCATGCTGTGAGATGGCATCCCGCAGTC 568
Db      101  SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY      569  TCCATTCACCTGGGCTGTGCGACCCCTCACCTCTCTCACGCTGTCTACTGTGGGAGC 628
Db      121  SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
QY      629  AGTGCCTCATTTCCGGCTGGGGGAGCAGCAGCTCCAGCCCGCAGTTACGCTGCTCACACC 688
Db      141  SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY      689  TTGGGATGGCCACATCATCATGAGACAGACAGAGTGTGAGACCGCTTACCCGGCC 748
Db      161  LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaValProGly 180
QY      749  AACATCAGACAGACCATGATGTGTGCCAGCTGAGAGAGGGGAGAGAGATCTGCGCAG 808
Db      181  AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 200
QY      809  GGTGACTCCGGGGGCCCTGTGCTGTGTACCATGCTCTTCAAGGCAATATCTCTGGGGC 868
Db      201  GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
QY      869  CAGATCCGTTGGGATCACCCGAAAGCTGTCTACAGCAAGTGTGAATATGTG 928
Db      221  GlnAspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTrpVal 240
QY      929  GACTGATCCAGAGAGAGATGAGACAAAT 958
Db      241  AspTrpIleGlnGlnThrMetLysAsnAsn 250

```

RESULT 6  
AAY99390  
ID AAY99390 standard; Protein: 250 AA.

AC AAY99390;

DT 08-AUG-2000 (first entry)

DE Human PRO1279 (UNQ649) amino acid sequence SEQ ID NO:170.

KM Human, PRO polypeptide; membrane bound protein; receptor; diagnosis;  
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.

OS Homo sapiens.

PN WO200012708-A2.

PD 09-MAR-2000.



XX	01-SEP-1999;	99WO-USZ0111
XX		
PR	01-SEP-1999;	98US-00987116
PR	01-SEP-1999;	98US-00987419
PR	01-SEP-1999;	98US-00988703
PR	02-SEP-1999;	98US-00988750
PR	02-SEP-1999;	98US-00988821
PR	02-SEP-1999;	98US-00988843
PR	02-SEP-1999;	98US-00989536
PR	03-SEP-1999;	98US-00989596
PR	03-SEP-1999;	98US-00989598
PR	03-SEP-1999;	98US-00996502
PR	03-SEP-1999;	98US-00996442
PR	10-SEP-1999;	98US-00997411
PR	10-SEP-1999;	98US-00997554
PR	10-SEP-1999;	98US-00997634
PR	10-SEP-1999;	98US-00997912
PR	10-SEP-1999;	98US-00998108
PR	10-SEP-1999;	98US-00998208
PR	10-SEP-1999;	98US-00998616
PR	15-SEP-1999;	98US-01003885
PR	15-SEP-1999;	98US-01003980
PR	15-SEP-1999;	98US-01003988
PR	16-SEP-1999;	98US-01005844
PR	16-SEP-1999;	98US-01006227
PR	16-SEP-1999;	98US-01006621
PR	16-SEP-1999;	98US-01006642
PR	16-SEP-1999;	98US-01006644
PR	17-SEP-1999;	98US-01006883
PR	17-SEP-1999;	98US-01006884
PR	17-SEP-1999;	98US-01007010
PR	17-SEP-1999;	98US-01007111
PR	17-SEP-1999;	98US-01009319
PR	17-SEP-1999;	98US-01009330
PR	18-SEP-1999;	98US-01008448
PR	18-SEP-1999;	98US-01008449
PR	18-SEP-1999;	98US-01010144
PR	18-SEP-1999;	98US-01010668
PR	18-SEP-1999;	98US-01010701
PR	22-SEP-1999;	98US-01012729
PR	22-SEP-1999;	98US-01014771
PR	22-SEP-1999;	98US-01014772
PR	22-SEP-1999;	98US-01014774
PR	22-SEP-1999;	98US-01014775
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PR	24-SEP-1999;	98US-01017368
PR	24-SEP-1999;	98US-01017411
PR	24-SEP-1999;	98US-01017433
PR	24-SEP-1999;	98US-01019155
PR	24-SEP-1999;	98US-01019166
PR	25-SEP-1999;	98US-01022407
PR	25-SEP-1999;	98US-01022470
PR	25-SEP-1999;	98US-01023207
PR	25-SEP-1999;	98US-01023209
PR	28-SEP-1999;	98US-01023311
PR	30-SEP-1999;	98US-01024884
PR	30-SEP-1999;	98US-01024887
PR	30-SEP-1999;	98US-01025700
PR	30-SEP-1999;	98US-01025711
PR	01-OCT-1999;	98US-01026884
PR	01-OCT-1999;	98US-01026887
PR	02-OCT-1999;	98US-01028657
PR	06-OCT-1999;	98US-01033558
PR	07-OCT-1999;	98US-01034449
PR	07-OCT-1999;	98US-01033114
PR	07-OCT-1999;	98US-01033155
PR	07-OCT-1999;	98US-01033228
PR	07-OCT-1999;	98US-01033965
PR	07-OCT-1999;	98US-01033996

PR	07-OCT-1998;	98US-0103401.
PR	08-OCT-1998;	98US-0103633.
PR	08-OCT-1998;	98US-0103678.
PR	08-OCT-1998;	98US-0103679.
PR	08-OCT-1998;	98US-0103711.
PR	14-OCT-1998;	98US-0104257.
PR	20-OCT-1998;	98US-0104987.
PR	20-OCT-1998;	98US-0105000.
PR	20-OCT-1998;	98US-0105002.
PR	21-OCT-1998;	98US-0105104.
PR	22-OCT-1998;	98US-0105165.
PR	22-OCT-1998;	98US-0105266.
PR	26-OCT-1998;	98US-0105693.
PR	26-OCT-1998;	98US-0105694.
PR	27-OCT-1998;	98US-0105807.
PR	27-OCT-1998;	98US-0105881.
PR	27-OCT-1998;	98US-0105882.
PR	27-OCT-1998;	98US-0106062.
PR	28-OCT-1998;	98US-0106023.
PR	28-OCT-1998;	98US-0106029.
PR	28-OCT-1998;	98US-0106030.
PR	28-OCT-1998;	98US-0106032.
PR	28-OCT-1998;	98US-0106033.
PR	28-OCT-1998;	98US-0106178.
PR	29-OCT-1998;	98US-0106248.
PR	29-OCT-1998;	98US-0106384.
PR	29-OCT-1998;	98US-0108500.
PR	30-OCT-1998;	98US-0106466.
PR	03-NOV-1998;	98US-0106856.
PR	03-NOV-1998;	98US-0106902.
PR	03-NOV-1998;	98US-0106905.
PR	03-NOV-1998;	98US-0106919.
PR	03-NOV-1998;	98US-0106932.
PR	03-NOV-1998;	98US-0106934.
PR	10-NOV-1998;	98US-0107783.
PR	17-NOV-1998;	98US-0108775.
PR	17-NOV-1998;	98US-0108779.
PR	17-NOV-1998;	98US-0108787.
PR	17-NOV-1998;	98US-0108788.
PR	17-NOV-1998;	98US-0108801.
PR	17-NOV-1998;	98US-0108802.
PR	17-NOV-1998;	98US-0108806.
PR	17-NOV-1998;	98US-0108807.
PR	17-NOV-1998;	98US-0108867.
PR	17-NOV-1998;	98US-0108925.
PR	18-NOV-1998;	98US-0108848.
PR	18-NOV-1998;	98US-0108849.
PR	18-NOV-1998;	98US-0108850.
PR	18-NOV-1998;	98US-0108851.
PR	18-NOV-1998;	98US-0108852.
PR	18-NOV-1998;	98US-0108855.
PR	18-NOV-1998;	98US-0108856.
XX	(GETH ) GENENTECH INC.	98US-0108904.
PA		
PI	Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;	
DR	WPI: 2000-237871/20.	
XX		
XX	N-PSDB; AAA37072.	
XX		
XX	New mammalian DNA sequences encoding transmembrane, receptor or	
PT	secreted PRO polypeptides, useful for screening of potential peptide or	
PT	small molecule inhibitors of the relevant receptor/ligand interactions	
XX		
PS	Claim 12; Fig 102; 773pp; English.	
XX		
XX	AAA37022 to AAA37144 encode the new isolated human transmembrane,	
CC	receptor or secreted PRO polypeptides given in AA99340 to AA99462. The	
CC	transmembrane and receptor PRO proteins can be used for screening of	
CC	potential peptide or small molecule inhibitors of the relevant	
CC	receptor/ligand interactions. The polypeptides and nucleotide sequences	
CC	encoding them have various industrial applications, including uses as	
CC	pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent	

CC PCR primers and hybridisation probes used in the isolation of the PRO  
CC polypeptides from the present invention.

SO Sequence 250 AA:

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 2.68e-97	250	250	0	0	0	0
Percent Similarity: 100.00%						
Best Local Similarity: 100.00%						
Query Match: 57.17%						
DB: 21						

US-09-856-320a-1 (1-1301) x AA99390 (1-250)

```

OY 209 ATGAGGATTCGACGATTATTCCTGCTGCTGGCAACAGGGCTGTGAGGGAGAGACC 268
DB 1 MetArgIleLeuGlnIleuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyIthr 20
OY 269 AGCATCATCAAGGGGTTGAGTGCAGAGCTGCTCCAGCCCTGGCAGGACGCTGTTC 328
DB 21 ArgIleIleuysGlyPheGlyCysIleysProHisSerGlnProTyrGlnAlaAlaLeuPhe 40
OY 329 GAGAGAGAGGGGCTACTGCTGAGGGGCGAGCTCAATCGCCGACATGGCTCTGTGACACGA 388
DB 41 GlnuysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrPleuLeuThrAla 60
OY 389 GCCCACTGCTCAAGCCCGCTACATAGTTACCTGGGGGAGCAGCAACCTCAGAGAGAG 448
DB 61 AlaHisCysIleuysProArgTyrIleValHisIleuGlyGlnHisAsnLeuGlnIleu 80
OY 449 GAGGGCTGTGAGCAGACCCGAGCAGCCAGCTGCTCCACCCGCTTCAACAC 508
DB 81 GlnuysCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 100
OY 509 AGCTCCGCAACAAAGACACCCGACATGATGATGCGTGGTGAAGATGGATCGGCACTC 568
DB 101 SerIleuProAsnIleuysAspHisArgAsnAspIleuMetLeuValIleuysMetAlaSerProVal 120
OY 569 TCCATACCTGGGCTGTGAGACCCCTCACCCTCTCAGCTGTGTCATGCTGGCAC 628
DB 121 SerIleuThrPalalaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
OY 629 AGTGGCGCATTCGCGGCTGGGGGAGCAGCTCCAGCCCGGCAATACCGCTCCGACACCC 688
DB 141 SerCysLeuIleSerGlyTyrPglySerThrSerSerProGlnLeuArgLeuProHisThr 160
OY 689 TTGGGATGGCCCAACATCACCATCATTTGAGCAGCAGAAAGTGTGAGAAAGCCTACCCGAGC 748
DB 161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnIleuysCysGlnAsnAlaIleTyrProGly 180
OY 749 AACATCACAGACACCATGCTGTGTCGACGCTGAGAGAGGGGCGCAAGGACTCTGCCAG 808
DB 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnIleuysAspSerCysGln 200
OY 809 GGTACACCGGGGGGCGCTGCTGTGTTAACCAGTCTCTCAAGCATATATCTCTGGAGC 868
DB 201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnIleIleSerTyrPgly 220
OY 869 CAGATCGATGCTGATGATCAGCCGAAAGCTGTGCTTACAGCAAGAGCTGCAATATGTC 928
DB 221 GlnAspProCysAlaIleThrArgIleysProGlyValIleTyrThrIleValCysIleTyrVal 240
OY 929 GACTGATCCAGAGAGCAGTGAAGACAT 958
DB 241 AspTyrIleGlnGlnIleuThrMetIleAsnAsn 250

```

RESULT 7

ABBS0479 standard: Protein: 250 AA.

XX ABB50479;  
AC ABB50479;  
XX

DT 07-FEB-2002 (first entry)  
XX  
DE Human secreted protein encoded by gene 179 SEQ ID NO:427.  
XX

Human: secreted protein; immunomodulatory; antisclerotic; anti-HIV; dermatological; immunosuppressive; antiinflammatory; immunostimulant; cytoskeletal; cardiac; vascular; anti-angiogenic; ophthalmological; neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnery; antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder; multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer; human immunodeficiency virus; hyperproliferative disorder; wound healing; Gaucher's disease; cardiovascular disease; Scleritar syndrome; chemotaxis; Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder; corneal graft neovascularisation; diabetic retinopathy; regeneration; neurological disorder; Huntington's chorea; Alzheimer's disease; Parkinson's disease; infectious disease.

OS Homo sapiens.

PN WO200162891-A2.

PD 30-AUG-2001.

PE 21-FEB-2001; 2001WO-US05614.

PR 24-FEB-2000; 2000US-184836P.

PR 29-MAR-2000; 2000US-193170P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Nt J, Edner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;

PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;

PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrle AM, Fan P;

PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;

PI Zeng Z, Greene JM;

XX WPI: 2001-625724/72.

DR N-PSDB: ABA83372.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:
Score: 2.68e-97	250	250	0	0
Percent Similarity: 100.00%				
Best Local Similarity: 100.00%				

Claim 11, Page 1181-1182; 1533pp: English.

ABBS0301 to ABB51287 and ABA83194 to ABA83441 represent human secreted proteins (I) and polynucleotide (II) sequences. (I) and (II) have various activities based on the tissues and cells the genes are expressed in. Example of these activities include: immunomodulatory; antisclerotic; dermatological; immunosuppressive; antiinflammatory; immunostimulant; anti-HIV; cytoskeletal; cardiac; anti-angiogenic; ophthalmological; neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular; antiparkinsonian; antimicrobial; and vulnery. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) can be used in the prevention, diagnosis and treatment of immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immunodeficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases (e.g. Scleritar syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to ABA83193 and ABB50300 represent sequences used in the exemplification of the present invention.

```

Query Match:      57.17%      Indels:      0
DB:               22          Gaps:         0
US-09-856-320A-1 (1-1301) x ABB50479 (1-250)

QY 209 ATGAGAGATTCGTCAGTAAATCTGCTGTGCTGGCAACAGGGCTGTAGGGGAGAGACC 268
DB 1 MetArgIleLeuGlnLeuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyIuThr 20
QY 269 AGCATCATCAAGGGGTGCGAGTGAAGCCTCACTCCAGCCCTGGAGGACCCCTGTTC 328
DB 21 ArgIleIleLysGlyPheGlnLysLysProHisSerGlnProTyrPheIleAlaLeuPhe 40
QY 339 GAGAAAGCGGGCTACTGTGTGGGAGACGCTATCGCCCGAGATGGCTCTGTGACAGA 388
DB 41 GlnLysThrArgLeuLeuLysGlyAlaThrLeuIleAlaProArgTyrLeuThrAla 60
QY 389 GCGCCACTGCTCAACCCCGCTACATAGTCACTGGGGGACAGACAACTCCAGAAAGAG 448
DB 61 AlaHisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisLeuGlnLysGln 80
QY 449 GAGGCTGTGAGCAGACCCGAGCAGCCACTGAGTCTCCCGCCGCGCTTCAACAGAC 508
DB 81 GlnGlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 100
QY 509 AGCTTCCCAACAAAGACACCGCAATGATCATGCTGTGAGATGGCATCGCCAGTTC 568
DB 101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY 569 TCATATCACTGGGCTGTGCGACCCCTCACTCTCTCAAGCTGTGTCACTGTGGCACC 628
DB 121 SerIleThrIlePheAlaValAlaArgProLeuThrLeuSerSerArgCysValThrIleGlyThr 140
QY 629 AGCTGCTCATATTCCGGCTGGGGGAGCAGCAGTCCAGCCCGCAATGACGCTGCGCTCAAC 688
DB 141 SerCysIleIleIleSerGlyTyrPheLysSerThrSerSerProGlnIleuArgLeuProHisThr 160
QY 689 TTGCGATGCGCCACATCATCAATCATTTGACACAGAAAGTGTGAGAACGCTTACCCCGGC 748
DB 161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaIleTyrProGly 180
QY 749 AACATCACAGACACCATGTGTGTGCGACGCTGTGCGAGAAAGGGGGAGAGAGCTCTGCCAG 808
DB 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 200
QY 809 GGTGACTCGGGGGCCCTGTGTGTGAACAGTCTCTTCAAGGCAATATCTCTGGGGC 868
DB 201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrPgly 220
QY 869 CAGATTCGCTGTGCGATCAACCGAAAGCCTGTGTACACGAAAGTCTGCAATATGTG 928
DB 221 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 240
QY 929 GACTGTGATCGAGAGACGATGAGAAACAAT 958
DB 241 AspThrIleGlnGlnThrMetLysAsnAsn 250

RESULT 8
AAU12424
ID AAU12424 standard; Protein: 250 AA.
XX
AC AAU12424;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO1279 polypeptide sequence.
XX
KM Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KM breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KM cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KM adipocyte; A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.

```

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XX XX
PN WO200140466-A2.
XX
XX 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32678.
XX
XX 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
XX (GENTH ) GENENTECH INC.
XX
XX Baker RP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI. 2001-408281/43.
DR N-PSDB; MAS21496.
XX
XX Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical.
XX
XX Claim 12; Fig 506; 813pp; English.
XX
XX AAU12172-AAU12446 represent novel human secretory and transmembrane
XX PRO polypeptides. The PRO polypeptides are useful to detect other
XX PRO polypeptides, to link bioactive molecules to cells expressing
XX PRO polypeptides, to modulate biological activities of cells expressing
XX PRO polypeptides, and to detect the presence of mammalian lung, colon,
XX breast, prostate, rectal, cervical or liver tumours by comparing PRO
XX polypeptide expression in a cell sample to that in a control sample.
XX Some of the 275 sequences are also useful to stimulate the release of
XX tumour necrosis factor-alpha (TNF-alpha) from human blood, the
XX proliferation or differentiation of chondrocytes, the proliferation or
XX gene expression in pericyte cells, the release of proteoglycans from
XX cartilage, the proliferation of inner ear utricular supporting cells or
XX of T-lymphocytes, the release of a cytokine from peripheral blood
XX monocytes (PBMCs), or the proliferation of endothelial cells. Some of
XX the PRO polypeptides may modulate glucose or free fatty acid uptake by
XX skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
XX to factor VIIA. The PRO polypeptides can be used in assays to identify
XX molecules involved in binding interactions. The polynucleotides encoding
XX PRO polypeptides can be used to generate probes, antisense RNA/DNA,
XX transgenic or knock out animals and can be used in gene therapy.
XX
XX Sequence 250 AA;
SQ

```

## Alignment Scores:

Pred. No.: 2,686-97 Length: 250  
 Score: 1355.00 Matches: 250  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 57.17% Indels: 0  
 DB: 22 Gaps: 0

US-09-856-320A-1 (1-1301) x AAB6139 (1-250)

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QY 209 ATGAGATTTCGACGTTAATCTGCTGCTGGCAACAGGGCTTGTAGGGGAGAGACC 268
    |||||||
Db 1 MetArglleuGlnleuIleleuAlaLeuAlaThrGlyLeuValGlyGluThr 20
QY 269 AGGATCATCAAGGGGTTTCAAGTGCAGAGCTTCCAGCCCTGGAGGAGAGCCCTGTTTC 328
    |||||||
Db 21 ArgIlelleuGlyPheGlnCysGlyProHisSerGlnProThrPrglnAlaAlaLeuPhe 40
QY 329 GAGAAAGCGGGCTACTCTGTGGGGGAGAGCTCATCGCCCAAGATGGCTCTGACAGCA 388
    |||||||
Db 41 GluIysThrArgleuLeuGlyAlaThrleuIleAlaProArgTrpLeuLeuThrAla 60
QY 389 GCCCACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGAGCAACCTCCAGAGAGAG 448
    |||||||
Db 61 AlaHisCysleuLysProAlaGlyTyrIleValHisleuGlyGlnHisAsnleuGlnGly 80
QY 449 GAGGGCTGTGAGACAGCCGAGACAGCACTGAGTCTTCCCGACCCGCTTCAACAC 508
    |||||||
Db 81 GluIleGlySerGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsn 100
QY 509 AGCCTCCCAACAAAGACCCAGCAATGACATGCTGCTGGAGAGAGTGGCATCCGACATC 568
    |||||||
Db 101 SerleuProAsnLysAspHisAspAsnAspIleMetleuValLysMetAlaSerProVal 120
QY 569 TCCATCACTGGGCTGTGAGACCCCTGACCTCTCTCAACGCTGTGCTGCTGAGCACC 628
    |||||||
Db 121 SerIleThrTrpAlaValArgProleuThrleuSerSerArgCysValThrAlaGlyThr 140
QY 629 AGTGGCTCATTTCCGGCTGGGGGAGAGAGCTGACAGCCCGAGTTACGCTGCTGACACC 688
    |||||||
Db 141 SerCysleuIleSerGlyTrpGlySerThrSerSerProGlnleuArgleuProHisThr 160
QY 689 TTGGGATGGCGCAACATACCATGATGAGACAGCAAGTGTGAGAACGCTTACCAGGCG 748
    |||||||
Db 161 LeuArgGlyAlaAsnIleThrIleleuGlnHisGlnLysCysGlnAsnAlaTyrProGly 180
QY 749 AACATCAAGACACCATGATGTGTGCGAGGCTGAGAGAGGGGAGAGAGACTCTGCGCAG 808
    |||||||
Db 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 200
QY 809 GGTGACTCCGGGGGCTCTGTGCTGTGTACCAAGTCTTCAAGGCAATTAATCTCTGGGCG 868
    |||||||
Db 201 GlyAspSerGlyGlyProleuValCysAsnGlnSerleuGlnGlyIleIleSerTrpGly 220
QY 869 CAGGATCCGTTGGGATGACCCAGCAAGCTGTGTCTACACAGAAAGTCTGCAATATGTG 928
    |||||||
Db 221 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 240
QY 929 GACTGATCCAGAGAGCATGAGAACAAAT 958
    |||||||
Db 241 AspTrpIleGlnGlnIleuThrMetLysAsnAsn 250
  
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RESULT 9

AAB6139 ID AAB6139 standard; protein: 250 AA.

AC AAB6139;

DT 02-APR-2001 (first entry)

DE Protein of the invention #51.

KW Secreted; transmembrane; gene therapy.

XX OS Unidentified.

XX PN WO200078961-A1.

XX PD 28-DEC-2000.

XX PF 18-FEB-2000; 2000WO-US04342.

XX PR 23-JUN-1999; 99US-0141037.

XX PR 20-JUL-1999; 99US-0144758.

XX PR 26-JUL-1999; 99US-0145638.

XX PR 01-SEP-1999; 99WO-US20111.

XX PR 29-OCT-1999; 99US-0162506.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 02-DEC-1999; 99WO-US28551.

XX PR 16-DEC-1999; 99WO-US30095.

XX PR 05-JAN-2000; 2000WO-US00219.

XX PR 06-JAN-2000; 2000WO-US00376.

XX PA (GENTH ) GENENTECH INC.

XX PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;

XX PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

XX PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;

XX PI Watanabe CK, Williams PM, Wood WI;

XX PI WPI; 2001-071395/08.

XX PS Claim 1; Fig 102; 787pp; English.

XX CC The present invention relates to secreted and transmembrane proteins.

XX CC These proteins and the DNA encoding them may be used as hybridization

XX CC probes, in chromosome and gene mapping and in the generation of

XX CC anti-sense RNA and DNA. They may also be used to generate either

XX CC transgenic animals or knockout animals which are in turn useful for

XX CC development and screening of therapeutically useful reagents.

XX CC The nucleic acids may also be used in gene therapy.

XX SQ Sequence 250 AA;

## Alignment Scores:

Pred. No.: 2,686-97 Length: 250  
 Score: 1355.00 Matches: 250  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 57.17% Indels: 0  
 DB: 22 Gaps: 0

US-09-856-320A-1 (1-1301) x AAB6139 (1-250)

```

QY 209 ATGAGATTTCGACGTTAATCTGCTGCTGGCAACAGGGCTTGTAGGGGAGAGACC 268
    |||||||
Db 1 MetArglleuGlnleuIleleuAlaLeuAlaThrGlyLeuValGlyGluThr 20
QY 269 AGGATCATCAAGGGGTTTCAAGTGCAGAGCTTCCAGCCCTGGAGGAGAGCCCTGTTTC 328
    |||||||
Db 21 ArgIlelleuGlyPheGlnCysGlyProHisSerGlnProThrPrglnAlaAlaLeuPhe 40
QY 329 GAGAAAGCGGGCTACTCTGTGGGGGAGAGCTCATCGCCCAAGATGGCTCTGACAGCA 388
    |||||||
Db 41 GluIysThrArgleuLeuGlyAlaThrleuIleAlaProArgTrpLeuLeuThrAla 60
QY 389 GCCCACTGCTCAAGCCCGCTACATAGTTCACTGGGGGAGAGCAACCTCCAGAGAGAG 448
    |||||||
Db 61 AlaHisCysleuLysProAlaGlyTyrIleValHisleuGlyGlnHisAsnleuGlnGly 80
QY 449 GAGGGCTGTGAGACAGACCCGAGACAGCACTGAGTCTTCCCGACCCGCTTCAACAC 508
  
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Db      81 GluGlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsn 100
QY      509 AGCCTCCCAACAAAGACACCCGAAATGACATCATCTGGTGAAGATGGCATGCCAGTC 568
Db      101 SerLeuProAsnIlyAspHisArgAsnAspIleMetLeuValIlyMetAlaSerProVal 120
QY      569 TCCATCATCTGGGCTGTGGACCCCTCACCCCTCTCTCTCAAGCTGTGTCACTGTGGCACC 628
Db      121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgGlyValThrAlaGlyThr 140
QY      629 AGCTGCTCATATTCCGGCTGGGGGACAGCTCCAGCTCCAGCCCACTTACGCCCTGCACACC 688
Db      141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY      689 TTGCGATGGCCCAACATCAATCATATGAGACACCAAGATGTGAGAACGCCCTACCCGGC 748
Db      161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnIlyCysGlnAsnAlaTrpProGly 180
QY      749 AACATCAACAGACACCATGTGTGTGTGGCAGCGTGCAGGAAGGGGCAAGACTCTGCCAG 808
Db      181 AsnIleThrAspThrMetValCysAlaSerValGlnGlyGlyLysAspSerCysGln 200
QY      809 GGTGACTCGGGGGCCCTGTGCTGTACACAGCTCTTCAAGGCAATTATCTCTGGGCG 868
Db      201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnIleIleSerTrpGly 220
QY      869 CAGGATCCGTGTGCATCACCCGAAAGCCTGTGTGTACAGAACTGTGCAATATGTG 928
Db      221 GlnAspProCysAlaIleThrArgLysProGlyValTrpThrIlyValCysLysTrpVal 240
QY      929 GACTGGATCCAGAGACGATGAAGAACAAT 958
Db      241 AspTrpIleGlnIleThrMetLysAsnAsn 250

RESULT 10
ABG61816
ID      ABG61816 standard; Protein; 250 AA.
XX
AC      ABG61816;
XX
DT      15-AUG-2002 (first entry)
XX
DE      Prostate cancer-associated protein #17.
XX
KM      Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
XX
OS      Mammalia.
XX
PN      WO200230268-A2.
XX
PD      18-APR-2002.
XX
PF      12-OCT-2001; 2001WO-US32045.
XX
PR      13-OCT-2000; 2000US-0687576.
PR      08-DEC-2000; 2000US-0733288.
PR      06-DEC-2000; 2000US-0733742.
PR      24-JAN-2001; 2001US-263957P.
PR      16-MAR-2001; 2001US-276791P.
PR      16-MAR-2001; 2001US-276888P.
PR      06-APR-2001; 2001US-281922P.
PR      24-APR-2001; 2001US-286214P.
PR      30-APR-2001; 2001US-0847046.
PR      04-MAY-2001; 2001US-288589P.
XX
PA      (BOSB-) EOS BIOTECHNOLOGY INC.
PI      Gish KC, Mack DH, Wilson KE, Afar D, Hvezzi P;
XX
DR      WPI; 2002-471335/50.
XX
N-PSDB; ABR92131.
XX

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PT      Detecting a prostate cancer-associated transcript in a cell in a
PT      patient, useful for diagnosing prostate cancer (PC) or screening
PT      modulators of PC, by determining if prostate cancer-associated genes
PT      are expressed in a prostate tissue
PS      Claim 27; Page 314; 436pp; English.
XX
XX      The present invention relates to methods of detecting a prostate
CC      cancer-associated transcript in a cell from a patient. The method
CC      comprises contacting a biological sample from the patient with
CC      prostate cancer-associated polynucleotides (designated PC genes) that
CC      selectively hybridise to a sequence that is at least 80% identical
CC      to them. The prostate cancer-associated polynucleotide sequences
CC      are differentially expressed in prostate tumour tissue or in
CC      prostate cancer and are derived from the tissues of various
CC      organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC      The methods of the invention are useful for diagnosing and treating
CC      prostate cancer in mammals. The prostate cancer-associated genes are
CC      useful for diagnosing or treating prostate cancer, as well as for
CC      identifying modulators of prostate cancer or agents that inhibit
CC      prostate cancer. The nucleic acid sequences are particularly useful
CC      in gene therapy, as a vaccine or in antisense applications.
CC      ABG61800-ABG61944 represent prostate cancer-associated proteins.
XX
SQ      Sequence      250 AA:

Alignment Scores:
Pred. No.:      2,68e-97      Length:      250
Score:      1355.00      Matches:      250
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      57.17%      Indels:      0
DB:      23      Gaps:      0

US-09-856-320A-1 (1-1301) x ABG61816 (1-250)
QY      209 ATGAGGATTCGAGTAAATCTGTCCTGTGTGGCAACAGGCTGTAGGGAGAGACC 268
Db      1 MetArgIleLeuGlnIleuIleLeuAlaLeuAlaThrGlyLeuValGlyGlyIuThr 20
QY      269 AGGATCATCAAGGGGTTCAGTGCAGGCTCATCTCCAGCCCTGGAGGACGCCCTGTTC 328
Db      21 ArgIleIleLysGlyPheGlyCysLysProHisSerGlnProTrpIlnAlaIleuPhe 40
QY      329 GAGAGAGCCGCGTACTCTGTGGGGGAGCGCTCATGCCCCGAGTGGCTCTGCAGACA 388
Db      41 GlnLysThrArgLeuLeuGlyGlyAlaThrIleuIlnAlaProArgTrpLeuThrAla 60
QY      389 GCCCACTGCCCTCAAGCCCGCTACATAGTTCACTTGGGGCAGCACAACTCCAGAGAG 448
Db      61 AlaHisCysLeuLysProArgTrpGlyIleValIlnHisLeuGlyGlnHisAsnLeuGlnLys 80
QY      449 GAGGCTGTGAGACACCCGGACAGCCACTGAGTCTTCCCGACCCCGGCTTCAACAA 508
Db      81 GluGlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsn 100
QY      509 AGCCTCCCAACAAAGACACCCGAAATGACATCATCTGGTGAAGATGGCATGCCAGTC 568
Db      101 SerLeuProAsnIlyAspHisArgAsnAspIleMetLeuValIlyMetAlaSerProVal 120
QY      569 TCCATCATCTGGGCTGTGGACCCCTCACCCCTCTCTCTCAAGCTGTGTCACTGTGGCACC 628
Db      121 SerIleThrTrpAlaValArgProLeuThrLeuSerSerArgGlyValThrAlaGlyThr 140
QY      629 AGCTGCTCATATTCCGGCTGGGGGACAGCTCCAGCTCCAGCCCACTTACGCCCTGCACACC 688
Db      141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY      689 TTGCGATGGCCCAACATCAATCATATGAGACACCAAGATGTGAGAACGCCCTACCCGGC 748
Db      161 LeuArgCysAlaAsnIleThrIleIleGlnHisGlnIlyCysGlnAsnAlaTrpProGly 180
QY      749 AACATCAACAGACACCATGTGTGTGTGGCAGCGTGCAGGAAGGGGCAAGACTCTGCCAG 808

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Db      181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyGlyLysAspSerGln 200
QY      809 GGTGACTCCGGGGCCCTGTGCTGTACCAAGCTCTTCAAGGATTATCTCCGGGCG 868
Db      201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
QY      869 CAGGATCCGTGTGCATACCCGGAAGCCCTGTGCTACACGAAAGTCTGCAATATGTG 928
Db      221 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 240
QY      929 GACTGATCCAGAGAGCATGAGACAAT 958
Db      241 AspTrpIleGlnGlnThrMetLysAsn 250

RESULT 11
ID      ABB95526
AC      ABB95526 standard; Protein; 250 AA.
XX      ABB95526;
XX      19-JUL-2002 (first entry)
DE      Human angiogenesis related protein PRO1279 SEQ ID NO: 208.
XX      Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW      atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW      cardiac; cytosolic; antiangiogenic; hypotensive; vulnery;
OS      antiarteriosclerotic.
XX      Homo sapiens.
XX      W0200208284-A2.
XX      31-JAN-2002.
XX      09-JUL-2001; 2001WO-US21735.
XX      20-JUL-2000; 2000US-219556P.
XX      25-JUL-2000; 2000US-220624P.
XX      28-JUL-2000; 2000US-220664P.
XX      02-AUG-2000; 2000US-222695P.
XX      17-AUG-2000; 2000US-0643657.
XX      23-AUG-2000; 2000US-0523522.
XX      24-AUG-2000; 2000WO-US23328.
XX      07-SEP-2000; 2000US-230978P.
XX      15-SEP-2000; 2000US-000000P.
XX      18-SEP-2000; 2000US-0664610.
XX      18-SEP-2000; 2000US-0655350.
XX      24-OCT-2000; 2000US-242922P.
XX      08-NOV-2000; 2000US-0709238.
XX      08-NOV-2000; 2000WO-US30952.
XX      01-NOV-2000; 2000WO-US30873.
XX      01-DEC-2000; 2000WO-US32678.
XX      20-DEC-2000; 2000US-0747259.
XX      20-DEC-2000; 2000WO-US4956.
XX      22-JAN-2001; 2001US-0767609.
XX      28-FEB-2001; 2001US-0796498.
XX      28-FEB-2001; 2001WO-US06520.
XX      01-MAR-2001; 2001WO-US06666.
XX      09-MAR-2001; 2001US-0802706.
XX      14-MAR-2001; 2001US-0808689.
XX      22-MAR-2001; 2001US-0816744.
XX      05-APR-2001; 2001US-0828366.
XX      10-MAY-2001; 2001US-0854208.
XX      10-MAY-2001; 2001US-0854280.
XX      25-MAY-2001; 2001US-0866028.
XX      25-MAY-2001; 2001US-0866034.
XX      30-MAY-2001; 2001US-0870574.
XX      30-MAY-2001; 2001WO-US17443.
XX      01-JUN-2001; 2001WO-US17800.

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PR      20-JUN-2001; 2001WO-US19692.
PR      28-JUN-2001; 2001WO-US00000.
XX      (GETH ) GENENTECH INC.
PA      (BAKE) BAKER K P.
PA      (FERR) FERRARA N.
PA      (GERB) GERBER H.
PA      (GERR) GERRITSEN M E.
PA      (GODD) GODDARD A.
PA      (GODO) GODOWSKI P J.
PA      (GURN) GURNEY A L.
PA      (HILL) HILLAN K J.
PA      (MARS) MARSTERS S A.
PA      (PANU) PAN J.
PA      (PAON) PAONI N F.
PA      (STEP) STEPHAN J F.
PA      (WATA) WATANABE C K.
PA      (WILL) WILLIAMS P M.
PA      (WOOD) WOOD W I.
XX      Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI      Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI      Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX      WPI: 2002-171999/22.
DR      N-PSDB; ABL95664.
XX      One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PI      useful in diagnosis and treatment of cardiovascular (e.g myocardial
PI      infarction), endothelial or angiogenic disorders in a mammal -
XX      Claim 11; Fig 208; 567PP; English.
XX      The present invention provides the protein and coding sequences of human
CC      PRO proteins. These are useful for treating or diagnosing a
CC      cardiovascular, endothelial or angiogenic disorder, including cardiac
CC      hypertrophy, trauma, cancer, age-related macular degeneration,
CC      atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC      angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC      angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC      healing. The present sequence is a PRO protein of the invention.
XX      SEQ Sequence 250 AA;
XX      Alignment Scores:
XX      Pred. No.: 2,686-97 Length: 250
XX      Score: 1355.00 Matches: 250
XX      Percent Similarity: 100.00% Conservative: 0
XX      Best Local Similarity: 100.00% Mismatches: 0
XX      Query Match: 57.17% Indels: 0
XX      DB: 23 Gaps: 0
XX      US-09-856-320A-1 (1-1301) x ABB95526 (1-250)
QY      209 ATGAGGATTCGGCAGTTAATCTCTGCTGTGCGAACAGGGCTTGTAGGGGAGAGACC 268
Db      1 MetArgIleLeuGlnIleuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlnThr 20
QY      269 AGGATCATCAAGGGGGTTCGAGTGCAGACCTTCACCTCCAGGCCCTGGCAGGAGCCCTGTC 328
Db      21 ArgIleIleLeuGlnIleuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlnThr 20
QY      329 GAGAAGACGGCGCTACTCTGTGGGGCAGCCTCATCGCCGCCAGATGGCTCTGACAGCA 388
Db      41 GluIleThrArgLeuLeuGlnGlyAlaIleThrLeuIleAlaProArgTrpLeuThrAla 60
QY      389 GCCCAGTCCCTCAAGCCCCCGCTACATAGTTCACCTGGGGGAGACCAACCTCCAGAGGAG 448
Db      61 AlaHisCysLeuIleuGlnProArgTyrIleValAlaHisIleuGlnIleHisAsnLeuGlnGln 80
QY      449 GAGGGCTGTGAGCAGACCGGAGACGACCATGAGAGCTTCCGCCACCCGGGCTTCACCAAC 508
Db      81 GluIleCysGlnGlnIleThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsn 100

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QY 509 AGCTCCCAACAAAGACCGCAATGATCATCTGTGAAAGTGCATCGCCAGTC 568
Db 101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal 120
QY 569 TCCATACCTGGGGCTGGGAGCCCTCACCTCTCTCAAGCTGTGCTCACTGTGGCACC 628
Db 121 SerIleThrTrpAlaAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140
QY 629 AGCTGCCATATTCGGCTGGGGCAGACAGCTCCAGCCCACTTACGCTGCCCTCACACC 688
Db 141 SerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThr 160
QY 689 TTGCGATGGCCCAACATCACCATCATGAGCAGACAGAGTGTGAGAGCCCTACCCGGC 748
Db 161 LeuArgCysAlaAsnIleThrIleLeuHisGlnLysCysGlnAsnAlaTyrProGly 180
QY 749 AACATCAGACAGACCATGTGTGTGTCAGCAGCTGCGAAGAGGGGCAAGACATCTCCAG 808
Db 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlyLysAspSerCysGln 200
QY 809 GGTGACTCCGGGGGCGCTGTGCTGTAAACAGTCTCTCAAGGCAATATCTCTGGGGC 868
Db 201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
QY 869 CAGGATCCGTGTGCGATCACCCGAAAGCCTGTGTCTACAGAAAGTGTGCAAAATATGTC 928
Db 221 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrVal 240
QY 929 GACTGATCCAGAGACGATGAAGAACAT 958
Db 241 AspTrpIleGlnGlnIleThrMetLysAsnAsn 250

RESULT 12
ABR84920
ID ABR84920 standard; Protein: 250 AA.
XX
XX ABR84920:
AC
DE 16-MAY-2002 (first entry)
XX
XX Human PRO1279 protein sequence SEQ ID NO:208.
DE
XX
XX Human; angiogenesis; cardiast; cytosatic; antiangiogenic; hypotensive;
XX
XX Vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;
XX
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX
XX age-related macular degeneration; arterial restenosis; angina;
XX
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
XX
XX wound healing; chromosome mapping; gene mapping.
XX
XX Homo sapiens.
OS
XX
XX WO200200690-A2.
PN
XX
XX 03-JAN-2002.
PD
XX
XX 20-JUN-2001; 2001WO-US19692.
PF
XX
XX 23-JUN-2000; 2000US-213637P.
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222659P.
PR 17-AUG-2000; 2000US-064365P.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 18-SEP-2000; 2000US-066410.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.

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PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0806589.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 30-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 01-JUN-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX
XX (GENTECH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gertlsen ME, Goddard A;
XX
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
XX
XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX WPI; 2002-090516/12.
XX
XX N-PSDB; ABL88175.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX
XX infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 11; Fig 208; 565pp; English.
XX
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABR84817 to
XX
XX ABR85003. The PRO proteins and polynucleotides have cardiast, cytosatic,
XX
XX antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
XX
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX
XX a cardiovascular, endothelial or angiogenic disorder in a mammal,
XX
XX e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX
XX degeneration, atherosclerosis, hypertension, arterial restenosis,
XX
XX rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
XX
XX lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
XX
XX carcinoma) and wound healing. The PRO polynucleotides have applications
XX
XX in molecular biology, including use as hybridisation probes, and in
XX
XX chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX
XX probes used in the exemplification of the present invention.
XX
XX
XX Sequence 250 AA:
SQ
XX
XX
XX Alignment Scores:
XX
XX Pred. No.: 2.68e-97 Length: 250
XX
XX Score: 1355.00 Matches: 250
XX
XX Percent Similarity: 100.00% Conservative: 0
XX
XX Best Local Similarity: 100.00% Mismatches: 0
XX
XX Query Match: 57.17% Indels: 0
XX
XX DB: 23 Gaps: 0
XX
XX
XX US-09-856-320A-1 (1-1301) x ABR84920 (1-250)
QY 209 ATGAGGATCTGTCAGTATATCTGCTGTGCGCAAGGCGCTTGTAGGGGAGAGACC 268
Db 1 MetArgIleLeuGlnLeuIleLeuAlaLeuAlaThrGlyLeuValGlyGlyThr 20
QY 269 AGCATCATCAAGGGGTTCAGTGTGCAAGCCTTCACCTCCAGGCGGAGGACCGCTGTTTC 328
Db 21 ArgIleIleValGlyPheGlnCysLysSPProHisSerGlnProTrpPheIleAlaLeuPhe 40

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OY 329 GAGAGAGCGCGCTACTGTGTGGGGCAGCGCTCATCGCCGCCAGATGGCTCTGTGACAGCA 388
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Db 41 GlutylserthrargleuleucysglYAlaIthrleulleaIaProargTyrPleuleuthrAla 60
OY 389 GCCACACTCCCAAGACCCCGCTACATAGTTCACCTGGGGGAGCAACCTCCAGAGAG 448
    |||||||
Db 61 AlaIhscysleuLysProargTyrIleValaIhscysleuGlnhIsaIhscysleuGln 80
OY 449 GAGGCGTGTGAGCAGACCCGAGCAGCCAGCTAGTCCTTCCGCCACCCCGCTTCAACAC 508
    |||||||
Db 81 GluGlycysgluGlnThrArgThrAlaThrGluSerPheProhIsProGlyPheasn 100
OY 509 AGCCTCCCAACAAAGACACCCAGCAATACATCATCTGCGGAGATGGATCGGCAATC 568
    |||||||
Db 101 SerleuProasnLysAspHisArgAsnaspIleMetleuValLysMetAlaSerProVal 120
OY 569 TTCATACACTGGGCTGTGCGACCCCTCACCCTTCCTCAGCTGTGCTGCTGCGAC 628
    |||||||
Db 121 SerIleThrTrpAlaValArgProleuThrleuSerSerAlaGlyValThrAlaGlyThr 140
OY 629 AGCTGCTCATTTCCGCGCTGGGGAGCAGCAGCTCAGCCCGCCAGTTACGCTGCTCACAC 688
    |||||||
Db 141 SerCysleuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProhIsThr 160
OY 689 TTGGGATGCGCCGACATCATCATCATATGAGCAGCAGAAAGTGTGAGAACGCTTACCCGCGC 748
    |||||||
Db 161 LeuArgCysAlaAsnIleThrIleIleGlnhIsGlnLysCysGlnAsnAlaIaTyrProGly 180
OY 749 AACATCAGACAGACCATGCTGTGTCCAGCTGACAGAGAGGGGCAAGAGCTCCGCGCAG 808
    |||||||
Db 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnLysGlyLysAspSerCysGln 200
OY 809 GGTGACTCCGGGGGCGCTGTGCTGTGTATACAGTCTCTTCAAGGCATTATCTCTGGGGC 868
    |||||||
Db 201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerleuGlnGlyIleIleSerTrpIy 220
OY 869 CAGATCCGCTGGGATCACCAGAAAGCTGTCTCATCAGAAAGTGTGCAATATGTCG 928
    |||||||
Db 221 GlnAspProCysAlaIleThrArgLysProGlyValIyThrLysValCysLysIyVal 240
OY 929 GACTGATCCAGAGACGATGAGAACAAAT 958
    |||||||
Db 241 AspIrpIleGlnGlnIuThrMetLysAsn 250

```

RESULT 13  
 AA083684  
 ID AA083684 standard; Protein: 250 AA.  
 XX  
 AC AA083684;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE Human PRO protein, Seq ID No 186.  
 XX  
 KW Human: secreted protein: PRO: tumour; lung cancer; colon cancer;  
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
 KW pericyte cell proliferation; chondrocyte cell proliferation;  
 KW tumour necrosis factor-alpha.  
 KW  
 OS Homo sapiens.  
 XX  
 PN MO200208288-A2.  
 XX  
 PD 31-JAN-2002.  
 XX  
 PE 29-JUN-2001; 2001WO-US21066.  
 XX  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220585P.  
 PR 25-JUL-2000; 2000US-220605P.  
 PR 25-JUL-2000; 2000US-220607P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220638P.

```

PR 25-JUL-2000; 2000US-220664P.  

PR 25-JUL-2000; 2000US-220666P.  

PR 26-JUL-2000; 2000US-220893P.  

PR 28-JUL-2000; 2000WO-US20710.  

PR 23-AUG-2000; 2000WO-US23522.  

PR 24-AUG-2000; 2000WO-US23328.  

PR 15-SEP-2000; 2000US-000000P.  

PR 10-NOV-2000; 2000WO-US30873.  

PR 28-NOV-2000; 2000US-253646P.  

PR 01-DEC-2000; 2000WO-US32678.  

PR 20-DEC-2000; 2000US-0747259.  

PR 20-DEC-2000; 2000WO-US34956.  

PR 28-FEB-2001; 2001WO-US06520.  

PR 10-MAY-2001; 2001US-0854280.  

PR 25-MAY-2001; 2001WO-US17092.  

XX  

PA (GENE) GENENTECH INC.  

XX  

PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,  

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  

XX  

XX WPI; 2002-172001/22.  

XX N-PSDB; ABK33628.  

XX  

XX  

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  

XX useful for treating a PRO related disorder and for diagnosing tumours  

XX such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  

XX tumour or liver tumour -  

XX  

XX  

XX Claim 11; Figure 186; 359pp; English.  

XX  

XX The invention relates to one hundred and twenty two nucleic acids  

XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  

XX encode human secreted proteins. The PRO nucleic acids, polypeptides,  

XX agonists and antagonists are useful for treating a PRO related disorder.  

XX The PRO polypeptides are useful for diagnosing tumours, especially lung  

XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  

XX liver tumour. The PRO polypeptides are useful for stimulating the  

XX proliferation of, or gene expression, in pericyte cells, for stimulating  

XX the proliferation or differentiation of chondrocyte cells, for  

XX stimulating the release of tumour necrosis factor-alpha from human blood,  

XX for stimulating or inhibiting the proliferation of normal human dermal  

XX fibroblast cells. The PRO polypeptide may also be used as molecular  

XX weight markers and for tissue typing. The PRO nucleic acids have  

XX applications in molecular biology, including use as hybridisation probes,  

XX and in chromosome and gene mapping. AA083592-AA083713 represent human PRO  

XX protein sequences of the invention.  

XX  

XX  

XX Sequence 250 AA;  

XX  

XX  

XX  

XX Alignment Scores:  

XX Pred. No.: 2,68e-97 Length: 250  

XX Score: 1355.00 Matches: 250  

XX Percent Similarity: 100.00% Conservative: 0  

XX Best Local Similarity: 100.00% Mismatches: 0  

XX Query Match: 57.17% Indels: 0  

XX DB: 23 Gaps: 0  

XX  

XX US-09-856-320A-1 (1-1301) x AA083684 (1-250)  

OY 209 ATGAGGATTCGCGAGTTATCTCTGCTGTGCAACAGGGCTTGTAGGGGAGAGACC 268
    |||||||
Db 1 MetArgIleuGlnIleuIleuIleuAlaIleuAlaThrGlyIleuValGlyGlyIuThr 20
OY 269 AGGATCATCAAGGGGTTGAGTGCAGCTCAGCCAGCCGCGGAGGAGAGCCGCTTC 328
    |||||||
Db 21 ArgIleIleuysGlyPheGlyLysProhIsSerInProIrpGlnAlaAlaLeuPhe 40
OY 329 GAGAGAGCGCGCTACTGTGTGGGGCAGCAGCTCATCGCCCGCCAGATGGCTCTGACAGCA 388
    |||||||
Db 41 GlutylserthrargleuleucysglYAlaIthrleulleaIaProargTyrPleuleuthrAla 60
OY 389 GCCACACTCCCAAGACCCCGCTACATAGTTCACCTGGGGGAGCAACCTCCAGAGAG 448

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Db      |||||
61 AlaHisCysLeuIysProAlaGlyTyrIleValHisLeuGlyGlnHisAsnLeuGlnIysGln 80
QY      449 GAGGGCTGTGACAGACACCGGACAGACGACTGATGCTTCCGCCACCCGGCTTCAACAC 508
Db      81 GluGlyCysGluGlnThrArgThrAlaThrGlnUserPheProHisProIlePheAsn 100
QY      509 AGCTCCGCCAACAAACACCGACCGCAATGACATCATGCTGGTGAAGATGGCATCGCCATC 568
Db      101 SerLeuProAsnIlysPheHisArgAsnAspIleMetLeuValIysMetAlaSerProVal 120
QY      569 TGCATCACCTGGGCTGGGAGCCCTCACCCTCTCTCAAGCTGTGTCACTGCTGGCACC 628
Db      121 SerIleThrTrpAlaValAlaArgProLeuThrIleSerSerArgCysValThrAlaGlyThr 140
QY      629 ACCTGCTCATTTCCGGCTGGGAGCAGACGTCACAGCCCGACGATACGCTGCTCAGCC 688
Db      141 SerCysLeuIleSerClyTrpIleSerThrSerSerProGlnLeuArgLeuProHisThr 160
QY      689 TTGCGATGCGCCACATCACATCATTTGAGCACACGAGTGTGAGAACGCTACCCCGGC 748
Db      161 LeuAlaGlyCysAlaAsnIleThrIleIleGlnHisGlnIysCysGlnAsnAlaTyrProGly 180
QY      749 AACATCACAGACACCATGGTGTGTGCCACCGTCGACGAGGAGGGGCGACGACTCTGCCAG 808
Db      181 AsnIleThrAspThrMetValCysAlaSerValGlnGluGlyCylLysAspSerCysGln 200
QY      809 GGTGACTCCGGGGGCCCTGTGCTGTATACAGTCTCTTCAAGGCTTATCTCTGGGGC 868
Db      201 GlyAspSerClyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220
QY      869 CAGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTTACACGAAAGTGTGCAAAATATGTG 928
Db      221 GlnAspProCysAlaIleThrArgLysProGlyValTyrThrIysValCysLysTyrVal 240
QY      929 GACTGGATCCAGACGATGAGAACAT 958
Db      241 AspTrpIleGlnGlnThrMetLysAsnAsn 250

RESULT 14
ID      AB066822 standard; Protein; 250 AA.
XX      AB066822;
XX      23-MAY-2003 (first entry)
XX      Human PRO polypeptide #253.
DE      Human; PRO polypeptide; secreted and transmembrane protein;
KW      tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW      differentiation; chondrocyte; tumour; genetic disorder;
KW      cytosolic.
XX      Homo sapiens.
OS      US2003036180-A1.
XX      20-FEB-2003.
XX      09-MAY-2002; 2002US-0143114.
XX      31-MAR-1997; 97WO-US05230.
XX      12-JUN-1998; 98WO-US12456.
XX      14-JUL-1998; 98WO-US14552.
XX      28-AUG-1998; 98WO-US17888.
XX      10-SEP-1998; 98WO-US18824.
XX      14-SEP-1998; 98WO-US19093.
XX      14-SEP-1998; 98WO-US19094.
XX      14-SEP-1998; 98WO-US19177.
XX      16-SEP-1998; 98WO-US19330.
XX      17-SEP-1998; 98WO-US19437.
XX      07-OCT-1998; 98WO-US21141.
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PR      29-OCT-1998; 98WO-US22991.
PR      29-OCT-1998; 98WO-US22992.
PR      01-DEC-1998; 98WO-US24855.
PR      05-JAN-1999; 98WO-US25108.
PR      08-MAR-1999; 98WO-US250106.
PR      10-MAR-1999; 98WO-US05190.
PR      20-APR-1999; 98WO-US08615.
PR      14-MAY-1999; 98WO-US10733.
PR      02-JUN-1999; 98WO-US12252.
PR      01-SEP-1999; 98WO-US20111.
PR      08-SEP-1999; 98WO-US20594.
PR      13-SEP-1999; 98WO-US20944.
PR      15-SEP-1999; 98WO-US21090.
PR      15-SEP-1999; 98WO-US21547.
PR      05-OCT-1999; 98WO-US23089.
PR      29-NOV-1999; 98WO-US28214.
PR      30-NOV-1999; 98WO-US28313.
PR      30-NOV-1999; 98WO-US28409.
PR      01-DEC-1999; 98WO-US28301.
PR      01-DEC-1999; 98WO-US28634.
PR      02-DEC-1999; 98WO-US28551.
PR      02-DEC-1999; 98WO-US28564.
PR      02-DEC-1999; 98WO-US28565.
PR      16-DEC-1999; 98WO-US30095.
PR      20-DEC-1999; 98WO-US30911.
PR      20-DEC-1999; 98WO-US30999.
PR      22-DEC-1999; 98WO-US30720.
PR      30-DEC-1999; 98WO-US31243.
PR      30-DEC-1999; 98WO-US31274.
PR      05-JAN-2000; 2000WO-US00219.
PR      06-JAN-2000; 2000WO-US00277.
PR      06-JAN-2000; 2000WO-US00376.
PR      11-FEB-2000; 2000WO-US03565.
PR      18-FEB-2000; 2000WO-US04341.
PR      18-FEB-2000; 2000WO-US04342.
PR      22-FEB-2000; 2000WO-US04414.
PR      24-FEB-2000; 2000WO-US04914.
PR      24-FEB-2000; 2000WO-US05004.
PR      02-MAR-2000; 2000WO-US05601.
PR      02-MAR-2000; 2000WO-US05746.
PR      02-MAR-2000; 2000WO-US05841.
PR      10-MAR-2000; 2000WO-US06319.
PR      15-MAR-2000; 2000WO-US06884.
PR      20-MAR-2000; 2000WO-US07377.
PR      21-MAR-2000; 2000WO-US07532.
PR      30-MAR-2000; 2000WO-US08439.
PR      17-MAY-2000; 2000WO-US13705.
PR      22-MAY-2000; 2000WO-US14042.
PR      30-MAY-2000; 2000WO-US14941.
PR      02-JUN-2000; 2000WO-US15264.
PR      28-JUL-2000; 2000WO-US20710.
PR      11-AUG-2000; 2000WO-US22031.
PR      23-AUG-2000; 2000WO-US23522.
PR      24-AUG-2000; 2000WO-US23328.
PR      08-NOV-2000; 2000WO-US30952.
PR      10-NOV-2000; 2000WO-US30873.
PR      01-DEC-2000; 2000WO-US32678.
PR      20-DEC-2000; 2000WO-US34956.
PR      28-FEB-2001; 2001WO-US06520.
PR      01-MAR-2001; 2001WO-US06666.
PR      25-MAY-2001; 2001WO-US17092.
PR      01-JUN-2001; 2001WO-US17800.
PR      20-JUN-2001; 2001WO-US19692.
PR      22-JUN-2001; 2001WO-US20116.
PR      29-JUN-2001; 2001WO-US21066.
PR      09-JUL-2001; 2001WO-US21735.
PR      20-DEC-2000; 2000US-0747259.
PR      28-FEB-2001; 2001US-0796498.
PR      09-MAR-2001; 2001US-0803706.
PR      14-MAR-2001; 2001US-0808689.
PR      22-MAR-2001; 2001US-0816744.
PR      05-APR-2001; 2001US-0826366.
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PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 18-MAY-2001; 2001US-0860216.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 01-JUN-2001; 2001US-0872035.  
PR 05-JUN-2001; 2001US-0874503.  
PR 14-JUN-2001; 2001US-0882636.  
PR 19-JUN-2001; 2001US-0886342.  
PR 21-JUN-2001; 2001US-0887879.  
PR 18-JUL-2001; 2001US-0908827.  
PR 06-AUG-2001; 2001US-0924419.  
PR 09-AUG-2001; 2001US-0927796.  
PR 16-AUG-2001; 2001US-0931836.  
PR 19-DEC-2001; 2001US-0028072.  
PR (GENTH ) GENTECH INC.  
XX  
XX Baker RP, Beresini M, DeForge L, Desnoyers L, Flivaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S,  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX WPI; 2003-332040/31.  
DR N-PSDB; ACA03855.  
XX  
XX New secreted and transmembrane PRO nucleic acids, useful for gene  
PT therapy, in chromosome and gene mapping, as chromosome markers, in  
PT tissue typing, and in chromosome identification -  
XX  
XX Claim 12; Fig 506; 660pp; English.  
PS  
XX The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The  
CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for  
CC linking bioactive molecules to cells expressing PRO polypeptides,  
CC for modulating biological activities of cells expressing PRO  
CC polypeptides, and for identifying agonists or antagonists.  
CC The PRO polypeptides are useful for stimulating the release of  
CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating  
CC the proliferation or differentiation of chondrocytes, and detecting the  
CC presence of tumours. The polynucleotide sequences encoding PRO  
CC polypeptides are useful as hybridisation probes, in chromosome and  
CC gene mapping, in the generation of antisense RNA and DNA, in the  
CC preparation of PRO polypeptides, for generating transgenic animals or  
CC knockout animals, for the genetic analysis of individuals with genetic  
CC disorders, and in gene therapy. AB06570-AB066844 represent the human  
CC PRO polypeptides of the invention.  
CC Note: The sequence data for this patent was obtained in electronic  
CC format directly from the USPTO web site at  
CC seqdata.uspto.gov/psipdsidentity.html.  
XX  
XX  
XX Sequence 250 AA:  
SO  
Alignment Scores:  
Pred. No.: 2,68e-97 Length: 250  
Score: 1355.00 Matches: 250  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 57.17% Indels: 0  
DB: 24 Gaps: 0  
US-09-856-320a-1 (1-1301) x AB066822 (1-250)  
OY 209 ATGAGATTCCTGCAAGTTAACTCTGCTTGCGCAACAGGGCTTGAAGGGAGAGACC 268  
DB 1 MetArgileuenglInleuileLeuLeuAlaLeuAlaThrGlyLeuValGlyGluThr 20  
OY 269 AGGATCATCAAGGGCTTGCAGTGAACCTTCACCTCCAGCCCTGGCAGGAGACCCCTGTC 328  
DB 21 ArgilelleuysgIlypneglucylsProlHisSerGlnProItrpGlnAlaAlaLeuPhe 40  
OY 329 GAGAAAGACGGGGCTACTCTGTGGGGGCGAGCGTATCGCCGCCCAAGATGGCTCTTCACAGCA 388

DB 41 GluIysThrArgLeuLeuCysGlyAlaThrLeuLeuLeuProArgItrpLeuThrAla 60  
OY 389 GGGCAGCTGCTCAAGCCCCGGCTACATAGTTACCTGGGGGCGCAACCTCCACAGAG 448  
DB 61 AlaniscysLeuIysProlArgItrpGlyLeuValHisLeuGlnHisAsnLeuGlnLysGlu 80  
OY 449 GAGGCGCTGTAGCAGACCCGGAGCAGCCAGTACGTCTTCCGCCAGCCCGGCTTCACAC 508  
DB 81 GluGlyCysGluGlnThrArgThrAlaThrGluSerPhePronHisProlGlyPheAsn 100  
OY 509 AGCTCCGCCAACAAAGACCCAGCAGTACATGCTGCTGGTGAAGATGSGATGCGGAC 568  
DB 101 SerLeuProlAsnLysAspHisAspHisAspIleMetLeuValLysMetAlaSerProVal 120  
OY 569 TCCATCAGCTGGGCTGTGCGACCCCTGACCTTCTCTCAGCCTGTGACGTGGGAC 628  
DB 121 SerIleThrItrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140  
OY 629 AGTGCCTCATTTCCGGCTGGGGGAGCAGCTGCAGCCCGGAGTTACGCTGCTACACC 688  
DB 141 SerCysLeuIleSerGlyItrpGlySerThrSerSerProGlnLeuArgLeuPronHisThr 160  
OY 689 TTGGGATGGCGGCACATCACCATCATGATGAGCAGCAGAGTGTGAGACGGCTACCCGGC 748  
DB 161 LeuArgCysAlaAsnIleThrIleLeuGlnHisGlnLysCysGlnAsnAlaItrpGly 180  
OY 749 AACATCAGACAGACCATAGTGTGTGCGAGCTGCAGAGGAGGGGCGAGCATCTGCGCAG 808  
DB 181 AsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGln 200  
OY 809 GGTACTCCGGGGGCGCTGTGTTACCAAGTCTTTCAAGGATTAATCTCTGGGCG 868  
DB 201 GlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGly 220  
OY 869 CAGATCGGTGTGATCACCCGGAAGCTGTGTACAGAAAGTGTCAATATAGTG 928  
DB 221 GlnsProlCysAlaIleThrArgLysProlGlyValItrpLysValCysLysItrpVal 240  
OY 929 GACTGTATCCAGGAGCATGACAGAACAT 958  
DB 241 AspItrpIleGlnItrpThrMetLysAsn 250  
RESULT 15  
AB067098  
ID AB067098 standard; Protein; 250 AA.  
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XX AB067098;  
AC  
XX  
XX 27-MAY-2003 (first entry)  
DE  
XX  
XX Human secreted/transmembrane, PRO, protein SEQ ID 506.  
DE  
XX  
XX Human; secreted protein; transmembrane protein; PRO;  
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
KW infertility; birth defects; premature aging; AIDS; biosensor;  
KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
KW bioreactor; tumour.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2003032155-A1.  
PN  
XX  
XX 13-FEB-2003.  
PD  
XX  
XX 03-MAY-2002; 2002US-0137865.  
PF  
XX  
XX 31-MAR-1997; 97WO-US05230.  
PR 12-JUN-1998; 98WO-US12456.  
PR 14-JUL-1998; 98WO-US14552.  
PR 28-AUG-1998; 98WO-US17888.  
PR 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19093.

PR 14-SEP-1998: 98MO-US19094.  
 PR 14-SEP-1998: 98MO-US19177.  
 PR 16-SEP-1998: 98MO-US19330.  
 PR 17-SEP-1998: 98MO-US19437.  
 PR 07-OCT-1998: 98MO-US21141.  
 PR 29-OCT-1998: 98MO-US22991.  
 PR 29-OCT-1998: 98MO-US22992.  
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 PR 13-SEP-1999: 98MO-US20944.  
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 PR 29-NOV-1999: 98MO-US28214.  
 PR 30-NOV-1999: 98MO-US28313.  
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 PR 24-AUG-2000: 2000MO-US23328.  
 PR 08-NOV-2000: 2000MO-US30952.  
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 PR 20-DEC-2000: 2000MO-US34956.  
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 PR 25-MAY-2001: 2001MO-US17092.  
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 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI: 2003-331925/31.  
 DR N-PSDB: NCA04276.  
 XX  
 PT New secreted and transmembrane nucleic acids and polypeptides,  
 PT designated as PRO, useful for treating inflammation, organ failure,  
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature  
 PT aging, AIDS, or cancer -  
 PS  
 XX  
 PS Claim 12: Fig 506; 655pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising, or which is  
 CC at least 80% identical to, or the full-length coding sequence of, any of  
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide  
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid  
 CC further comprises the full-length coding sequence of the DNA deposited  
 CC under American Type Culture Collection (ATCC) accession number in a list  
 CC given in the specification. Also included are vectors and host  
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO  
 CC antibodies, PRO extracellular domains and mature sequences, methods  
 CC of detecting PRO proteins, methods for stimulating the release of  
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,  
 CC (and the proliferation of differentiation of chondrocyte cells, the  
 CC proliferation of, or gene expression in pericyte cells, the release or  
 CC proteoglycans from cartilage, proliferation of inner ear utricular  
 CC supporting cells, the proliferation of T-lymphocyte cells, the release  
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the  
 CC proliferation of endothelial cells), a method for modulating the uptake  
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,  
 CC a method for inhibiting the binding of A-peptide to factor VIIA,  
 CC or the differentiation of adipocyte cells, a method for detecting the  
 CC presence of a tumour in a mammal and an oligonucleotide probe derived  
 CC from any of the nucleotide sequences cited above. The nucleic acids and  
 CC polypeptides are useful for treating inflammatory diseases, organ  
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,  
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or  
 CC diabetic complications. The nucleic acids are useful as hybridisation  
 CC probes, in chromosome and gene mapping, and in generating antisense RNA  
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors. Both are useful in tissue typing.  
 CC The present sequence represents a PRO protein of the invention.  
 XX  
 SQ Sequence 250 AA:  
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 Score: 1355.00 Matches: 250

Percent Similarity: 100.008  
Best Local Similarity: 100.008  
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Conservative: 0  
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US-09-856-320a-1 (1-1301) x AB067098 (1-250)

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Job time : 67.1889 secs

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4738.816 Million cell updates/sec

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Searched: 328717 seqs, 42310858 residues

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Minimum DB seq length: 0  
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Maximum Match 100%  
Listing first 45 summaries

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- 6: /cgcn2\_6/plodata/2/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	1324	55.9	248	4	US-08-944-483-24 Sequence 24, Appl
4	1279	54.0	246	4	US-09-205-258-1149 Sequence 1149, Ap
5	1232	52.0	289	4	US-09-386-642-14 Sequence 14, Appl
6	1197	50.5	228	4	US-09-205-258-1150 Sequence 1150, Ap
7	698.5	29.5	260	3	US-09-025-059-3 Sequence 3, Appl1
8	690	29.1	260	4	US-09-070-526-2 Sequence 2, Appl1
9	689	29.1	288	4	US-09-386-642-13 Sequence 13, Appl
10	682	28.8	260	3	US-09-008-271A-7 Sequence 7, Appl1
11	650.5	27.4	293	4	US-09-996-243-309 Sequence 309, Appl
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15	604.5	25.5	263	2	US-08-790-137-4 Sequence 4, Appl1
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17	604.5	25.5	263	3	US-08-807-151-5 Sequence 5, Appl1
18	604.5	25.5	263	3	US-09-210-084-5 Sequence 5, Appl1
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21	600.5	25.3	246	2	US-08-978-404B-44 Sequence 4, Appl
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43	580	24.5	262	2	US-08-790-137-3 Sequence 3, Appl1
44	580	24.5	262	2	US-08-681-151-4 Sequence 4, Appl1
45	580	24.5	262	2	US-08-824-874-4 Sequence 4, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-025-059-1  
; Sequence 1, Application US/09025059  
; Patent No. 6075136  
GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: Guegler, Karl J.  
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,059  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0481 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166





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1  EARLIER APPLICATION NUMBER: 60/048, 9114
2  EARLIER FILING DATE: 1997-06-06
3  EARLIER APPLICATION NUMBER: 60/048, 9454
4  EARLIER FILING DATE: 1997-06-06
5  EARLIER APPLICATION NUMBER: 60/048, 9744
6  EARLIER FILING DATE: 1997-06-06
7  EARLIER APPLICATION NUMBER: 60/048, 8833
8  EARLIER FILING DATE: 1997-06-06
9  EARLIER APPLICATION NUMBER: 60/048, 8892
10 EARLIER FILING DATE: 1997-06-06
11 EARLIER APPLICATION NUMBER: 60/048, 8898
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14 EARLIER FILING DATE: 1997-06-06
15 EARLIER APPLICATION NUMBER: 60/048, 9626
16 EARLIER FILING DATE: 1997-06-06
17 EARLIER APPLICATION NUMBER: 60/048, 9666
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21 EARLIER APPLICATION NUMBER: 60/048, 8787
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23 EARLIER APPLICATION NUMBER: 60/070, 9232
24 EARLIER FILING DATE: 1997-12-18
25 EARLIER APPLICATION NUMBER: 60/092, 9211
26 EARLIER FILING DATE: 1998-07-15
27 EARLIER APPLICATION NUMBER: 60/094, 6575
28 EARLIER FILING DATE: 1998-07-30
29 NUMBER OF SEQ IDS NOS: 1227
30 SOFTWARE: PatentIn Ver. 2.0
31 SEQ ID NO 427
32 LENGTH: 250
33 TYPE: PRT
34 ORGANISM: Homo sapiens
35 OS-09-205-258-427

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US-08-944-483-24

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Score: 1324.00 Matches: 248  
Percent Similarity: 99.208 Conservative: 0  
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Query Match: 55.868 Indels: 2  
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US-09-856-320a-1 (1-1301) x US-08-944-483-24 (1-248)

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RESULT 4  
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Sequence 1149, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1

CURRENT APPLICATION NUMBER: US/09/205,258  
CURRENT FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
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EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877

EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1149  
LENGTH: 246  
TYPE: PRF  
ORGANISM: Homo sapiens  
US-09-205-258-1149

Alignment Scores:  
Pred. No.: 5,29e-101 Length: 246  
Score: 1279.00 Matches: 244  
Percent Similarity: 98.79% Conservative: 0  
Best Local Similarity: 98.79% Mismatches: 2  
Query Match: 53.97% Indels: 1  
DB: 4 Gaps: 0

US-09-856-320A-1 (1-1301) x US-09-205-258-1149 (1-246)

209 ATGAGATCTGTCAGATTATCTGCTGTGGCAACAGGCTTGTAGGGAGAGACC 268  
1 MetArgIleLeuGlnLeuIleLeuAlaLeuAlaThrGlyLeuValGlyGlnThr 20  
269 AGATATCAACAGGGGTTCAGTGCAGACCTCCACCTGGCAGCAGCCCTGTTTC 328  
21 ArgIleIleLeuGlyPheGlnCysLysLeuHisSerGlnProTrpIleAlaLeuPhe 40  
329 GAGAAAGCCGCTACTCTGTGGGGGAGGCTCATGCCCCCAGATGGCTCTGCAGACA 388  
41 GlyLysThrArgLeuLeuLeuGlyAlaThrIleuIleAlaProArgTrpLeuThrAla 60  
389 GCCCACTGCTCAAGCCCGCTACATAGTTCACTGGGAGCAGACAACTCCAGAAAGAG 448  
61 AlaHisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisLeuGlnLysGln 80  
449 GAGGGCTGTGAGCAGACCCGAGCAGACCTGATGCTTCCGCCCGCTTCAACAAC 508  
81 GlnGlyCysGlnGlnThrArgThrAlaThrGlnUserPheProHisProGlyPheAsn 100  
509 AGCTTCCCAACAAGACCCGAGCAGATGATCATGCTGTGTAAGATGGCATGCCAGTC 568  
101 SerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProAl 120  
569 TCATCATCCTGGGCTGTGGAGCCCGCAGCCCTCTCTCAGGCTGTGCTGAGCAGC 628  
121 SerIleThrThrAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThr 140  
629 AGCTGCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCGCATAGCCCTGCTCAGACC 688  
141 SerCys-SerPheProAlaGlyAlaAlaAlaArgProAspProSerThrAlaCysLeuThr 160  
689 TTGGCATGGCCCAACATCACCATATTGAGCAGCAGAACTGTGAGAACCCCTAACCCGGC 748  
160 OCysAspAlaProHisSerProSerLeuSerThrArgSerValArgThrProThrProAl 180  
749 AACATCAGACACCATGCTGTGTGTGACAGCTGAGGAAGGGGCAAGAGCTCTCCAG 808  
180 aThrSerGlnThrProTrpCysValProAlaCysArgLysGlyAlaArgThrProAlaArg 200  
809 GGTGACTCGGGGGCCCTGTGGTGTGTAAACAGTCTTCAAGGCAATTATCTCTGGGCG 868  
200 gValThrProGlyAlaLeuThrSerValThrSerLeuPheLysAlaLeuSerProGlyAl 220  
869 CAGGATCCGTGTGGCATCACCCGAAAGCTGGTGTACACGAAAGTCTGCAATATGTG 928

220 aArgIleArgValArgSerProGlnSerLeuValSerThrArgLysSerAlaAsnMetTr 240  
929 GACTGGATCCAGAGACGA 947  
240 pThrArgLysSerArgArgArg 246

RESULT 5  
US-09-386-642-14  
Sequence 14, Application US/09386642  
Patent No. 6420157  
GENERAL INFORMATION:  
APPLICANT: Dartow, Andrew  
APPLICANT: Qi, Jensen  
APPLICANT: Andrade-Gordon, Patricia  
TITLE OF INVENTION: Zymogen Activation System  
FILE REFERENCE: ORT-1028  
CURRENT APPLICATION NUMBER: US/09/386,642  
CURRENT FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 289  
TYPE: PRF  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
OTHER INFORMATION: With homo sapien serine protease catalytic domain  
US-09-386-642-14

Alignment Scores:  
Pred. No.: 5,57e-97 Length: 289  
Score: 1232.00 Matches: 233  
Percent Similarity: 86.12% Conservative: 9  
Best Local Similarity: 82.92% Mismatches: 17  
Query Match: 51.98% Indels: 22  
DB: 4 Gaps: 3

US-09-856-320A-1 (1-1301) x US-09-386-642-14 (1-289)

203 CAGGCCATGAGGATTTCTGAGTTATTCG-----CTTGCTGTGGCAACAGGCTT 253  
8 GlnLysSerArgLeuLeuLeuValSerAsnLeuLeuLysGlnGlyVal 27  
254 GTAGG----- 259  
28 ValSerAspTrpLysAspAspAspValAspAlaAlaLeuAlaAlaProPheAsp 47  
260 GAGAGACCAAGATCATCAAGGGGTTCAGTGC---AAGCTTCACTCCAGCCCTGGCAG 316  
48 AspAspAspLysIleValGlyGlyTrpAsnCysLeuGlnLysHisSerGlnProTrpGln 67  
317 GGAGCCCTGTGGAGAAGACGGGCTACTGTGGGGGAGCAGCTCATGCCCCCAATAGG 376  
68 AlaAlaLeuPheGlnLysThrArgLeuLeuLysGlyAlaThrIleuIleAlaProArgTrp 87  
377 CTCTGACAGCAGCCCATGCTCAAGCCCGCTACATAGTTACCTGGGGCAGCACAAC 436  
88 LeuLeuThrAlaAlaHisCysLeuLysProArgTrpIleValHisLeuGlnHisAsn 107  
437 CTCACAGAGAGAGGGCTGTGAGCAGACCCGAGACAGCAGTGAAGTCTTCCGCCAGCC 496  
108 LeuGlnLysGlnGlnLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 127  
497 GGCTTCAACAACAGCTCCCAACAAGACCAAGCCCAAGATGATCATGCTGTGGGAAGAG 556  
128 GlnPheAsnAsnSerLeuProAsnLysAspHisArgAsnAspIleLeuValLysMet 147  
557 GCATGCCAGTCTCATCACTGAGCTGTGAGCAGCCCTCACTCTCTCAGCTGTGTGC 616  
148 AlaSerProValSerIleThrThrAlaValArgProLeuThrLeuSerSerArgCysVal 167  
617 ACTGCTGGCAGCAGCTGCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCGCATAGTC 676

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Db      168 ThrAlaGlyThrSerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArg 187
QY      677 CTGCCTCAGACCTTGCGATGCGCCACATCACCATTGAGCACCAGAGTGTGAGAC 736
Db      188 LeuProHISThrLeuArgCysAlaAsnIleThrIleIleGlnHISGlnIlyscysGlnsn 207
QY      737 GCCTCCCCCGCAACATCAGACAGACACCATGGTGTGTGCCAGCGTCCAGAGAGGGGCAAG 796
Db      208 AlaTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnIlyGlyLys 227
QY      797 GACTCTCCAGAGGAGTCTCCGGGGCCCTCTGCTCTTAACAGTCTCTTCAAGGCAATT 856
Db      228 AspSerCysGlnGlyAspSerCylGlyProLeuValCysAsnGlnSerLeuGlnIlyIle 247
QY      857 ATCTCTGGGGGCGAGATCCGTGTGCGATCACCAGAAAGCCTGTGTCTACAGAAAGTC 916
Db      248 IleserTprGlyGlnAspProcysAlaIleThrArgLysProGlyValTyrThrLysVal 267
QY      917 TGCAATATGTGACTGATCGAGGAGCATGAGAAACAATTACACTGAGACCCACCCAC 976
Db      268 CysLysTyrValAspTPrIleGlnIlyThrMetLysAsnAsnSerArgHISHisHis 287
QY      977 CAC 979
Db      288 His 288

RESULT 6
US-09-205-258-1150
; Sequence 1150, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER APPLICATION NUMBER: 1998-12-04
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
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; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892

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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
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; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
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; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1150
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-1150

Alignment Scores:
Pred. No.: 4,99e-94 Length: 228
Score: 1197.00 Matches: 226
Percent Similarity: 98.69% Conservative: 0
Best Local Similarity: 98.69% Mismatches: 2
Query Match: 50.51% Indels: 1
DB: 4 Caps: 0

US-09-856-320A-1 (1-1301) x US-09-205-258-1150 (1-228)
QY      263 GAGACGAGATCATCAAGGGTTGAGTGCAGGCTTCCAGCCCTGGCAGGACCC 322
Db      1 GluThrArgIleIleIlysglyPheGlnCysLysLeuHISserGlnProTprGlnAla 20
QY      323 CTGTTGAGAGAGGCGGTACTCTGTGGGGCGACGCTCATCCGCCCAATGGCTCTCTG 382
Db      21 LeuPheGlnLysTyrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTPrLeuLeu 40
QY      383 ACAGCAGCCCACTGCTCAAGCCCGGCTACATAGTTCACCTGGGGCAGCAGCACTCCAG 442
Db      41 ThrAlaIleHIScysLeuLysProArgTyrIleValHisLeuGlyGlnHISAsnLeuGln 60

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QY 443 MAGGAGAGGCTGTGAGACAGACCGGAGACGCACTGAGTCTTCCCGGAGCCCGGCTTC 502
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    LysGluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPhe 80
Db 61
QY 503 AACACAGGCTCCCGGACAAAGACCGCCCAATGATCATGCTGTGGAAGATGATG 562
    |||||
    AsnAsnSerLeuProAsnLysAspHisAlaGlnAsnAspIleMetLeuValLysMetAlaSer 100
Db 81
QY 563 CCAGTCTCATCATCAGCTGGGCTGTGCGACCCCTCACCCCTCCCTCCTCAGCTGTGCTGCT 622
    |||||
    ProValSerIleThrThrProAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAla 120
Db 101
QY 623 GGCACACAGCTGCTCATTTCCGGCTGGGAGACAGCTCCAGCCCGCATTTAGCCTGCT 682
    |||||
    GlyThrSerCys-SerPheProAlaGlyAlaAlaArgProAspProSerThrAlaCysLe 140
Db 121
QY 683 CACACCTGGCAGTGGCGGCAACATCACCATCATGTGACACCAAGAGTGAGAGCGCTAC 742
    |||||
    ValThrProCysAspAlaProThrSerProSerLeuSerThrArgSerValAlaArgThrPro 160
Db 140
QY 743 CCGGCAACATCATCAGACACACATGCTGTGCGACGCTCAGAGAGGAGCAAGACATCC 802
    |||||
    rProAlaThrSerGlnThrProThrCysValProAlaCysArgLysGlyAlaArgThrPr 180
Db 160
QY 803 TGCCAGGTGACTCCGGGGCCCTGTGTGTAAACCACTCTCTTCAGCATTTATCTCC 862
    |||||
    AlaAlaArgValThrProGlyAlaLeuThrSerValThrSerLeuPheLysAlaLeuSerPr 200
Db 180
QY 863 TGGGGCAGAGTCCGTGTGCGATCACCAGCAAGCCCTGGTGTACACGAAAGCTTCGAA 922
    |||||
    200 oGlyAlaArgIleAlaGlyAlaArgSerProIleSerValSerThrArgLysSerAlaAs 220
Db 200
QY 923 TAGTGACTGATCCAGGAGAGCA 947
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    220 nMetThrThrGlySerArgArgArg 228
Db 220

RESULT 7
US-09-025-059-3
; Sequence 3, Application US/09025059
; Patent No. 6075136
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guejler, Karl J.
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0481 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:

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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1020091
; US-09-025-059-3

Alignment Scores:
Pred. No.: 1,49e-51 Length: 260
Score: 698.50 Matches: 129
Percent Similarity: 66.13% Conservative: 35
Best Local Similarity: 52.02% Mismatches: 77
Query Match: 29,47% Indels: 7
DB: 3 Gaps: 3

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US-09-856-320A-1 (1-1301) x US-09-025-059-3 (1-260)

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QY 227 ATCCGCTGTGCTGTGCGACACAGGCTTTGAGGGGAGAGACGAG----- 271
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    IleLeuLeuLeuLeuPheMetGlyAlaThrAlaGlyLeuThrArgAlaGlnGlySerLys 32
Db 13
QY 272 ATCATCAAGGGGCTTCAAGTGCAGCTCACTCCACGCTGGCAGGACGCGCTGTGCGAG 331
    |||||
    IleLeuGlnGlyArgGlnCysIleProHisSerGlnProThrGlnAlaAlaLeuPheGln 52
Db 33
QY 332 AAGACGGGCTACTGTGTGGGGGAGCGCTATCGCCCGAGATGGCTGTGACGACGCG 391
    |||||
    53 GlyLysArgLeuLeuLeuLecysGlyGlyValLeuValGlyAspArgThrValLeuThrAla 72
Db 53
QY 392 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGACACACACCTCCAGAGAGAG 451
    |||||
    73 HisCysLysLysGlnLysIleArgSerValArgLeuGlyAspHisSerLeuGlnSerArgAsp 92
Db 73
QY 452 GGCCTGTGACAGACCCCGGACAGGCACTGATGCTCCCGGCGGCTTCAACACACAG 511
    |||||
    93 GlnProGluGlnGlnIleGlnValAlaGlnSerIleGlnHisProCysIleArgAsnSer 112
Db 93
QY 512 CTCGCCACAAAGACCCGCAATGATCATCTGTGTGAAGATGGCATCGCCAGTCTCC 571
    |||||
    113 AsnPro--GlnAspHisSerHisAspIleMetLeuIleArgLeuGlnAsnSerAlaAsn 131
Db 113
QY 572 ATCACCTGGGCTGTGGACCCCTCACCCCTCTCTCAGCGTGTGTCTGTGCGACGAG 631
    |||||
    132 LeuGlyAspLysValLysProValGlnLeuAlaAsnLeuCysProLysValGlyGlnLys 151
Db 132
QY 632 TGCTTCATTTCCGGCTGGGGGACAGACGCTCCAGCCCGCATGAGCTGCTCCACACTTG 691
    |||||
    152 CysIleIleSerGlyThrProGlyThrValThrSerProGlnGlnAsnPheProAsnThrLeu 171
Db 152
QY 692 CGATGGCCACATCATCATTCATTGACACCCAGAGATGTGAGAGACCTTACCCCGGCAAC 751
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    172 AsnCysAlaGlnValLysIleIleThrSerGlnAsnLysCysGlnArgAlaIleThrProGlyLys 191
Db 172
QY 752 ATCACAGACACCATGCTGTGCTGCCAGCGGACGAGAGGGGCAAGACCTCCCGCGGCT 811
    |||||
    192 IleThrGluGlnMetValCysAlaGly---SerSerAsnGlyAlaAspThrCysGlnGly 210
Db 192
QY 812 GACTCCGGGGGCTGTGCTGTGTACAGCTCTTCAAGGATTAATTCCTGGGGCGAG 871
    |||||
    211 AspSerGlyGlyProLeuValLysAspGlyMetLeuGlnGlyIleThrSerThrProLysSer 230
Db 211
QY 872 GATCGGTGCGATCACCCGAAAGCCTGTGTCTACAGAAAGTGTGCAAAATATGTGAGC 931
    |||||
    231 AspProCysGlyLysProGlnLysProGlnLysProGlyValThrLysIleCysArgThrThr 250
Db 231
QY 932 TGGATCCAGGAGACGATGAAGAAC 955
    |||||
    251 ThrIleLysLysThrMetAspAsn 258
Db 251

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RESULT 8  
US-09-070-526-2  
Sequence 2, Application US/09070526  
Patent No. 6100059  
GENERAL INFORMATION:  
APPLICANT: SOUTHAN, CHRISTOPHER  
APPLICANT: CLINKENBEARD, HELEN  
APPLICANT: BURGESS, NICOLA  
TITLE OF INVENTION: No. 6100059e1 Compounds  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RATNER & PRESTIA  
STREET: P. O. BOX 980  
CITY: VALLEY FORGE  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070.526  
FILING DATE: 30-APR-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9711952.3  
FILING DATE: 9-JUN-1997  
APPLICATION NUMBER: EP 97309646.4  
FILING DATE: 1-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: PRESTIA, PAUL F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GH-30353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-070-526-2  
  
Alignment Scores:  
Pred. No.: 7,92e-51 Length: 260  
Score: 690.00 Matches: 125  
Percent Similarity: 66.93% Conservative: 45  
Best Local Similarity: 49.21% Mismatches: 80  
Query Match: 29.11% Indels: 4  
DB: 3 Gaps: 3  
  
US-09-856-320a-1 (1-1301) x US-09-070-526-2 (1-260)  
QY 188 CGCTCTCCCTCCCTCCAGCCATGAGATTCTGAGTAACTCTGCTT-----GCTCTG 241  
DB 3 ArgProArgProArgAlaAlaLysThrTrpMetHethLeuLeuLeuGlyAlaLys 22  
QY 242 GCACACAGGCGTTGAGGGGAGACACAGATCTACAGGGGTTGAGTGCACACCTCAC 301  
DB 23 AlaGlyHisSerArgAlaGlnGlnLysValLeuGlyGlnHisGlyGlnProHis 42  
QY 302 TCCAGCCCTGAGGAGCCCTGTTGAGAGACGCGGCTACTGTGGGGGAGACCTC 361  
DB 43 SerLysProTyrGlnAlaAlaLeuPheGlnGlnGlnLeuLeuGlyGlyValLeu 62  
QY 362 ATGCCCCCAGATGGCTCTGACAGACACCCACTGCTCAAGCCCGCTACATAGTTTAC 421  
DB 63 ValGlyLysAsnTyrValLeuThrAlaAlaHisCysLysTyrTyrValArg 82

QY 422 CTGGGGCAGACACACTTCACAGAGAGGAGGCTGTGACAGACCCGAGACCCACTGAG 481  
DB 83 LeuGlyAspHisSerLeuGlnAsnLysAspGlyProGlnGlnGlnIleProValValGln 102  
QY 482 TCCTTCCCGCCCGCGGTTGACACACAGCCTCCCGACAAAGACACCCGAAATGACATC 541  
DB 103 SerLysProHisProCysTyrAsnSerSer---AspValGlnAspHisAsnHisAspLeu 121  
QY 542 ATGTGTGTAAGATGCGCATCCGACATCCATACACCTGGCTGTGCGACCCCTCACCTC 601  
DB 122 MetLeuLeuGlnLeuArgAspGlnAlaSerLeuGlnSerTyrValLysProIleSerLeu 141  
QY 602 TCCTCAGCCTGTGTCATGCTGCGACACAGCTCCCTCATTTCCGCTGGGGAGACAGTCC 661  
DB 142 AlaAspHisCysThrGlnProGlyGlnLysCysThrValSerGlyTyrGlyThrValThr 161  
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DB 162 SerProArgGlnAsnProAspThrLeuAsnCysAlaGlnValLysIlePheProGln 181  
QY 722 CAGAAGTGTGAGAACGCTTACCCGCGCAATCACAGACACCATGAGTGTGCGACGCTG 781  
DB 182 LysLysCysGlnAspAlaTyrProGlyGlnIleThrAspGlyMetValCysAlaGlySer 201  
QY 782 CAGGAGGGGCGAAGGACTCCTGCCAGGGTCACTCCGGGGCCCTTGTGTTAACCCAG 841  
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DB 221 AlaLeuGlnGlyIleThrSerTyrProLysSerAspProCysGlyLysSerAspLysPro 240  
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RESULT 9  
US-09-386-642-13  
Sequence 13, Application US/09386642  
Patent No. 6420157  
GENERAL INFORMATION:  
APPLICANT: Darrow, Andrew  
APPLICANT: OI, Jemson  
APPLICANT: Andrade-Gordon, Patricia  
TITLE OF INVENTION: Zymogen Activation System  
FILE REFERENCE: ORT-1028  
CURRENT APPLICATION NUMBER: US/09/386.642  
CURRENT FILING DATE: 1999-08-31  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 13  
LENGTH: 288  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
OTHER INFORMATION: With homo sapien serine protease catalytic domain  
US-09-386-642-13  
  
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US-09-856-320a-1 (1-1301) x US-09-386-642-13 (1-288)  
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DB 8 GlnLysSerArgLeuLeuLeuValValSerAsnLeuLeuLeuGlyGlnGlyVal 27

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QY 254 GTAGG----- 259
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QY 260 GGAGAGACACGAGTCAATCAAGGGTCCGAGTGC---AAGCTTACATCCCAAGCCCTGGCAG 316
Db 48 AspAspAspLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 67
QY 317 GCAGCCCTGTTCGAGAGACGCGCTACTCTGTGGGGCGAGCGCTACATCCGCGCCAGATGG 376
Db 68 AlaAlaLeuPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 87
QY 377 CTCCTGACAGACACCCAGTCCATGAGCCCGCTACATGATGATGATGATGATGATGATGATGATGAT 436
Db 88 ValLeuThrAlaAlaHisCysLysLysProLysTyrThrValArgLeuGlyAspHisSer 107
QY 437 CTCACAAAGAGAGAGGGCTGTGTGACGACGCCGAGACGACGACGACGACGACGACGACGACGACGAC 496
Db 108 LeuGlnAsnLysAspLysProGlnGlnLysLeuProValGlnSerLeuProHisPro 127
QY 497 GCGTTCACACACGAGCTCCCAACAAAGACACCGGACGACGACGACGACGACGACGACGACGACGACGAC 556
Db 128 CysTyrAsnSerSer---AspValGlnAspHisAsnHisAspLeuLeuLeuGlnLeu 146
QY 557 GCATGCGCAGTCTCCATCACTGAGGCTGTGCGACCCCTCACCCTCTCTCAGCTGTATC 616
Db 147 ArgAspGlnAlaSerLeuLysSerLysValLysProLysLeuAlaAspHisCysThr 166
QY 617 ACTGCTGGAGCAGCAGCTGCTCATTTCCGGCTGGGGGAGACGACGACGACGACGACGACGACGACGACGAC 676
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QY 737 GCGTACCCCGGACATCAGACAGACACCATGCTGTGCGACGCTGACGAGAGGGGGGCAAG 796
Db 207 AlaTyrProGlnGlnLeuThrAspGlyMetValCysAlaGlySerSerLysGlyAla--- 225
QY 797 GACTCTGCGCAGGAGTACCCGCGGCGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 856
Db 226 AspThrCysGlnGlnLysAspSerGlyGlyProLeuValCysAspLysLeuLeuGlnGlyLeu 245
QY 857 ATCTCTGCGGCGCAGGATCCGTGCGCATCACCCGACGCTGCTGTACAGGAAGTTC 916
Db 246 ThrSerThrPheLysSerAspProCysGlyArgSerAspLysProGlyValTyrThrAsnIle 265
QY 917 TGCATAATATGTGACTGTGATCCAGAGAGAGATGAGAACAAATTGACTGAGCCACCCAC 976
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QY 977 CACAGCCCATCAG 989
Db 284 HisHis-HisHis 287

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RESULT 10
US-09-008-271A-7
; Sequence 7, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Puryi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

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; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheila
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLMNOT27
; CLONE: 1798496
; SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
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US-09-008-271A-7
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Pred. No.: 3,8e-50 Length: 260
Score: 682.00 Matches: 124
Percent Similarity: 66.54% Conservative: 45
Best Local Similarity: 48.82% Mismatches: 81
Query Match: 28.78% Indels: 4
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Db 3 ArgProArgProArgAlaAlaLysThrTrpMetPheLeuLeuLeuLeuGlyAlaTyr 22
QY 242 GCACACAGGAGCTGTAGGGGAGAGACGACGATCATCAAGGGTTCGAGGCAAGCTCAG 301
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QY 302 TCCACGCGCTGCGAGGACGCGCTGTTCAGAAAGCGGCTACTGTGTGGGGGAGCTC 361
Db 43 SerGlnProThrPheGlnAlaAlaLeuSerGlnGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 62
QY 362 ATCGCGCCGAGATGGCTCTGACAGACGACGCGCTGCTCAAGCCCGCTACATAGTTCAC 421
Db 63 ValGlyGlyAsnThrAlaLeuThrAlaAlaHisCysLysLysProLysTyrThrValArg 82
QY 422 CTGGGGGACAGACAACTCCAGAGAGAGAGGGCTGTGACGACGCGCGGACGACGACGACGACGACGACGACGACGACGAC 481
Db 83 LeuGlnAspHisSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 102
QY 482 TCCCTCCCGCCACCGCGCTTCAACACAGCCTCCCAACAAAGACCGCATGATCATC 541
Db 103 SerLysProHisProCysTyrAsnSerSer---AspValGlnAspHisAsnHisAspLeu 121
QY 542 ATGCGGTGAAGATGAGCATCGGACGATGCTCATCAGCTGCGGCTGTGCGACCCCTCAGCTC 601
Db 122 MetLeuLeuGlnLeuArgAspGlnAlaSerLeuGlySerLysValLysProLysLeu 141

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Db 162 SerProaTgGluAsPheProAsPheProAsPheProAsPheProAsPheProAsPheProAs 181  
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RESULT 11  
US-09-996-243-309  
Sequence 309, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996, 243  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-11-12  
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 PRIOR APPLICATION NUMBER: 60/091633

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 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
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 Best Local Similarity: 50.64% Mismatches: 67  
 Query Match: 27,458 Indels: 7  
 Gaps: 4

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QY 383 ACAGAGCCCACTGCTCAAGCCCGCTACATAGTTCACCTGGGCGAGACAACTCCAG 442  
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QY 443 AAG--GAGGAGGCTGTGTGAGGACGACCGGACGACCACTGAGTCTCCCGCCGCG 499  
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RESULT 12  
 US-08-824-874-1  
 ; Sequence 1, Application US/08824874  
 ; Patent No. 5962300  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Lal, Preeti

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: TITLE OF INVENTION: NOVEL KALLIKREIN
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/824, 874
: FILING DATE: Filed Herewith
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0252 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 268 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: KERAMOT02
: CLONE: 820694
: US-08-824-874-1
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: Pred. No.: 6.98e-44 Length: 268
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: Best Local Similarity: 45.13% Mismatches: 83
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: QY 171 CCAAGGAACCTGGGGCCCTCCCTCCAGGCGCATGAGATTCTGCAGTTAATCC 230
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: QY 315 AG-----CGAGCCCTGTCGAGAAACGCGGCTACTCTGTGGGGGAGGCTATGCGCC 370
:   |||  |||  |||  |||
:   :|:  :|:  :|:  :|:
:   :|:  :|:  :|:  :|:
: Db 56 GluAlaAlaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValIleuValHisPro 75
:
: QY 371 AGATGGCTCTGACAGAGCCGCTGCTGCTGAGCCCGCTACATAGTTCACCTGGGGCAG 430
:   |||  |||  |||  |||
:   :|:  :|:  :|:  :|:
:   :|:  :|:  :|:  :|:
: Db 76 GlnTrpLeuLeuThrAlaAlaHisCysArgLysValIlePheArgValArgLeuGlyHis 95
:
: QY 431 CACAACCTCGAGAG---GAGGAGGGGCTGTGACGACAGACCCGAGACGACCTAGTCTTC 487
:   |||  |||  |||  |||
:   :|:  :|:  :|:  :|:
:   :|:  :|:  :|:  :|:
: Db 96 TyrSerLeuSerProValTyrGlnSerGlyGlnIleMetPheGlnGlyValLysSerIle 115

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: QY 488 CCCCACCCGCTTCACACAGACCTCCCAACAAAGACACCGCATGACATCATGCTG 547
:   |||  |||  |||  |||
:   :|:  :|:  :|:  :|:
:   :|:  :|:  :|:  :|:
: Db 116 ThrHisProGlyTyrSer-----HisProGlyHisSerAsnAspLeuMetLeu 131
:
: QY 548 GTGAAGATGGCATGGCCATGTCATACCTCGGCTGGCGACCCCTCACCTCTCCCA 607
:   |||  |||  |||  |||
:   :|:  :|:  :|:  :|:
:   :|:  :|:  :|:  :|:
: Db 132 IleLysLeuAsnAlaArgAlaIleArgProThrLysAspValArgProIleAsnValSerSer 151
:
: QY 608 CGCTGTCTACCTGCTGGCAGCAGCTCCATTTCCGGCTGGGCGACAGCTCCAGCC 667
:   |||  |||  |||  |||
:   :|:  :|:  :|:  :|:
:   :|:  :|:  :|:  :|:
: Db 152 HisCysProSerAlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerPro 171
:
: QY 668 CAGTTAGCCCTGCTCACACCTTGCGATGGCCCAACATCACCATTCATGACCCAGAG 727
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:   :|:  :|:  :|:  :|:
: Db 172 GlnValHisPheProLysValIleuGlnCysLeuAsnIleSerValIleSerGlnLysArg 191
:
: QY 728 TGTGAGAACGCTACCCCGGACATGACACACACATGGTGTGGCAGCGTCAGGAA 787
:   |||  |||  |||  |||
:   :|:  :|:  :|:  :|:
:   :|:  :|:  :|:  :|:
: Db 192 CysGlnAspAlaTyrProArgGlnIleAspAspThrMetPheCysAlaGly---AspLys 210
:
: QY 788 GGGGCAAGACACTCTCGCAGCGTACTCCGGGGCCCTCTGTCTGTAAACAGTCTCT 847
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:   :|:  :|:  :|:  :|:
:   :|:  :|:  :|:  :|:
: Db 211 AlaGlyArgAspSerCysGlnGlyAspSerGlyLysProValValCysAsnGlySerLeu 230
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: QY 848 CAAGCATATCTCTCTGGGCGCAGATCCGTGTGCGATCACCCAAAGCTGTGTCTAC 907
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:   :|:  :|:  :|:  :|:
: Db 231 GlnGlyLeuValSerTrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyr 250
:
: QY 908 ACGAAGTCTCAATATATGTGACTGGATCCAGAGACGATGAGAACAAAT 958
:   |||  |||  |||  |||
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:   :|:  :|:  :|:  :|:
: Db 251 ThrIleuLeuCysLysPheThrLysTrpIleGlnIleThrIleGlnAlaAsn 267
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: RESULT 13
: US-09-210-084-1
: Sequence 1, Application US/09210084
: Patent No. 6197511
:
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Lal, Preeti
: TITLE OF INVENTION: NOVEL KALLIKREIN
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/210,084
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/824, 874
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0252 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 268 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear

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: IMMEDIATE SOURCE:
: LIBRARY: KERANOT02
: CLONE: 820694
US-09-210-084-1

Alignment Scores:
Pred. No.: 6,986-44      Length: 268
Score: 608.50           Matches: 125
Percent Similarity: 60.29%      Conservative: 42
Best Local Similarity: 45.13%   Mismatches: 83
Query Match: 25.68%            Indels: 28
DB: 3                      Gaps: 8

US-09-856-320A-1 (1-1301) x US-09-210-084-1 (1-268)

QY 171 CCAAGGAACCTGGGCGCGCTCCGCCCTCCAGGACATGAGATTCTGCAGTTAATCC 230
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Db 4 ProthmetmetPheProValThrThrProLeuThrPro----- 16

QY 231 TGCCTTGCTC-----TGCACAAGGGCTTGAGGGGAGAGACCAGGA--- 272
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Db 17 CysProLeuGlyAlaThrArgThrTrpGlnLeuGlyPro---GlyYsthrProGlyArg 35

QY 273 -----TCATCAAGGGTTCGAGTGCAGACCTCACTCCAGCCCTGGC 314
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Db 36 MethThrAlaAlaLaserSerMetAspProThrAlaIleCysThrProSerArgGly 55

QY 315 AG---GCAGCCCTGCTGCAGAAAGACGCGCTACTCTGGGGCGACGATCGCCCC 370
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Db 56 GlnAlaAlaLeuLeuLeuArgProAsnGlnLeuTyrcysGlyAlaValLeuValHisPro 75

QY 371 AGATGGCTTCGACAGACGCCACTGCCAAGCCCGCTACATAGTTCACCTGGGGCAG 430
   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db 76 GlnTrpLeuThrAlaAlaHisCysArgGlyLysValPheArgValArgLeuGlyHis 95

QY 431 CACAACCTCCACAGAG---GAGAGGGCTGTGACAGACCCGGACAGCCACTGAGTCTTC 487
   ::|   |||   |||   |||   |||   |||   |||   |||   |||
Db 96 TyrSerLeuSerProValTyTrGlnSerGlyGlnMetPheGlnIlyValLysSerIle 115

QY 488 CCCCCCGCGGCTTCGACAAACAGCCTCCCAACAAAGACCCGCAATGATCATGCTG 547
   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db 116 ProHisProGlyTyrSer-----HisProGlnHisSerAsnSpleuMetLeu 131

QY 548 GTGAAGATGGCATGCCAGCTCCATCACTGGGCTGTGCGACCCCTCAACCTTCCTCA 607
   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db 132 IleLysLeuAsnArgArgIleArgProThrLysAspValArgProIleAsnValSerSer 151

QY 608 CGCTGTGCATGCTGCGCACAGCTGCTCATTTCCGGCTGGGGCAGACGTCACCCCC 667
   ||   |||   |||   |||   |||   |||   |||   |||   |||
Db 152 HisCysProSerAlaGlyThrLysCysLeuValSerGlyTyrGlyThrThrLysSerPro 171

QY 668 CAGTTAGCCTGCGCCACACACTGGGATGGCGGCACATCAACATCATTTAGACACGAAG 727
   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db 172 GlnValHisPheProLysValLeuIleCysLeuAsnIleSerValLeuSerGlnLysArg 191

QY 728 TGTGAGACGCGCTACCCCGCGCAACATCAACACACATGATGTTGTGCCAGCGTACGAA 787
   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db 192 CysGlnAspAlaTyrProArgGlnIleAspAspThrMetPheCysAlaIleLys---AspLys 210

QY 788 GGGGCGAAGACTCTGCGCAGGGTACTTCGGGGGCGCTGTGCTGTGTAACCACTCTTT 847
   |||   |||   |||   |||   |||   |||   |||   |||   |||
Db 211 AlaGlyArgAspSerCysGlnGlyAspSerGlyGlyProValIValCysAsnGlySerLeu 230

QY 848 CAAGGATTAATCTCTGGGGCAGGATCGCTGTGGATGATCAACCCGAAAGCGGTGTCTAC 907
   |||   |||   |||   |||   |||   |||   |||   |||   |||
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QY 908 ACGAAGTCTCCAATATGTGACTGCATGCCAGAGACGATGAAGAACAAT 958
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Db 251 ThrAsnLeuCysLysPheThrLysTrpIleGlnGlnThrIleGlnAlaLsn 267

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; Sequence 1/, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Inl, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KERANOT02
; CLONE: 820694
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-764-762-1
;
Alignment Scores:
Pred. No.: 6.98e-44 Length: 268
Score: 608.50 Matches: 125
Percent Similarity: 60.29% Conservative: 42
Best local Similarity: 45.13% Mismatches: 83
Query Match: 25.68% Indels: 28
DB: 4 Gaps: 8
;
US-09-856-320A-1 (1-1301) x US-09-764-762-1 (1-268)
OY 171 CCAAGAACCTGGGCGCCGTCCGCCCTCAGACCATGAGATTTCGAGTTATACC 230
Db ||| ::||| ||| |||
4 ProThrMetkethProValThrThrProLeuThrPro----- 16
OY 231 TGGTTCCTC-----TGCCAACAGGGCTTGTAAGGGGAGACAGACA--- 272
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
17 CysProLeuclYalThrArgThrArgThrPrgIuLeuGlyPro--GlyLysThrProGlyArg 35
OY 273 -----TCATCAAAGGGGTTGAGATGCAGAAGCTCATCTCCAGCCCTGGC 314
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
36 MetThrAlaAlaAlaAlaSerSerMetAspProThrAlaIleCysThrProSerArgGly 55
OY 315 AG----GCAAGCCCTGTTGCAGAAAGACGGGCTACTGTGGGGGAGAGCGTACGGCCCC 370
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
56 GluAlaAlaLeuLeuLeuArgProAsnGlnLeuIryCysGlyAlaValLeuValHisPro 75
OY 371 AGATGGCTCTGTGACAGACAGCCCATGCTCAAGCCCCTACATAGTTTCACTGGGGCAG 430
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Db      76  GlnTrpLeuIwThrlAlaIlaHIScysAryglYsVal.PheArgValAlrLeuGIyHIS  95
OY      431  CACAACTCCAGAG---GAGGAGGGGCTGTGAGCAGACCCGGAGACCCCTGAGTCTTC  48
Db      96  TySerLeuSerProValIYrGlUserGIyGlnGImetPheGlnGlyAlaIYsSerIle  11
OY      488  CCCCACCCCGGCTTCAACAACAGCCTCCCAACMAAGACACCAGCATGATCATCTGTG  54
Db      116  ProHISProGIyIYrSer-----HISProGIYHISerASnIserASnIleu  13
OY      548  GTGAAGATGGCATTCGCCAGTCTCCATCCACTGGGCTGTGAGACCCCTACCCCTCTCA  60
Db      132  IleYsLeuASnIAlrGAlIleAlrProThrLYsASpAlAlrProIleASnIAlrSer  15
OY      608  CGCTGTTCACGTCTGTGACACAGCCTGCTCATTTCCGTGGGTGGGAGACAGCTCAGCCC  66
Db      152  HISysProSerAlaGIYrThrLYsCysLeuAlValSerGIYrProIYrThrIYrSerPro  17
OY      668  CAGTTACGCTGCTCAGCTCACCTTGGCATGGCCACATCATCATCATATGAGCACAGAG  72
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OY      728  TGTCAGAAAGCCCTACCCGGCAACATACAGACACCATGCTGTGTGGCCAGCTGAGAGA  78
Db      192  CysAlASpAlAlrYrProAlrGAlIleASpASpTHMetPheCysAlaIY---ASpLYs  21
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OY      848  CAAGGCATTTATCTCTCTGGGGCCAGGATCCGTGTGGCATACACCGAAAGCTGTGTCTAC  90
Db      231  GlndIleuValIserTrpGIYASpTYrProCysAlaAlrProASnIAlrProGIYAlIYr  25
OY      908  ACGAAATCTGCAATATGTGACTGATCCAGGAGACGATGAAGAACAAT  958
Db      251  ThrASnIeucysLYsPheThrLYsTrpIleGIYcysIleuThrIleGIYAlaASn  267

RESULT 15
US-08-790-137-4
; Sequence 4, Application US/08790137
; Patent No. 5840871
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
; TITLE OF INVENTION: KALLIKREIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,137
; FILING DATE: Filed Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0195 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555

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[illegible]

Thu Oct '16 09:48:32 2003

us-09-856-320a-1.rai

Page 15

Search completed: October 15, 2003, 20:28:58  
Job time : 29.2321 secs

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; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 1186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-211

Alignment Scores:
Pred. No.: 5,17e-162 Length: 1186
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-856-320a-2 (1-282) x US-10-205-823-211 (1-1186)

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QY 21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgLleLeuGlnLeuLleu 40
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Db 86 AAGGAACCTGGGCCCGGCTCTCCCTCCCTCCAGGCGCATGGCATGTGCGATTAACTCG 145

QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlyLeuThrArgLleLleLysGlyPheGly 60
   |||||
Db 146 CTTCCTCTGGCAACAGGGCTTTGAGGGGGAGAGACCAAGATCATCAAGGGGTTGAGTGC 205

QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLulysThrArgLeuLeuGly 80
   |||||
Db 206 AACCCCTACCTCCAGCCCTGGCAGGCGCCCTGTGAGAGAAAGCCGGCTACTCTGTGG 265

QY 81 AlaThrLeuLleAlaProAArgTrpLeuLeuThrAlaAlaHisCysLeuLysProAArgTyr 100
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Db 266 GCGACCTCATCGCCCCCAGATGGCTCTCCACAGCAGCCACACTGCTCAAGCCCCGCTAC 325

QY 101 IleValHisLeuGlyLnisHisLeuGlnLysGlyGlyGlyGlyGlnThrArgTrpThr 120
   |||||
Db 326 ATAGTTACACTGGGGCAGCACAACCTCCAGAAAGAGAGGGCTGTGAGACCGGAGAC 385

QY 121 AlaThrGlnSerPheProHisProGlyPheHisAsnSerLeuProAsnLysAspHisArg 140
   |||||
Db 386 GGCACAGAGTCTTCCCCACCCGGGCTTCAMACAGGCTCCCAACAAAGACACCGC 445

QY 141 AsnAspLleMetLeuValLysMetAlaSerProValSerLleThrTrpAlaValAlaPro 160
   |||||
Db 446 AATGACATATATGGTGTGAAGATGGCATGGCCAGTTCATCATCACTGGGGCTGGCACC 505

QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuLleSerGlyTrpGly 180
   |||||
Db 506 CTCACCCCTCCCTCCAGCGTGTGCATCGTGGGACCAAGCTGCTCATTTCCGGCTGGGG 565

QY 181 SerThrSerSerProGlnLeuArgLeuPheProHisThrLeuArgCysAlaAsnLleThrLle 200
   |||||
Db 566 AGCAGCTCCAGCCCAAGTTACCCCTGCTCACACCTTGCGATGCGCAACATCACACATC 625

QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnLleThrAspThrMetValCys 220
   |||||
Db 626 ATTGACACACAGAGGTGAAGAGCGCTTACCCCGGCAATCAACACACCATGATGTGT 685

QY 221 AlaSerValGlnGlnLysLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
   |||||
Db 686 GCCAGCGTGCAGGAAGGGGGCAAGGACCTCTGCGAGGGTACTCCGGGGGCCCTCTGTGTC 745
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QY 241 CysAsnGlnSerLeuGlnGlyLleLleSerTrpGlyGlnAspProCysAlaLleThrArg 260
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Db 746 TGTAAACAGCTCTTCAAGGCATTATCTCTGGGCCAGAGATCCGTGCGATCACCCCA 805

QY 261 LysProGlyValLyrThrLysValCysLysTyrValAspTrpLleGlnLthrMetLys 280
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Db 806 AACCTGTGTCTTACAGAAAGCTGCAATATATGTGACTGGATTCAGAGAGAGATGAAG 865

QY 281 AsnAsn 282
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Db 866 AACAAAT 871

RESULT 2
US-09-946-374-169
; Sequence 169, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Hong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
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Db 550 AGCAGCTCAGCCCCCACTACGCGCTGCTCAGACCTTGCATGCGCCACATCACCATC 609
Oy 201 ILeGIuHISgInLySgYsGluAsnAlaTyRProGlyAsnIleThrAspThrMetValCys 220
Db 610 ATTGAGCACCAGAAAGTGTGAGAACGCCCTACCCGGCAGACATCAGACCATGGTGTGT 669
Oy 221 AlaSerValGInGInGInGlyGlyLysAspSerCysGInGInGInGlyLysAspSerGlyGlyProLeuVal 240
Db 670 GCCAGCGTGCAGGAAGGGGGGCAAGGACTCTGCGCAGGGGTGACTCCGGGGGCTCTGTGTC 729
Oy 241 CysAsnGInSerLeuGInGlyIleIleSerTrpGlyGInAspProCysAlaIleThrArg 260
Db 730 TGTAAACCACTCTCTTCAAGGCATATATCTCTGGGGCCAGATCCGTGTGCATCACCAG 789
Oy 261 LysProGlyValTyRThrLysValCysLysTyRValAspTrpIleGInGInThrMetLys 280
Db 790 AAGCTGTGTCTCTACACGAAAGTCTGCMAATATGTGACTGATCCAGAGACGATGAAG 849
Oy 281 AsnAsn 282
Db 850 AACAAAT 855

RESULT 4
US-10-137-870-505
; Sequence 505, Application US/10137870
; Publication No. US20030138883a1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33081C15
; CURRENT APPLICATION NUMBER: US/10/137, 870
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-870-505

Alignment Scores:
Pred. NO.: 5,28e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-137-870-505 (1-1204)
Oy 1 MetGlnArgLeuAlaGTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
Db 10 ATGCAAGAGGTGAGGTGCTCGGAGACTGGAAGTCATCGGGCAAGAGGTCTCAGCAGCAGCC 69
Oy 21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnIleLeu 40
|||||
```

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Db 70 AAGGAACCTGGGGGCGCTCTCTCCCGCTCCAGGCCCATAGAGGATTTGCACTTAATCTTG 129
Oy 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlnTrpArgIleIleLysGlyPheGlyCys 60
Db 130 CTGTGCTGGCAACAGGGGCTGTGAGGGGAGAGACAGGATCATCAAGGGCTTCAGATGC 189
Oy 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLysThrArgLeuLeuGly 80
Db 190 AAGCTCACTCCACGCCCTGGAGGACAGCCCTGTTCGAGAGACGCCGCTACTCTGTGGG 249
Oy 81 AlaThrLeuIleAlaProArgTrpLeuThrAlaAlaHisCysLeuLysProArgTr 100
Db 250 GCGAGCTCATCGCCCCAGATGGCTCTGAGAGGAGCCACCTGCTTAAGCTCCGCTAC 309
Oy 101 ILeValHisLeuGInGInHisAsnLeuGInLysGInGInGlyCysGInGInThrArgThr 120
Db 310 ATAGTTCACCTGGGGCAGACACACCTCCAGAAAGAGAGAGGGGTGTGACAGACGCCGACA 369
Oy 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db 370 GCCACTGAGTCTTCCCGCCACCGCGCTTCAACAACAGCCTCCCAACAAAGACCAACCGC 429
Oy 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db 430 AATGACATCATGCTGTGTGAAGATGGCATGCGCAGTCTCATACACCTGGGCTGTGGACCC 489
Oy 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Db 490 CTCACCTCTCTCTCAGCGTGTGTCTACTGCTGTCGACACCACTGCTCTATTTCCGGCTGGGGC 549
Oy 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db 550 AGCAGCTCAGCCCCCACTACAGCTGCGCTCCACACCTTGCATGGCGCCACATCACCATC 609
Oy 201 ILeGIuHISgInLySgYsGluAsnAlaTyRProGlyAsnIleThrAspThrMetValCys 220
Db 610 ATTGAGCACCAGAAAGTGTGAGAACGCCCTACCCGGCAGACATCAGACCATGGTGTGT 669
Oy 221 AlaSerValGInGInGInGlyLysAspSerCysGInGInGInGlyLysAspSerGlyGlyProLeuVal 240
Db 670 GCCAGCGTGCAGGAAGGGGGGCAAGGACTCTGCGCAGGGGTGACTCCGGGGGCTCTGTGTC 729
Oy 241 CysAsnGInSerLeuGInGlyIleIleSerTrpGlyGInAspProCysAlaIleThrArg 260
Db 730 TGTAAACCACTCTCTTCAAGGCATATATCTCTGGGGCCAGATCCGTGTGCATCACCAG 789
Oy 261 LysProGlyValTyRThrLysValCysLysTyRValAspTrpIleGInGInThrMetLys 280
Db 790 AAGCTGTGTCTCTACACGAAAGTCTGCMAATATGTGACTGATCCAGAGACGATGAAG 849
Oy 281 AsnAsn 282
Db 850 AACAAAT 855

RESULT 5
US-10-140-018-505
; Sequence 505, Application US/10140018
; Publication No. US20030138885a1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
```







QY 281 AsnAsn 282  
| | | | |  
Db 850 AACAAAT 855

## RESULT 8

US-10-140-471-505

; Sequence 505, Application US/10140471  
; Publication No. US2003013887A1

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geriltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C163  
CURRENT APPLICATION NUMBER: US/10/140,471  
CURRENT FILING DATE: 2002-05-06  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 505  
LENGTH: 1204  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-140-471-505

## Alignment Scores:

Pred. No.: 5,28e-162 Length: 1204  
Score: 1523.00 Matches: 282  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-140-471-505 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20  
| | | | |  
Db 10 ATGCAAGAGGTGGAGGTGGGACTGGAGTCAATCGGGCGAGAGGTCTCACAGCAGCC 69  
| | | | |  
QY 21 LysGluProGlyValArgSerSerProLeuGlnAlaMetArgLleLeuGlnLeuIleLeu 40  
| | | | |  
Db 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGCCCATGAGATTCGAGTTAAATCCG 129  
| | | | |  
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgLleIleLysGlyPheGlyCys 60  
| | | | |  
Db 130 CTGGCTGTGGCAACAGGGCTGTGAGGGGAGACACAGATCATCAAGGGTTCCAGTGC 189  
| | | | |  
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly 80  
| | | | |  
Db 190 AAGCCTCATCCAGCCCTGGCAGGCGCTGTGAGAAAGACGGCGTACTCTGTGG 249  
| | | | |  
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100  
| | | | |  
Db 250 GGACCCCTATGCCCCCAGATGGCTTCGACAGCAGCCACCTGCTCAAGCCCGCTAC 309  
| | | | |  
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlnGlnThrArgTyr 120  
| | | | |  
Db 310 ATAGTTCACCTGGGGCAGCACAACCTCCAGAAAGAGAGAGGCTGTGACGACAGCCGAC 369  
| | | | |

QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140  
| | | | |  
Db 370 GCCACTGAGCTCTTCCCCACCCCGGCTTCAACAAACAGCTCCCAACAAAGACACCCG 429  
| | | | |  
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerLleThrTrpAlaValAlaPro 160  
| | | | |  
Db 430 AATGACATCATGTGTGAAGATGCGATCGCCAGTCTCATCATCTGGGCTGTGCGACCC 489  
| | | | |  
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180  
| | | | |  
Db 490 CTCACCTCTCCCTCAGCAGCTGTGTCACTGTGGACACAGTGCCTCATTTCCGGCTGGGG 549  
| | | | |  
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrLle 200  
| | | | |  
Db 550 AGCAGCTCCAGCCCGCAGTTACCGCTGCACACCTTCGATGCGCCAAATCACACATC 609  
| | | | |  
QY 201 IleGluHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220  
| | | | |  
Db 610 ATTGAGCACCAGAAAGTGTGAAGCGCTACCCCGGCAACATCACACACAGATGTGTGT 669  
| | | | |  
QY 221 AlaSerValGlnGlnLysGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240  
| | | | |  
Db 670 GCCAGGCTGAGGAAGGGGCAAGACTCTCGCAGAGTGACTCCGGGGCCCTGTGTC 729  
| | | | |  
QY 241 CysAsnGlnSerLeuGlnGlnLysLleSerTrpGlyGlnAspProCysAlaIleThrArg 260  
| | | | |  
Db 730 TGTAAACAGTCTCTTCAAGGCAATTAATCTCTGGGCGCAGAGATCCGTGTGATCACCCGA 789  
| | | | |  
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnLuhThrMetLys 280  
| | | | |  
Db 790 AAGCCTGGTGTCTACACGAAAGTCTCAATATATGTGACTGTGATCCAGGAGCAGTGAAG 849  
| | | | |  
QY 281 AsnAsn 282  
| | | | |  
Db 850 AACAAAT 855

## RESULT 9

US-10-140-807-505

; Sequence 505, Application US/10140807  
; Publication No. US2003013435A1

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geriltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C174  
CURRENT APPLICATION NUMBER: US/10/140,807  
CURRENT FILING DATE: 2002-05-07  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 505  
LENGTH: 1204  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-140-807-505

## Alignment Scores:

Pred. No.: 5,28e-162 Length: 1204

Score: 1523.00 Matches: 282  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-09-856-320a-2 (1-282) x US-10-140-807-505 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20  
 DB 10 ATGCAAGAGGTGAGGTGGCTGGGGAGTGAAGTATCGGGAGAGGCTCACAGCACC 69  
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetAlaGlyLeuGlnLeuLeu 40  
 DB 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCTCAGTTAATCTTG 129  
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGluThrArgIleIleLysGlyPheGluLys 60  
 DB 130 CTTCGCTGGCCACAGGGCTTGTAGGGGAGAGACAGCAGGATCATCAGGGGTTCAGTGC 189  
 QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLysGly 80  
 DB 190 AAGCTCACTCCAGCCCTGGCAGGACACCTGTTCCGAAAGAGCGGCTACTCTGTGG 249  
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100  
 DB 250 GCGACGCTCATCGCCGCCAGATGGCTCTGACAGACGCCCTCGTCAAGCCCGCTAC 309  
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThr 120  
 DB 310 ATAGTTCACTGGGGCCAGACACCTCCGAAAGGGAGGGCTGTGACAGACCCGGACA 369  
 QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140  
 DB 370 GCCACTGAGTCTCTCCGCCACCCCGGGCTTCAACAACAGCCTCCCAAAAGACACCGCC 429  
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160  
 DB 430 AATGACATCATGTGGTGTAAGATGGCATGCCAGTCTTCATCACCCTGGCTGTGGACCC 489  
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180  
 DB 490 CTCACCCCTCTCTCACGCTGTGTCACTGTGACACAGCTCCCTCATTTCCGGCTGGGC 549  
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200  
 DB 550 AGCAGCTCCAGCCGCCAGTACGCTGCTCACACCTTGCGATGGCCAAACATCAGCATC 609  
 QY 201 IleGluHisGlnLysCysGluAsnAlaIleThrProGlyAsnIleThrAspThrMetValCys 220  
 DB 610 ATTGAGCACCGAAGGTGTGAGAACGCTTACCCCGGCAACATCACAGACCATGTGTGT 669  
 QY 221 AlaSerValGlnGluGlyLysAspSerCysGlnGlyLysAspSerGlyLysProLeuVal 240  
 DB 670 GCCAGCGTGCAGGAAGGGGGCAAGACTCCCTGCCAGGCTGACCTCGGGGGCCCTCTGTC 729  
 QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpLysGlnAspProCysAlaIleThrArg 260  
 DB 730 TGTAAACAGTCTCTTCAAGGCAATATCTCTGGGGCCAGGATCCGTGGCATCACCGA 789  
 QY 261 LysProGlyValIleThrTrpLysValCysLysThrValAspTrpIleGlnGluThrMetLys 280  
 DB 790 AAGGCTGGTGTCTACAGAAAGTCTGCAAAATATGTGAGCTGATTCAGGAAGCATGAG 849  
 QY 281 AsnAsn 282  
 DB 850 AACAAAT 855

RESULT 10  
 US-10-140-922-505  
 ; Sequence 505, Application US/10140922  
 ; Publication No. US2003013889A1  
 ; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
 APPLICANT: Beresini, Maureen  
 APPLICANT: DeForge, Laura  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowsky, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K  
 APPLICANT: Wood, William  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 FILE REFERENCE: P3330R1C179  
 CURRENT APPLICATION NUMBER: US/10/140,922  
 PRIOR APPLICATION REMOVED - See Palm or File Wrapper  
 NUMBER OF SEQ ID NOS: 530  
 SEQ ID NO 505  
 LENGTH: 1204  
 TYPE: DNA  
 ORGANISM: Homo Sapien  
 US-10-140-922-505

#### Alignment Scores:

Pred. No.: 5,28e-162 Length: 1204  
 Score: 1523.00 Matches: 282  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-09-856-320a-2 (1-282) x US-10-140-922-505 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20  
 DB 10 ATGCAAGAGGTGAGGTGGCTGGGGAGTGAAGTATCGGGAGAGGCTCACAGCACC 69  
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetAlaGlyLeuGlnLeuLeu 40  
 DB 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCTCAGTTAATCTTG 129  
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGluThrArgIleIleLysGlyPheGluLys 60  
 DB 130 CTTCGCTGGCCACAGGGCTTGTAGGGGAGAGACAGCAGGATCATCAGGGGTTCAGTGC 189  
 QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLysGly 80  
 DB 190 AAGCTCACTCCAGCCCTGGCAGGACACCTGTTCCGAAAGAGCGGCTACTCTGTGG 249  
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100  
 DB 250 GCGACGCTCATCGCCGCCAGATGGCTCTGACAGACGCCCATGCTCAAGCCCGCTAC 309  
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThr 120  
 DB 310 ATAGTTCACTGGGGCCAGACACCTCCGAAAGGGAGGGCTGTGACAGACCCGGACA 369  
 QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140  
 DB 370 GCCACTGAGTCTTCCGCCACCCCGGGCTTCAACAACAGCCTCCCAAAAGACACCGCC 429  
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160  
 DB 430 AATGACATCATGTGGTGTAAGATGGCATGCCAGTCTTCATCACCCTGGGCTGTGGACCC 489  
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180

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|||||
490 CTCACCTCTCCACAGCTGTCTCAGTGGACACAGCTCATTTCCGGCTGGGC 549
Db
181 SerThrsSerProGlnLeuArgLeuProHisThrlLeuArgCysAlaAsnIleThrIle 200
Qy
550 AGACAGCTCCAGCCGCCAGTTACGCTCTCCACACCTCTGGGATGCCCAATCACCATC 609
Db
201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrsPthrMetValCys 220
Qy
610 ATTGAGACACCAAGAAGTGTAGAACGCCCTACCCCGCAACATCAAGACACATGTTGT 669
Db
221 AlaSerValGlnLeuLysGlyLysAspSerCysGlnLysAspSerGlyLysProLeuVal 240
Qy
670 GCCAGGCTGACGAGAGGGGCAAGAGCTCTGCGAGGGTACATCCGGGGCCCTGTGTC 729
Db
241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Qy
730 TGTAAACCAAGTCTTTCAAGGCAATTATCTCTGGGGCCAGGATCCGTGTGGATCACC 789
Db
261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnLysThrMetLys 280
Qy
790 AACCTGTGTCTACACGAAGTGTCAATATGTGACTGATCCAGAGCATGTAAG 849
Db
281 AsnAsp 282
Qy
850 AACAAAT 855
Db

RESULT 11
US-10-140-924-505
; Sequence 505, Application US/10140924
; Publication No. US20030134355A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C177
; CURRENT APPLICATION NUMBER: US/10/140,924
; PRIOR APPLICATION: 2002-05-07
; PRIOR Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Saplen
US-10-140-924-505

Alignment Scores:
Pred. No.: 5,28e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-2 (1-282) x US-10-140-924-505 (1-1204)
Qy 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyValArgGlyLeuThrAlaAla 20

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|||||
10 ATCAGAGAGTGTGAGTGGCTGCGGAGCTGGAACGTATCGGGGAGAGTCTCACAGCAGCC 69
Db
21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
Qy
70 AAGGAACTGTGGGCGCGCTCTCTCCCTCCAGGCCATGAGATGTGGAGTTAAATCTG 129
Db
41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLysThrArgIleIleLysGlyPheGlyCys 60
Qy
130 CTTCCTGTGGCAACAGGGGCTTGTAGGGGGAGAACACAGATCATCAAGGGGTTCCAGTGC 189
Db
61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLysGly 80
Qy
190 AACCTCAGCTCCAGGCTGTGGAGGAGCCCTGTGAGAMGACGGGCTACTCTGTGG 249
Db
81 AlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Qy
250 GCCAGGCTCATGCCGCCAGATGGCTCTGTACAGCAGCCACTGCTCAAGCCCGCTAC 309
Db
101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyLysGlyLysGlnLysThrArgThr 120
Qy
310 ATAGTTACCTGGGCGAGCACACCTCCAGAAAGAGAGGGGCTGTGAGCAGACCCGAGA 369
Db
121 AlaThrGluSerPheProHisPProGlyPheAsnAspSerLeuProAsnLysAspHisArg 140
Qy
370 GCCAGTGAAGTCTTCCGCCACCCCGCTTCACACAGACCTCCCAACAAAGACACCCG 429
Db
141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Qy
430 AATGACATCATGCTGTGGTGAAGATGGCATGCCAGTCTCCATCAGCTGGGCTGTGCCACCC 489
Db
161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Qy
490 CTCACCTCTCTCTACAGCTGTGTCTGCTGCGACACAGCTGCCTATTCGGGCTGGGC 549
Db
181 SerThrsSerProGlnLeuArgLeuProHisThrlLeuArgCysAlaAsnIleThrIle 200
Qy
550 AGCAGCTCCAGCCGCCAGTTACGCTGTGCTCACACCTTGGAGTGCACCAATCACCACATC 609
Db
201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrsPthrMetValCys 220
Qy
610 ATTGAGACACCAAGAAGTGTAGAACGCCCTACCCCGCAACATCACAACACATGTTGT 669
Db
221 AlaSerValGlnLysGlyLysAspSerCysGlnLysAspSerGlyLysProLeuVal 240
Qy
670 GCCAGGCTGACGAGAGGGGCAAGAGCTCTGCGAGGGTACATCCGGGGCCCTGTGTC 729
Db
241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Qy
730 TGTAAACCAAGTCTTTCAAGGCAATTATCTCTGGGGCCAGGATCCGTGTGGATCACC 789
Db
261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnLysThrMetLys 280
Qy
790 AACCTGTGTCTACACGAAGTGTCAATATGTGACTGATCCAGAGCATGTAAG 849
Db
281 AsnAsp 282
Qy
850 AACAAAT 855
Db

RESULT 12
US-10-140-926-505
; Sequence 505, Application US/10140926
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```

APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zhen  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P330R1C187  
CURRENT FILING DATE: 2002-05-07  
CURRENT FILING DATE: 2002-05-07  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 505  
LENGTH: 1204  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-140-926-505

Alignment Scores:  
Pred. No.: 5.28e-162 Length: 1204  
Score: 1523.00 Matches: 282  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-140-926-505 (1-1204)

QY 1 MetGlnArgLeuAgtTPrLeuAAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20  
DB 10 ATGAGAGAGTTGAGGTGGCTGCGGAGTCAAGTATCGGCGAGAGGCTTCACAGCAGCC 69  
QY 21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnIleLeu 40  
DB 70 AAGGAGCTGGGGCCGCTCTCCCTCCAGGCGCATGAGGATTCGACATTATCTGTG 129  
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLeuGlyPheGluCys 60  
DB 130 CTGCTCTGGCAGACAGGGCTGTAGGGGGAGAGACAGGATCATCAAGGGGTTGAGTGC 189  
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluCysThrArgLeuLeuGly 80  
DB 190 AAGCTCATCTCCAGCCCTGGCAGGAGCCCTGTTCGAGAGAGCGGCTACTGTGGG 249  
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysIleLysProArgTyr 100  
DB 250 GCGAGCTCATGCGCCCGAGATGGCTCTGACAGCAGCCCACTGCTCAAGCCCGCTAC 309  
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGluGlnThrArgThr 120  
DB 310 ATAGTTCACTGGGGGAGCAGACACCTCCAGAGAGAGAGGGCTGTGACAGACCCGACA 369  
QY 121 AlaThrGlnSerPheProHisSerProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140  
DB 370 GCCACTAGTCTCTCCCGCAGCCCGGCTTCAACAAGAGCTCCCAACAAGACACCGC 429  
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160  
DB 430 AATGACATCATGCGGTGAGATGAGCATGCGCAATCTCCATCACTGGGCTGTGAGCC 489  
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrPoli 180  
DB 490 CTCACCTCTCTCAGCGCTGTGTACAGTGTGACAGCAGTCCCTCATTTCCGGGTGGGC 549  
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200  
DB 550 AGCAGCTGTCAGCCCGCAGTGTACGCTGCTCAGACACTTGCATCGGCAACATCAGATC 609  
QY 201 IleGlnHisGlnLysCysGluAsnAlaTyrProGlyLysIleThrAspThrMetValCys 220

DB 610 ATTGAGCAGCAGAACTGTGAGAACCCCTAACCCCGCAGCATCAGACACCATGCTGT 669  
QY 221 AlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240  
DB 670 GCCAGCTGTCAGAGAGAGGGGAGAGACATCTCCAGAGGGTGAATCCGGGGCCCTGTGTC 729  
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260  
DB 730 TGTAACTGCTCTCTTCAAGGCAATATCTCTGGGGCCAGAGATCCGTGCGATCACCGGA 789  
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280  
DB 790 AAGCTGTGTCTACACAGAAAGTCTGCAAAATATGTGAGTGTATCAGAGACGATGAG 849  
QY 281 AsnAsn 282  
DB 850 AACAT 855

RESULT 13

US-10-141-698-505  
Sequence 505, Application US/10141698  
Publication No. US20030134357A1  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeFoyers, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zhen  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P330R1C206  
CURRENT FILING DATE: 2002-05-08  
CURRENT FILING DATE: 2002-05-08  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 505  
LENGTH: 1204  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-141-698-505

Alignment Scores:

Pred. No.: 5.28e-162 Length: 1204  
Score: 1523.00 Matches: 282  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-141-698-505 (1-1204)

QY 1 MetGlnArgLeuAgtTPrLeuAAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20  
DB 10 ATGAGAGAGTTGAGGTGGCTGCGGAGTCAAGTATCGGCGAGAGGCTTCACAGCAGCC 69  
QY 21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnIleLeu 40  
DB 70 AAGGAGCTGGGGCCGCTCTCCCTCCAGGCGCATGAGGATTCGACATTATCTGTG 129  
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGluCys 60

Db 130 CTTCGCTCTGGCAACAGGCGCTTGTAGGGGGAGACACGATCATCAAGGGCTTCAGCTGC 189  
QY 61 LysProHisSerSerGlnProTrpGlnAlaAlaLeuPheGluIuPstThrArgLeuLeuGly 80  
190 AAGCTTCACCTCCAGAGCCCTGGAGGAGCCCTGTGTGAGAAAGAGGGGCTACTGTGGG 249  
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100  
250 GCGACGCTCATCCGCCCAATGAGCTCTTCAGACAGCCACACGCCCTCAAGCCCGCTAC 309  
QY 101 TLeValHisLeuGlnLysGlnHisAsnLeuGlnLysGluLysGlnGlnThrArgThr 120  
310 ATAGTTCACCTCGGGGCGAGCAACCTCCAGAAAGAGAGGGCTGTGAGCAGACCCGAGCA 369  
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140  
370 GCCACTGAGCTCTCCCGCCACCGGGCTTCACACAGAGCTCCCGCAACAAAGACACCGC 429  
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160  
430 AATGACATCATGCTGTGGAAAGATGGCATCGCAGTCTCCATCAGCTGGGCTGTGCGACCC 489  
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180  
490 CTCACCTCTCTCCAGCGCTGTCTCACTGCTGGCAGCACGCTGCTCATTTCCGGCTGGGC 549  
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200  
550 AGCAGCTGACGCCCGCCAGTGTAGCGCTGACCTCACACCTTGGGATGGCGCAACATCACATC 609  
QY 201 TLeGluHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220  
610 ATTGAGACACCAAGAGTGTGAAAGCGCTACCCCGGCAACATCACAGCACCATGCTGTGT 669  
QY 221 AlaSerValGlnLysGlnLysAspSerCysGlnLysAspSerGlyGlyProLeuVal 240  
670 GCGAGCGTGCAGAGAGGGGCGCAAGACTCTGCCAGGGTGTACTCCGGGGCCCTGTGTC 729  
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260  
730 TGTAAACAGTCTCTTCAGGCAATTAATCTCTGGGGGCGAGATCCGTTGCGATCACCCGA 789  
QY 261 LysProGlyValIleThrIleLysValCysLysTyrValAspTrpIleGlnGlnIuThrMetLys 280  
790 AAGCTGTGTCTTACAGAAAGTCTGCAATATGTGACTGATCCAGGAGACGATGAAG 849  
QY 281 AsnAsn 282  
850 AACAAAT 855  
Db

RESULT 14  
US-10-141-702-505  
; Sequence 505, Application US/10141702  
; Publication No. US20030134358A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Geriltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P330R1C208  
; CURRENT APPLICATION NUMBER: US/10/141,702  
; CURRENT FILING DATE: 2002-05-08  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 505  
; LENGTH: 1204  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-141-702-505  
Alignment Scores:  
Pred. No.: 5.28e-162 Length: 1204  
Score: 1523.00 Matches: 282  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0  
US-09-856-320a-2 (1-282) x US-10-141-702-505 (1-1204)  
QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20  
10 ATGCAAGAGTTGAGTGGGCTGCGGAGCTGGAATCATCGGGCAGAGTCTCACAGCAGCC 69  
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40  
70 AAGGAACCTGGGGGCGGCTCTCTCCCGCTCCAGCCATGAGATTCGTGAGTTAACTCTG 129  
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIuThrArgIleIleLysGlyPheGlyCys 60  
130 CTTCGCTGTGCAACAGGGCTGTGTAGGGGAGAACACAGATCATCAAGGGGTTGCGAGTGC 189  
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluIuPstThrArgLeuLeuGly 80  
190 AAGCTTCACCTCCAGAGCCCTGGCAGGAGCCCTTTTGAGAAAGCGGGCTACTGTGGG 249  
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100  
250 GCGACGCTCATCCGCCCAATGAGCTCTTCAGACAGCCACATGCTCAAGCCCGCTAC 309  
QY 101 TLeValHisLeuGlnLysGlnHisAsnLeuGlnLysGluLysGlnGlnThrArgThr 120  
310 ATAGTTCACCTCGGGGCGAGCAACCTCCAGAAAGAGAGGGCTGTGAGCAGACCCGAGCA 369  
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140  
370 GCGACTGAGTCTTCCCGCCACCGGGCTTCACACAGAGCTCCCGCAACAAAGACACCGC 429  
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160  
430 AATGACATCATGCTGTGAAAGATGGCATCGCAGTCTCCATCAGCTGGGCTGTGCGACCC 489  
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180  
490 CTCACCTCTCTCCAGCGCTGTCTCACTGCTGGCAGCACGCTGCTCATTTCCGGCTGGGC 549  
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200  
550 AGCAGCTCCAGCCCGCCAGTGTAGCGCTGTGCTCACACCTTGGGATGGCGCAACATCACATC 609  
QY 201 TLeGluHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220  
610 ATTGAGACACCAAGAGTGTGAAAGCGCTACCCCGGCAACATCACAGACATGAGTGTGT 669  
QY 221 AlaSerValGlnLysGlnLysAspSerCysGlnLysAspSerGlyGlyProLeuVal 240  
670 GCGAGGTCAGAGAAAGGGGCGCAAGACTCTGCGAGGTCGACTCCCGGGGCGCTGTGTC 729  
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260  
730 TGTAAACAGTCTTCAAGGCAATTAATCTCTGGGGGCGAGATCCGTTGCGATCACCCGA 789

```

OY      261  LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGluThrMetLys 280
Db      790  AAGCTGTGTCTCTACAGAAAGTCTGCATAATATGTGACTGTGATCCAGAGACGATGAAAG 849

OY      281  AsnAsn 282
Db      850  AACAAAT 855

RESULT 15
US-10-141-704-505
; Sequence 505, Application US/10141704
; Publication No. US20030134359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvalet, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C209
; CURRENT APPLICATION NUMBER: US/10/141,704
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-704-505

Alignment Scores:
Pred. No.:      5,28e-162      Length:      1204
Score:          1523.00      Matches:      282
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              12          Gaps:          0

US-09-856-320a-2 (1-282) x US-10-141-704-505 (1-1204)

OY      1  MetClnArgLeuArgTyrPleuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
Db      10  ATGCAAGAGGTGAGTGAGTGGCTGGGACTGGAAGTCATCGGGCAGAGGCTTCACAGCAGCC 69

OY      21  LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnIleuLeu 40
Db      70  AAGGAACCTGGGGCCCTCTCCCTCCAGCCATGAGGATTCGACATTATCTCTG 129

OY      41  LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGluCys 60
Db      130  CTTCCTCTGGCAACAGAGGCTTGTAGGGGGAGAGACAGATCATCAAGGGGTTGAGAGTGC 189

OY      61  LysProHisSerGlnProTyrPglAlaAlaLeuPheGluLysThrArgLeuLeuCysGly 80
Db      190  AAGCCTCACTCCAGCCCTGGCAGGACCCCTGTTGAGAAAGACGCGCTACTCTGTGGG 249

OY      81  AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db      250  GCGACGCTCATGCCCCCAAGTGGCTCTGTCAGACAGCCCACTGCTCAAGCCCCCGGCTAC 309

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OY      101  IleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGluGlyCysGlnGlnThrArgThr 120
Db      310  ATAGTTCACCTGGGGCAGACACACACTCCAGAAAGAGGAGGGCTGTGACACACCCGGACA 369

OY      121  AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      370  GCCACTGAGTCTTCCCCACCCCGGCTTCAACACACACTTCCCAACAAAGACCCAGCCG 429

OY      141  AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db      430  AATGACATCATGTGTGTAAGATGGCATCGCAGTCTCCATACCTGGGCTGTGGACCC 489

OY      161  LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrPglY 180
Db      490  CTCACCCCTCTCCTCAGCGTGTGTACTCTGTGACACACACTCCATTTCCGGGCTGGGGC 549

OY      181  SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db      550  AGCAGCTCCACGCCCCCACTTACGCTGCTCACAACCTTGCATGCGCCACATCACCATC 609

OY      201  IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
Db      610  ATTGAGCCACAGAAAGTGTGAGAACGCTTACCCCGGCACACATCACAGACCATGGTGTCT 669

OY      221  AlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
Db      670  GCCAGCGTGCAGGAAGGGGGCAGAGACTCTGCCAGGGGTGACTCGGGGGGCTCTGTGTC 729

OY      241  CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db      730  TGTAAACCACTCTTCAAGGCATTATCTCTGGGGCCAGGATCCGTGTGCATCACCCGA 789

OY      261  LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGluThrMetLys 280
Db      790  AAGCCTGTGTCTACAGAAAGTCTGCATAATATGTGAGTGTGATCCAGAGACGATGAAAG 849

OY      281  AsnAsn 282
Db      850  AACAAAT 855

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Search completed: October 15, 2003, 23:04:17  
Job time : 318.352 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_pzn model

Run on: October 15, 2003, 20:58:42 ; Search time 78.364 Seconds

(without alignments)  
1588.358 Million cell updates/sec

Title: US-09-856-320A-2

Perfect score: 1523

Sequence: 1 MQRRLRLDMKSSGRGILTA.....GYTKCKYVDIQTMKNN 282

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-O=/cgn2\_1/USPTO.spool/P/US09856320/runat\_15102003\_105826\_10042/app.query.fasta\_1.846  
-DB=Issued\_Patents\_NA -OPMT=fastlap -SUFFIX=rni -MINMATCH=0.1 -LOOPCT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdd  
-LIST=45 -DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pco -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09856320.ecgn\_1.1.133.8runat\_15102003\_105826\_10042 -NCPV=6 -ICPV=3  
-NO\_MMAP -LARGEOUDRY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -MAIN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued\_Patents\_NA: \*  
1: /cgn2\_6/ptodata/2/1na/5A.COMB.seq: \*  
2: /cgn2\_6/ptodata/2/1na/5B.COMB.seq: \*  
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4: /cgn2\_6/ptodata/2/1na/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/2/1na/PCTUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/2/1na/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1523	100.0	1314	3	US-09-025-059-2
2	1519	99.7	1292	4	US-09-205-258-189
3	1410	92.6	1192	3	US-08-944-483-7
4	1398	91.8	1166	3	US-08-944-483-7
5	1284	84.3	1146	4	US-09-205-258-247
6	1233	81.0	833	2	US-08-790-137-2
7	1227	80.6	1052	4	US-09-386-642-10
8	916.5	60.2	618	4	US-09-280-116-3
9	739	48.5	472	4	US-09-280-116-136
10	690	45.3	944	3	US-09-070-526-1
11	682	44.8	994	3	US-09-008-271A-19
12	679	44.6	1049	4	US-09-386-642-9

13	650.5	42.7	1570	4	US-09-996-243-308	Sequence 308, App
14	637.5	41.9	1476	2 <td>US-08-824-874-2</td> <td>Sequence 2, App1</td>	US-08-824-874-2	Sequence 2, App1
15	637.5	41.9	1476	2 <td>US-09-210-084-2</td> <td>Sequence 2, App1</td>	US-09-210-084-2	Sequence 2, App1
16	637.5	41.9	1476	4 <td>US-09-764-762-2</td> <td>Sequence 2, App1</td>	US-09-764-762-2	Sequence 2, App1
17	634.5	41.7	1364	4 <td>US-09-280-116-20</td> <td>Sequence 20, App1</td>	US-09-280-116-20	Sequence 20, App1
18	596.5	39.2	822	3 <td>US-09-100-264-8</td> <td>Sequence 8, App1</td>	US-09-100-264-8	Sequence 8, App1
19	596.5	39.2	832	3 <td>US-08-768-859A-5</td> <td>Sequence 5, App1</td>	US-08-768-859A-5	Sequence 5, App1
20	596.5	39.2	832	3 <td>US-08-768-859A-5</td> <td>Sequence 5, App1</td>	US-08-768-859A-5	Sequence 5, App1
21	596.5	39.2	832	4 <td>US-08-622-046B-15</td> <td>Sequence 15, App1</td>	US-08-622-046B-15	Sequence 15, App1
22	596.5	39.2	832	4 <td>US-08-843-076D-4</td> <td>Sequence 4, App1</td>	US-08-843-076D-4	Sequence 4, App1
23	596.5	39.2	1341	4 <td>US-08-983-075D-6</td> <td>Sequence 6, App1</td>	US-08-983-075D-6	Sequence 6, App1
24	596.5	39.2	1358	4 <td>US-08-983-075D-8</td> <td>Sequence 8, App1</td>	US-08-983-075D-8	Sequence 8, App1
25	594	39.0	732	1 <td>US-08-361-395-2</td> <td>Sequence 20, App1</td>	US-08-361-395-2	Sequence 20, App1
26	593.5	39.0	832	3 <td>US-08-767-820A-20</td> <td>Sequence 20, App1</td>	US-08-767-820A-20	Sequence 20, App1
27	593.5	39.0	832	3 <td>US-08-767-820A-20</td> <td>Sequence 20, App1</td>	US-08-767-820A-20	Sequence 20, App1
28	593.5	39.0	832	3 <td>US-08-622-046B-4</td> <td>Sequence 4, App1</td>	US-08-622-046B-4	Sequence 4, App1
29	592.5	38.9	832	5 <td>PCT-US95-06157-5</td> <td>Sequence 5, App1</td>	PCT-US95-06157-5	Sequence 5, App1
30	587	38.5	897	2 <td>US-08-956-267A-1</td> <td>Sequence 1, App1</td>	US-08-956-267A-1	Sequence 1, App1
31	585.5	38.4	766	3 <td>US-08-768-859A-9</td> <td>Sequence 9, App1</td>	US-08-768-859A-9	Sequence 9, App1
32	585.5	38.4	766	3 <td>US-08-768-859A-9</td> <td>Sequence 9, App1</td>	US-08-768-859A-9	Sequence 9, App1
33	585.5	38.4	766	3 <td>US-08-622-046B-17</td> <td>Sequence 17, App1</td>	US-08-622-046B-17	Sequence 17, App1
34	585.5	38.4	766	3 <td>US-09-100-264-6</td> <td>Sequence 6, App1</td>	US-09-100-264-6	Sequence 6, App1
35	585.5	38.4	766	4 <td>US-08-843-076D-6</td> <td>Sequence 6, App1</td>	US-08-843-076D-6	Sequence 6, App1
36	583	38.3	1504	4 <td>US-09-280-116-1</td> <td>Sequence 1, App1</td>	US-09-280-116-1	Sequence 1, App1
37	582.5	38.2	766	5 <td>PCT-US95-06157-9</td> <td>Sequence 9, App1</td>	PCT-US95-06157-9	Sequence 9, App1
38	581.5	38.2	1089	5 <td>US-08-930-188-1</td> <td>Sequence 1, App1</td>	US-08-930-188-1	Sequence 1, App1
39	580	38.1	1089	3 <td>US-08-930-188-1</td> <td>Sequence 3, App1</td>	US-08-930-188-1	Sequence 3, App1
40	580	38.1	1089	5 <td>PCT-US96-04294-1</td> <td>Sequence 1, App1</td>	PCT-US96-04294-1	Sequence 1, App1
41	580	38.1	1089	5 <td>PCT-US96-04294-3</td> <td>Sequence 3, App1</td>	PCT-US96-04294-3	Sequence 3, App1
42	580	38.1	1089	5 <td>US-08-768-859A-7</td> <td>Sequence 7, App1</td>	US-08-768-859A-7	Sequence 7, App1
43	579.5	38.0	760	3 <td>US-08-767-820A-7</td> <td>Sequence 7, App1</td>	US-08-767-820A-7	Sequence 7, App1
44	579.5	38.0	760	3 <td>US-08-767-820A-7</td> <td>Sequence 7, App1</td>	US-08-767-820A-7	Sequence 7, App1
45	577.5	37.9	711	3 <td>US-08-622-046B-13</td> <td>Sequence 13, App1</td>	US-08-622-046B-13	Sequence 13, App1

#### ALIGNMENTS

RESULT 1  
US-09-025-059-2  
Sequence 2, Application US/09025059  
Patent No. 6075136

GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,059  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0481 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-845-0555  
TELEFAX: 650-845-4166

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TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1314 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: LONGTUT10
;   CLONE: 2723646
;
US-09-025-059-2

Alignment Scores:
Pred. No.:      5.95e-144      Length:      1314
Score:          1523.00      Matches:      282
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:               Gaps:      0

US-09-856-320a-2 (1-282) x US-09-025-059-2 (1-1314)

QY      1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
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Db      128 ATGCACAGGTGAGTGAGTGCGCGGACTGGAATCATCGGGCAGAGGTCTCACAGCAGCC 187
QY      21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
      |||
Db      188 AAGGAACCTGGGGGCGGCTCTCCCGCCCTCCAGGCGCATGAGATCTGCAGTAAATCTTG 247
QY      41 LeuAlaIleAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGlyLys 60
      |||
Db      248 CTTCCTCTGGCAGACAGGGCTGTAGGGGAGAGACCAGGATCATCAAGGGGTTGAGTGC 307
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly 80
      |||
Db      308 AAGCCTCAGCTCCAGCGCTGGCGAGGAGCGCCCTGTGAGAGACGCGGCTACTGTGGG 367
QY      81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
      |||
Db      368 GCGACGCTATCCGCCAGATGGCTCCGACAGCAGCCACAGCTCAAGCCCGCTAC 427
QY      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyLysGlnGlnThrArgTyr 120
      |||
Db      428 ATAGTTACCTGGGGGAGCACAACCTCCAGAAAGAGAGGGGCTGTAGCAGACCGGAGA 487
QY      121 AlaThrGlySerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
      |||
Db      488 GCGACGAGTCCCTCCGCCACCGCGGCTTCACACAGCCCTCCCAACAAAGACACCGG 547
QY      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
      |||
Db      548 AATGACATATGCTGTGAAGATGGCATGGCCAGTCTCATCCTGAGGCTGTGCAGACC 607
QY      161 LeuThrLeuSerSerArgCysValIleThrAlaGlyThrSerCysLeuIleSerGlyTyrPgly 180
      |||
Db      608 CTCACCTCTCCACAGCTGTGCATGCTGGGACCAAGCTGCTCATTTCCGGCTGGGGC 667
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
      |||
Db      668 AGCAGCTCAGCCGCCAGTTAGCCCTGCTCACACCTTGGAGAGGCCCAACATCACACATC 727
QY      201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
      |||
Db      728 ATTGAGCACCAAGAGTGAAGAACGCTTACCCCGGCAACATCACAGACCATGTGTGT 787
QY      221 AlaSerValGlnGlnGlyLysAspSerCysGlnGlyLysPserCylLysProLeuVal 240
      |||
Db      788 GCCAGCGTCAAGAAAGGGGCAAGGACTCTCTGCAGAGGGTACTCCGGGGCCCTTCGGTGC 847
QY      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyLysProCysAlaIleThrArg 260
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Db      848 TGTAAACCACTCTTCAAGGCATTAATCTCTGGGGGCGAGAGATCCGTGTGCATACCCGA 907
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QY      261 LysProGlyValIleThrLysValCysLysTyrValAspTrpIleGlnIleThrMetLys 280
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Db      908 AAGCTGAGTGTACACAGAAAGTCTCAATAATGTGAGTGCAGGAGAGATGAAG 967
QY      281 AsnAsn 282
      |||
Db      968 AACAAAT 973

RESULT 2
US-09-205-258-189
; Sequence 189, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
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: EARLIER APPLICATION NUMBER: 60/048,917
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,949
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,974
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,883
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,897
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,898
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,962
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,963
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,877
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/048,878
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/070,923
: EARLIER FILING DATE: 1997-12-18
: EARLIER APPLICATION NUMBER: 60/092,921
: EARLIER FILING DATE: 1998-07-15
: EARLIER APPLICATION NUMBER: 60/094,657
: EARLIER FILING DATE: 1998-07-30
: NUMBER OF SEQ ID NOS: 1227
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 189
: LENGTH: 1292
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-205-258-189

Alignment Scores:
Pred. No.: 1,47e-143      Length: 1292
Score: 1519.00           Matches: 281
Percent Similarity: 99.65%      Conservative: 0
Best Local Similarity: 99.65%      Mismatches: 1
Query Match: 99.74%           Indels: 0
                                Gaps: 0
DB: 4

US-09-856-320a-2 (1-282) x US-09-205-258-189 (1-1292)
QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
DB 111 ATGAGAGGTTGAGGTGGCTGGCGGAGCTGGAAGTCATCGGCGACAGGCTCTACAGCACC 170
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnIleLeu 40
DB 171 AAGGAACTGGGGCCCTCTCCCTCCCTCCAGGCGCATGAGGATTGTGAGTTAATCCTG 230
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIleThrArgIleIleLysGlyPheGlnCys 60
DB 231 CTTCCTCTGGCAACAGGAGCTGTGAGGGGAGAGACAGGATCAAGAGGGGTTGAGTGC 290
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysTrpArgLeuLeuCysGly 80
DB 291 AAGCTCAGTCCAGCCCTGGAGGAGCCCTGTTTCAGAAAGACGGGCTACTCTGTGGG 350
QY 81 AlaThrIleLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrp 100
DB 351 GCGAGGCTCATCGCCCAATGGCTCTCTGACAGCAGCCCACTGCTCAAGCCCGCTAC 410
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlyGlnThrArgThr 120
DB 411 ATAGTTACCTGGGGGCGACACACCTCCAGAGAGAGAGGGCTGTGACAGACCCGAGCA 470
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 471 GCCACGTAGTCTCTCCCGCCAGCCCGGCTTCACAGAACAGCCCTCCCAACAAAGACACCGC 530
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
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DB 531 AATGACATCATGCTGGTGAAGATGGCATCGCAGTCTCCATCATCCTGGGCTGTGACCC 590
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
DB 591 CTCACCTCTCTCTACAGCTGTGTCTCTGCTGTGACCTGCTGTCTATTTCCGCTGGGGC 650
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB 651 AGCAGCTCCAGCCCACTTACGCTGCTGCTACACCTTGCGATGGCCAAATCACCATC 710
QY 201 IleGluHisGlnLysCysGlyAsnAlaTrpProGlyAsnIleThrAspThrMetValCys 220
DB 711 ATTGAGCACAGAGTGTGAGACACCCCTAACCCCGCAACATCACAGACCATGTGTGT 770
QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnLysAspSerGlyProLeuVal 240
DB 771 GCCAGCGTGCAGAGAGGGGCAAGGACTCTGCGCAGGGGTGACTCGGGGGCTCTGTGTC 830
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
DB 831 TGTAAACAGTCTCTTCAAGGCATTAATCTCGGGGCGCAGATCCGTGTGCAATCACC 890
QY 261 LysProGlyValTrpThrLysValCysLysTrpValAspTrpIleGlnIleThrMetLys 280
DB 891 AAGCTGTGTCTACACGAAAGTCTGCAAAATATGTGAGCTGATTCAGACAGACATGAAG 950
QY 281 AsnAsn 282
DB 951 AACAAAT 956

RESULT 3
US-08-944-483-8
: Sequence 8, Application US/08944483
: Patent No. 6232456
: GENERAL INFORMATION:
: APPLICANT: COHEN, MAURICE
: APPLICANT: GOLPIYTS, TRACEY L.
: APPLICANT: FRIEDMAN, PAULA N.
: APPLICANT: GRANADOS, EDWARD N.
: APPLICANT: KLAAS, MICHAEL R.
: APPLICANT: RUSSELL, JOHN C.
: APPLICANT: STEWART, KENT D.
: APPLICANT: STROUPE, STEVEN D.
: TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
: TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
: NUMBER OF SEQUENCES: 76
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Abbott Laboratories
: STREET: 100 Abbott Park Road
: CITY: Abbott Park
: STATE: IL
: COUNTRY: USA
: ZIP: 60064-3500
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/944,483
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Becker, Cheryl L.
: REGISTRATION NUMBER: 35,441
: REFERENCE/DOCKET NUMBER: 6183 US-01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 847/935-1729
```

TELEFAX: 847/938-2623  
TELEX: 111  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1192 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-944-483-8

## Alignment Scores:

pred. No.:	1,22e-132	Length:	1192
Score:	1410.00	Matches:	261
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	92.58%	Indels:	0
DB:	3	Gaps:	0

US-09-856-320a-2 (1-282) x US-08-944-483-8 (1-1192)

22 GIUProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuLeu 41  
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74 GAACCTGGGGCCCGCTCTCCCTCCAGGCCATGAGATTGTGAGTTAACTGCTT 133  
|||||  
42 AlAlaLeuAlaThrGlyLeuValGlyGlyGluThrArgIleIleLeuGlyPheGlyCysLys 61  
|||||  
134 GCTCTGGCAACAGGCTGTAGGGGAGAGACAGCATCATCAAGGGGTTCGAGTCAAG 193  
|||||  
62 ProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuGlyCysGlyAla 81  
|||||  
194 CCTCACTCCAGCGCTGGGAGGAGCGCTGTTCGAGAAGCGGGTACTGTGGGGCG 253  
|||||  
82 ThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrpIle 101  
|||||  
254 AGGCTATGCGCCCGCATGGCTCCCTGACAGCGCCGCTGCTCAAGCCCGCTCAATA 313  
|||||  
102 ValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThrAla 121  
|||||  
314 GTTCACCTGGGGAGAGCAACCTCCAGAAAGAGAGGGCTGTGAGAGCAACCGGACAGCC 373  
|||||  
122 ThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArgAsn 141  
|||||  
374 ACTGATCTTCTCCCGCCCGCTTCAACACAGCTCCCGCCCAACAAAGCCAGCAAT 433  
|||||  
142 AspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgProLeu 161  
|||||  
434 GACATCATGCTGGTGAAGATGGCATGCGCATCTCCATCAGCTGGGCTGGCAGCCCTC 493  
|||||  
162 ThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGlySer 181  
|||||  
494 ACCCTCTCTCAGCGTGTCACTGTGACACAGCTGCTCTATTCCGGCTGGGGCAGC 553  
|||||  
182 ThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIleIle 201  
|||||  
554 AGCTCCAGGCCCGCATGTACGCTGCTCACACCTTCCGATGGCCCAACATCCACATCAT 613  
|||||  
202 GIUHisGlnLysCysGlnAsnAlaTrpProGlyAsnIleThrAspThrMetValCysAla 221  
|||||  
614 GAGCACCAGAAAGTGAAGAACGCTTACCCCGGCAACATACAGACACCAATGGTGTGGC 673  
|||||  
222 SerValGlnGluGlyLysAspSerCysGlnGlyAspSerGlyLysIleProLeuValCys 241  
|||||  
674 ACCGTGACAGAAAGGGGCAAGGACTCTCCAGAGGTGACTCCGGGGGCTGTGCTGTG 733  
|||||  
242 AsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArgLys 261  
|||||  
734 AACCGATCTCTTCAAGGCAATTAATCTCTGGGGCAGAGATCCGTGTCCGATCCCAAG 793  
|||||  
262 ProGlyValIleTrpThrLysValCysLysTrpValAspTrpIleGlnGlnThrMetLysAsn 281  
|||||  
794 CTTGTGTCTACACGAAAGTCTGCAAAATATGTGAGCTGATCCAGAGACGATGAAGAAC 853  
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QY 282 Asn 282  
DB 854 AAT 856

## RESULT 4

US-08-944-483-7

Sequence 7, Application US/08944483  
Patent No. 6232456  
GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLETTIS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLAAS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROUPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
TITLE OF INVENTION: OF THE PROSTATE  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1166 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-944-483-7

## Alignment Scores:

pred. No.:	1.9e-131	Length:	1166
Score:	1398.00 <td>Matches:</td> <td>259</td>	Matches:	259
Percent Similarity:	99.23% <td>Conservative:</td> <td>0</td>	Conservative:	0
Best Local Similarity:	99.23% <td>Mismatches:</td> <td>2</td>	Mismatches:	2
Query Match:	91.79% <td>Indels:</td> <td>0</td>	Indels:	0
DB:	3	Gaps:	0

US-09-856-320a-2 (1-282) x US-08-944-483-7 (1-1166)

22 GIUProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuLeu 41  
|||||  
70 GAACCTGGGGCCCGCTCTCCCGCTCCAGGCCATGAGATTCTGAGTTAACTGCTT 129  
|||||  
42 AlAlaLeuAlaThrGlyLeuValGlyGlyGluThrArgIleIleLeuGlyPheGlyCysLys 61  
|||||  
130 GCTCTGGCAACAGGCTGTAGGGGAGAGACAGCATCATCAAGGGCTTCGAGTCAAG 189  
|||||



```

: NAME/KEY SITE
: LOCATION: (20)
: OTHER INFORMATION: n equals a,t,g, or c
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (35)
: OTHER INFORMATION: n equals a,t,g, or c
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (36)
: OTHER INFORMATION: n equals a,t,g, or c
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (37)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-247

Alignment Scores:
Pred. No.: 5,53e-120 Length: 1146
Score: 1284.00 Matches: 246
Percent Similarity: 92.57% Conservative: 3
Best Local Similarity: 91.45% Mismatches: 16
Query Match: 84.31% Indels: 4
DB: Gaps: 2

US-09-856-320A-2 (1-282) x US-09-205-258-247 (1-1146)
QY 18 ThrAlaAlaLysGlnProGlyAlaArgSerProLeuGlnAlaMet--ArgLleu 36
Db 8 ACCCAGGGGAAcNTWTGGGGGCGCTTNNNTTCCCCCTCAGGCATTTGGGAATCTTC 67
QY 37 GlnLleuLleuLleu---AlaLleuAlaThrGlyLeuVal-GlyGlyGluThr-ArgLleI 55
Db 68 AAcTTATCTCTGCTTGTCTTGCTGGCCACACAGGGCTTGTAAGGGGGAGAGACCCAGGTCA 127
QY 55 LelysGlyPheGluCysLysProHisSerGlnProTrrpGlnAlaAlaLleuPheGluYst 75
Db 128 TCAAGGGGTTCAAGTCCAAAGCCTCACTCCAGACCCCTGGCAGGACCCCTGTTCCAGAGA 187
QY 75 hrArgLeuLeuCysGlyAlaThrLleuLleuLleuAlaProArgTrrpLeuLeuThrAlaLhsc 95
Db 188 CGCGGTACTACTGTGGGGGAGCGCTCATGCGCCCAATGGAGCTCTGACAGCCCACT 247
QY 95 ystLeuLysProArgTrrpLleuValHisLleuGlyGlnHisAsnLeuGlnLysGluGlyc 115
Db 248 GCGTCAGAGCCCGCTCATAGTTCACCTGGGGCACACAACTCCAGAAAGAGAGGGCT 307
QY 115 ysgGlnInThrArgThrAlaThrGlnUserPheProHisProGlyPheAsnAsnSerLeup 135
Db 308 GTAGAGACACCGGAGACGCCACTGAGTCTTCCCCACCCGGGCTTCAACACAGCTCC 367
QY 135 roAsnLysAspHisArgAsnAspLleMetLeuValLysMetAlaSerProValSerLleI 155
Db 368 CCAACAAAGACCCAGCATGACATCATGCTGGTGAAGATGGATCGGACAGTCCATCA 427
QY 155 hrTrrpAlaValArgProLeuThrLleuSerSerArgCysValThrAlaGlyThSerCysL 175
Db 428 CCGGGGCTGTGGACCCCTCACCCCTCTCTCAGCTGTGTACAGCTGGCACCGCTGYC 487
QY 175 eulLleSerGlyTrrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeuArgc 195
Db 488 TCATTTCCGGCTGGGGGACGACGTCAGGCCCAAGTTAGGCTGCTCACACCTTGGAT 547
QY 195 ysaAlaAsnLleThrLleLleGlnHisGlnLysCysGlnAspAlaTyrProGlyAsnLleI 215
Db 548 GCGCCAAATCAACATCATTTAGACACAGAAAGTGGAGAAAGCCTACCCCGGCAACTCA 607
QY 215 hrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnLysAsp 235
Db 608 CAACACACATGATGATGTGCCACGTCGAGAAAGGGGGCAAGACTCTGCCAGGGTGACT 667
QY 235 eArgGlyProLeuValCysAsnGlnSerLeuGlnGlyLleLleSerTrrpGlyGlnAsp 255

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Db      668  CCGGGGGCCCTCTGTCGTGTAAACCAATCTCTTCAAGCAATTATCTCCCTGGGGCCAGATC  72
QY      255  roCysAlaIlethraArgLysProGlyValIYrThrLysValcLysLysTyraValspTRI  275
Db      728  CGTTCGTGCATCCACCCGAAAGCCCTGCTGTACACGAAAGTCTGCAAAATATGTGGACTGGA  785
QY      275  legInguIthrMetLysAsnAsn 282
Db      788  TTCAGGAGACGATGAAGAACAAAT 810

RESULT 6
US-08-790-137-2
; Sequence 2, Application US/08790137
; Patent No. 5840871
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
; TITLE OF INVENTION: KALLIKREIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,137
; FILING DATE: Filed Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0195 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-4166
; TELEFAX: 415-845-0555
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-790-137-2

Alignment Scores:
Pred. No.: 4.67e-115 Length: 833
Score: 1233.00 Matches: 227
Percent Similarity: 91.15% Conservative: 10
Best Local Similarity: 87.31% Mismatches: 17
Query Match: 80.96% Indels: 6
DB: 2 Gaps: 1

US-09-856-320A-2 (1-282) x US-08-790-137-2 (1-833)
QY      29  ProLeuGlAlaMetArgIleLeuGlnLeuIleLeuAlaLeuAlaIthrgIleuVal 48
Db      6  CCGCTGGACACCTCTGTACCAATGTGGTTCCTGCTGTGCTGCGCCCTGTCCCTGGGG 65
QY      49  gIglYIY-----gIglYrArgIleIleLysgIglYpHeGluCysLysPro 62
Db      66  GGGACTGTGTCTCGCCGCCCGCCGATTCAGTCTCCGGAATTGTGGAGCGCTGGAGTGTGACAG 123
QY      63  HisSerGlnProTrpGlnAlaIleuPheGluIYrThrArgLeuLeuCYsGlyAlaThr 82

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|||||
Db 126 CATGCCAGCCCTGGCAGGCGGCTGTACAGAAAGCGGGCTACTGTGGGGCAGC 185
OY 83 LeuIleAlaProArgTTPLeuLeuThrAlaAlaHisCysLeuLysProArgTyrIleVal 102
Db 186 MTCAATNGCCCAATGGTTCTGTGACAGACCCACCTGCTTAAGCCCCGGCTACATAGTT 245
OY 103 HisLeuGlyGlnHisAsnLeuGlnLysGlnLysGlnLysGlnLysGlnLysGlnLys 122
Db 246 CACCTGGGGCAGCACAACCTCCAGAAAGAGAGAGGGCTGTGAGCAGACCAGCCGACCCCT 305
OY 123 GluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArgAsnAsp 142
Db 306 GAGGCTTCCCCCAACCCGGGCTTCAACACAGCCTCCCAACAAAGACACCGCAATGAC 365
OY 143 IleMetLeuValLysMetAlaSerProValSerIleThrTyrAlaValArgProLeuThr 162
Db 366 ATCATGCTGTGAGAGATGGCATCCGACATCCATCACTGCGGTGTCGACCCCTGAC 425
OY 163 LeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGlySerThr 182
Db 426 CTCCTCCACGCTGTGTACATGCTGGCAGCAGCTGCTCATTTCCGGCTGGGGCAGCAGC 485
OY 183 SerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIleLeu 202
Db 486 TCCAGCCCCCGATTACGCTCTGCTACACCTTGCGATGGCCACATCATCATATTAG 545
OY 203 HisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCysAlaSer 222
Db 546 CACCAAGAAAGTGTGAAAGCGCTACCCGGCAGACATCAGACACATGCTGTGCGCAGC 605
OY 223 ValGlnLysGlyLysAspSerSerGlnLysAspSerGlyLysProLeuValCysAsn 242
Db 606 GTGAGAGAAAGGGGCAAGGACTCCTGCCAGGGTACTCCGGGGCCCTCTGTGTGTAAC 665
OY 243 GlnSerLeuGlnGlyIleLeuSerTyrGlyAspProCysAlaIleThrArgLysPro 262
Db 666 CAGCTCTTCAAGGCATTAATCTCTGGGGCCAGCATCCGTTGGCATCACCCGAAAGCTT 725
OY 263 GlyValLysThrLysValCysLysTyrValAspTyrIleGlnLysThrMetLysAsn 282
Db 726 GGTTCTACAGAAAGTCTGCAATATGTGACTGATCCAGAGACGATGAACAACAT 785

RESULT 7
US-09-386-642-10
; Sequence 10, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Ol, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1052
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo saplen serine protease catalytic domain
US-09-386-642-10

Alignment Scores:
Pred. No.: 2,666-114 Length: 1052
Score: 1227.00 Matches: 231
Percent Similarity: 87.59% Conservative: 9
Best Local Similarity: 84.31% Mismatches: 12
Query Match: 80.56% Indels: 22
DB: 4 Gaps: 3
```

```
US-09-856-320a-2 (1-282) x US-09-386-642-10 (1-1052)
OY 31 GlnAlaMetArgIleLeuGlnLeuIleLeu-----LeuAlaLeuAlaThrGlyLeu 47
Db 34 CAGAAATCCCGCTCTCTCTGTGTGGTGGTCAATCTACTTGTGTGCCAGGGTGTG 93
OY 48 ValGly----- 49
Db 94 GTCTCCGACTCAAGAGCAGACGACGCTGACAGCGCGCCGCTTGTGCCCCCTTTGAT 153
OY 50 GlyIuThrArgIleIleLysGlyPheGlyCys---LysProHisSerGlnProTyrGln 68
Db 154 GATGATGCAAGATCTGTGGGGCTTACACAGCTGTGAAAGACATCCACGCTCCAGCGGAG 213
OY 69 AlaAlaLeuPheGlnLysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyr 88
Db 214 GCAGCCCTGTTCGAAAGACGCGGCTACTCTGTGGGGGAGCGTCAATGCCCCCAGATGG 273
OY 89 LeuLeuThrAlaAlaHisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsn 108
Db 274 CTCCTGACAGCAGCCCACTGCTCAAGCCCGCTACATAGTTCACTGCGGAGCAGACAC 333
OY 109 LeuGlnLysGlnLysGlyCysGlnLysThrArgThrAlaThrGlySerPheProHisPro 128
Db 334 CTCACAGAGGAGGAGGGCTGTGACAGACCGGACAGCAGCTGAGTCTCCCAACCC 393
OY 129 GlyPheAsnAsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMet 148
Db 394 GGCTTCAACACACAGCTCCCAACAAAGACACGCAATGACATCATGCTGTGAAAGATG 453
OY 149 AlaSerProValSerIleThrTyrAlaValArgProLeuThrLeuSerSerArgCysVal 168
Db 454 GCATGCGCAGCTCCATCATCACTGGCGCTGTGGAGACCCCTCACCCCTCTCCAGCGTGTTC 513
OY 169 ThrAlaGlyThrSerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArg 188
Db 514 ACTCTGGCAGCAGCTGCTCTATTTCGGCGGGGACAGCTCAGGCCACGCTCAAGTACGC 573
OY 189 LeuProHisThrLeuArgCysAlaAsnIleThrIleLeuGlnLysGlnLys 208
Db 574 CTGCTCAGACACTTGCAGATGGCCCAACATCCATCATTTGAGCAGCAAGATGTGAGAAC 633
OY 209 AlaTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnLysGlyLys 228
Db 634 GCTTACCCCGGCAACATCAGACACCATGTTGTGTGCGACGTCAGAGAGGGGGCAG 693
OY 229 AspSerSerGlnGlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyLe 248
Db 694 GACTCTGCGCAGGGTGACTCCGGGGCCCTCTGTGTATACAGTCTCTTCAAGGCATT 753
OY 249 IleSerTyrGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysVal 268
Db 754 ATCTCTCGGGGGCCAGGATCCGTGTGCATATCCCGAAAGCCTGTGTCTACAGAAAGTC 813
OY 269 CysLysTyrValAspTyrIleGlnLysThrMetLysAsn 282
Db 814 TGCAAATATGTGAGCTGGATCCAGAGACGATGAAGAACAAT 855

RESULT 8
US-09-280-116-3
; Sequence 3, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 618
```



```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-3
```

## Alignment Scores:

Pred. No.:	2,16e-83	Length:	618
Score:	916.50	Matches:	184
Percent Similarity:	90.78%	Conservative:	3
Best Local Similarity:	89.32%	Mismatches:	4
Query Match:	60.18%	Indels:	16
DB:	4	Gaps:	2

US-09-856-320a-2 (1-282) x US-09-280-116-3 (1-618)

```

QY ArgLeuLeuCySGlYAlaThrLeuIleAlaPro-ArgTrpLeuLeuThrAlaAlaIscy 95
   |||||
DB  CGGCTACTGTGTGGGCGAC---TCATGCCCTCAATGCTCTTGCACAGCAGCCACTG 58
   |||||
QY  sLeuIysProArgTrpIleValHisLeuGlnHisAsnLeuGlnLysGlnIscy 115
   |||||
DB  CCTCAAGCCCCGCTACATGATTCACCTGGGGCAGCAACCTCCAGAAAGAGAGGCGCTG 118
   |||||
QY  115 sGlnIleThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuP 135
   |||||
DB  119 TGGCAGACCCCGGACGCCACCTAGTCCTCCCGCCCGGCTCAACAGCCCTCC 178
   |||||
QY  135 oAnIysAspHisArgAsnAspIleMetLeuValIysMetAlaSerProVal-SerIle 155
   |||||
DB  179 CACCAAGACCCCGCAATGACATCATGCTGGGAAGATGGCATCCCGACTGCTCATCA 238
   |||||
QY  155 hTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysAl 175
   |||||
DB  239 CCGGGCTGTGGCACCCTCACCCTCTCATGCTGTGTCACTGCTGGCAGCCAGCTGCC 298
   |||||
QY  175 eutIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeuArgC 195
   |||||
DB  299 TCATTTCCGGCTGGGCGACAGCTCCAGCCCGCATTTAGCCCTGCACACCTTGCGAT 358
   |||||
QY  195 ysaAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaIleProGlyAsnIle 215
   |||||
DB  359 GCGCCAAATCACCACATTCATGAGCAGACAGAGTGTAGAAAGCGCTACCCCGGCAATCA 418
   |||||
QY  215 hAspThrIleValCysAlaSerValGlnGlnIleGlyLysAspSerCysGlnGlyAspS 235
   |||||
DB  419 CAGACACCATGTGTGTGCCAGCGTGAAGGAAGGGGCAAGGACTCTGCCAA----- 471
   |||||
QY  235 eGlyLeuProLeuValCysAsnGlnSerLeuGlnGlnIleIleSerTrp-GlyGlnAsp 254
   |||||
DB  472 -----GCTCTCTTC-AAAGGCATTATCTCTGGGGCCAGAC 507
   |||||
QY  255 -ProCysAlaIleThrArgLysProGlyValIleThrIleValCysLysThrValAspTr 274
   |||||
DB  508 TCGGTGTGGATCACCAGAAAGCGTGTGTCTACAGAAAGTGTGCAATATGTGACATG 567
   |||||
QY  274 pIleGlnIle 277
   |||||
DB  568 GATCCAGAA 577

RESULT 9
US-09-280-116-136
; Sequence 16, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
```

```

; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-136
```

## Alignment Scores:

Pred. No.:	1,06e-65	Length:	472
Score:	739.00	Matches:	138
Percent Similarity:	99.28%	Conservative:	0
Best Local Similarity:	99.28%	Mismatches:	1
Query Match:	48.32%	Indels:	0
DB:	4	Gaps:	0

US-09-856-320a-2 (1-282) x US-09-280-116-136 (1-472)

```

QY  3 ArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAlaIscy 22
   |||||
DB  56 AGATTGAGGTGGTGGGAGCTGGAAGTCATCGGCGAGAGGCTTCACAGCAGCCAGAA 115
   |||||
QY  23 ProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeuAla 42
   |||||
DB  116 CCGGGGCCCCCTCTCCCTCCCGCCAGCCATGAGATTCTGCAGTTATCTCTGCTGCT 175
   |||||
QY  43 LeuAlaThrGlyLeuValGlyGlyIleThrArgIleIleLysGlyPheGlnCysLysPro 62
   |||||
DB  176 CTGGCAACAGGCTGTAGAGGAGAGACAGCATCATCAAGGGGTTGAGTGCAGAGCCT 235
   |||||
QY  63 HisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuGlyAlaThr 82
   |||||
DB  236 CACTCCAGCCCTGGGAGGAGCCCTGTTCGAAAGACCGGCTACTGTGTGGGCGAGG 295
   |||||
QY  83 LeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrpIleVal 102
   |||||
DB  296 CTCATGCCGCCGAGATGGTCTCTGACAGACGCCACTGCTCAAGCCCGGCTACATAGT 355
   |||||
QY  103 HisLeuGlyGlnHisAsnLeuGlnLysGlnIleGlyGlnIleThrArgThrAlaThr 122
   |||||
DB  356 CACCTGGGCGAGACCAACTCCAGAAAGAGAGGCTGTGAGCAGACCGGAGCCAGCT 415
   |||||
QY  123 GlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArgAsn 141
   |||||
DB  416 GAGTCTTCCCTCCACCCCGGCTTCACACAGCTTCCCAACAAAGCACCGCAAT 472
   |||||
```

## RESULT 10

```

US-09-070-526-1
; Sequence 1, Application US/09070526
; Patent No. 6100059
; GENERAL INFORMATION:
```

```

; APPLICANT: SOOTHAN, CHRISTOPHER
; APPLICANT: CLINKENBEARD, HELEN
; APPLICANT: BURGESS, NICOLA
; TITLE OF INVENTION: No. 6100059el Compounds
; NUMBER OF SEQUENCES: 4
```

## CORRESPONDENCE ADDRESS:

```

ADDRESSER: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
```

## COMPUTER READABLE FORM:

```

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
```

## SOFTWARE: FastSeq for Windows Version 2.0

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,526
FILING DATE: 30-APR-1998
CLASSIFICATION:
```

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9711952.3
```

FILING DATE: 9-JUN-1997  
APPLICATION NUMBER: EP 97309646.4  
FILING DATE: 1-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: PRESTIA, PAUL F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GH-30353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 944 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-070-526-1

Alignment Scores:  
Pred. No.: 2.57e-60 Length: 944  
Score: 690.00 Matches: 129  
Percent Similarity: 64.81% Conservative: 46  
Best Local Similarity: 47.78% Mismatches: 82  
Query Match: 45.31% Indels: 14  
DB: 3 Gaps: 4

US-09-856-320A-2 (1-282) x US-09-070-526-1 (1-944)

OY 10 TTPlySerSerGlyArgGlyLeuThrAlaAlaLysGluProGlyAlaArgSerPro 29  
DB 91 TGAAGACCTCA-----CCATG-GGACGCCCGGCGACT 122  
OY 30 LeuGlnAlaMetArgIleLeuGlnLeuLeuLeu-----AlaLeuAlaThrGlyLeu 47  
DB 123 CGTGGCCCAAGAGCGTGAATCTCTCTCTGGGGGAGCGCTGGCGACACTCC 182  
OY 48 ValGlyGlyLeuThrArgIleIleLysGlyPheGlyCysLysProHisSerGlnProTrp 67  
DB 183 AGGCGACAGAGAGAGAGAGTGGTGGGGGTCATGATGCCAACCCCATTCGACACCTGG 242  
OY 68 GlnAlaAlaLeuPheGlyLysThrArgLeuLeuGlyGlyAlaThrLeuAlaProArg 87  
DB 243 CAGCGCGCTGTGTCCAGGGCGACCAATCTGTGGCGGTCTCTGTGAGTGGCAAC 302  
OY 88 TTPLeuThrAlaAlaHisCysLeuLysProArgTyrIleValHisLysGlyGlnHis 107  
DB 303 TGGGTCTTACAGCTGCCCTGTAAACCCGAAATACACAGTACCGCTGGAGACAC 362  
OY 108 AsnLeuGlnLysGluGlyLysGlyGluGlnThrArgThrAlaThrGlnSerPheProHis 127  
DB 363 AGCTTACAGATTAAGATGAGCCAGACCAAGAAATACCTGTGTTGATCCATCCACAC 422  
OY 128 ProGlyPheAsnAsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLys 147  
DB 423 CCGGTATACACACAC-----GATGTGAGAGCACCAACCATGTGATGCTTCTCA 479  
OY 148 MetAlaSerProValSerIleThrThrAlaValArgProLeuThrLysSerArgCys 167  
DB 480 CTGGGTACCAAGGATCTCTGGGGTCCAAAGTGAAAGCCCATCAGCTGGGCGATCATTGC 539  
OY 168 ValThrAlaGlyThrSerCysLeuIleSerGlyTyrPylSerThrSerProGlnLeu 187  
DB 540 ACCAGCGCTGGCGAGAGTGCACCGTCTCAGCGCTGGGGGACGTGCACAGCCCGAGAG 599  
OY 188 ArgLeuProHisThrLeuArgCysAlaAsnIleThrIleGluHisGlnLysCysGlu 207  
DB 600 AATTTCCTGACATCTCACTGTGAGAGTAAATCTTCCCGAAGAAAGTGTGAG 659  
OY 208 AsnAlaTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlyGly 227  
DB 660 GATGCTTACCGGGGCGAGATCACAGATGGCATGTGTGTGAGGCGACGCAAGAGGGGCT 719

OY 228 LysAspSerCysGlnGlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGly 247  
DB 720 --GACACGTGCCAGGGGATTCGAGAGCCCGGTGTGATGTGACATCCAGGCG 776  
OY 248 IleIleSerTyrGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLys 267  
DB 777 ATCACATCCGTGGGGCTGAGACCCCTGTGGAGAGTCCGACAAACCTGGCGCTATACCAAC 836  
OY 268 ValCysLysTyrValAspThrIleGlnGlu 277  
DB 837 ATGTCCGCTACTGAGCTGATCAAGAG 866

RESULT 11  
US-09-008-271A-19  
Sequence 19, Application US/09008271A  
Patent No. 6203979  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
Hillman, Jennifer L.  
Yue, Henry  
Guegler, Karl J.  
Corley, Neil C.  
Tang, Tom Y.  
Shah, Purvi  
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/008,271A  
FILING DATE: 16-Jan-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mohan-Peterson, Sheila  
REGISTRATION NUMBER: 41,201  
REFERENCE/DOCKET NUMBER: PF-0458 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 994 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: COLANOT27  
CLONE: 1798496  
SEQUENCE DESCRIPTION: SEQ ID NO: 19 :  
US-09-008-271A-19  
Alignment Scores:  
Pred. No.: 1.77e-59 Length: 994  
Score: 682.00 Matches: 128  
Percent Similarity: 64.44% Conservative: 46  
Best Local Similarity: 47.41% Mismatches: 83  
Query Match: 44.78% Indels: 14  
DB: 3 Gaps: 4  
US-09-856-320A-2 (1-282) x US-09-008-271A-19 (1-994)



RESULT 13  
 US-09-996-243-308  
 ; Sequence 308, Application US/09996243  
 ; Patent No. 6478825  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Bolstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gottfries, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kijavlin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2730P1C13  
 ; CURRENT APPLICATION NUMBER: US/09/996,243  
 ; CURRENT FILING DATE: 2001-11-14  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/065186  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/065311  
 ; PRIOR FILING DATE: 1997-11-13  
 ; PRIOR APPLICATION NUMBER: 60/066770  
 ; PRIOR FILING DATE: 1997-11-24  
 ; PRIOR APPLICATION NUMBER: 60/075945  
 ; PRIOR FILING DATE: 1998-02-25  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/083322  
 ; PRIOR FILING DATE: 1998-04-28  
 ; PRIOR APPLICATION NUMBER: 60/084600  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/087106  
 ; PRIOR FILING DATE: 1998-05-28  
 ; PRIOR APPLICATION NUMBER: 60/087607  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/087609  
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 ; PRIOR APPLICATION NUMBER: 60/087759  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/087827  
 ; PRIOR FILING DATE: 1998-06-03  
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 ; PRIOR FILING DATE: 1998-06-04  
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 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088028  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088029  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088030

;; PRIOR FILING DATE: 1998-06-04  
 ;; PRIOR APPLICATION NUMBER: 60/088033  
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 ;; PRIOR APPLICATION NUMBER: 60/088167  
 ;; PRIOR FILING DATE: 1998-06-05  
 ;; PRIOR APPLICATION NUMBER: 60/088202  
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 ;; PRIOR APPLICATION NUMBER: 60/088212  
 ;; PRIOR FILING DATE: 1998-06-05  
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 ;; PRIOR FILING DATE: 1998-06-22  
 ;; PRIOR APPLICATION NUMBER: 60/090252  
 ;; PRIOR FILING DATE: 1998-06-22  
 ;; PRIOR APPLICATION NUMBER: 60/090254  
 ;; PRIOR FILING DATE: 1998-06-22  
 ;; PRIOR APPLICATION NUMBER: 60/090349  
 ;; PRIOR FILING DATE: 1998-06-23



REFERENCE/DOCKET NUMBER: PF-0252 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1476 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: KERANOT02  
 CLONE: 820694  
 US-08-824-874-2

Alignment Scores:  
 Pred. No.: 9.65e-55 Length: 1476  
 Score: 637.50 Matches: 118  
 Percent Similarity: 67.95% Conservative: 41  
 Best Local Similarity: 50.43% Mismatches: 67  
 Query Match: 41.86% Indels: 8  
 DB: 2 Gaps: 4

US-09-856-320A-2 (1-282) x US-08-824-874-2 (1-1476)

OY 52 ThrAgtlletlelysglypHeGlucylsProhlsSerGlnProTrp-GlnAlaAla-- 70  
 Db 469 AGCGGCATCATCATGATCGACTGCGATGATGCACACCGCGTGGGAGCGCGCT 528  
 OY 71 -LeupheglulysThrArgleuLeuCyglAlaThrleuLeuAlaProAgtTPrleu 90  
 Db 529 GTTGCTAAGGCCCAACAGCTCTACTGCGGGCGGTGTGGTGCATCCAGTGGCTCT 588  
 OY 90 uThrAlaAlaHiscysleuysProAgtTylleValHlsleuglyGlnHlsasnleugl 110  
 Db 589 CACGCGCCCGCCACGAGAGAAAGTTTCAGAGTCGCTCCGCCACTCTCCCTGTC 648  
 OY 110 nlys---GluglucylsGlnGlnThrArgThrAlaThrGlsuSerPheProHlsProgl 129  
 Db 649 ACCAGTTTATGAACTGGGCGAGAGTGTCCAGGGGGTCAAAATCCATCCCGCCCTGG 708  
 OY 129 yPheasnAsnSerleuProAsnLysAspHlsArgAsnAspIleMetleuValLysMetAl 149  
 Db 709 CTACTCC-----CACCGTGGCCACTTACGACCTCACTCACTCACTCACTCACT 756  
 OY 149 aSerProValSerIleThrTrpAlaValArgProleuThrleuSerSerArgCysValTh 169  
 Db 757 CAGAGAAATTCGTCCCACTAAAGATGTCAGACCATCACTCTCTCTCTCTCTCTCT 816  
 OY 169 rAlaGlyThrSerCysleuIleSerGlyTTPGlySerThrSerSerProGlnLeuArgle 189  
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 OY 189 uProHlsThrleuArgCysAlaAsnIleThrIleleuGlnHlsleuGlnLysCysGluAsnAl 209  
 Db 877 CCTCAAGGCTCTCAAGCTTGAATATCAGGCTCTAAGTCAAGAAAGTCCGAGGAGTCC 936  
 OY 209 aTyProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAs 229  
 Db 937 TTACCCGAGACATAGTACACCATTTCTGGCCCGT---GACAAAGCAGGTAGAGA 993  
 OY 229 pSerCysGlnLysAspSerGlyGlyProleuValCysAsnGlnSerleuGlnGlyIleAl 249  
 Db 994 CTCTGCGACAGGATCTCTGGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1053  
 OY 249 eSerTrpGlyLysProCysAlaIleThrArgLysProGlyValYThrLysValCy 269  
 Db 1054 GTCTGGGAGATTAACCTTGTCCCGCGCCCAACAGCCGGGTCTACACGAACCTCTG 1113  
 OY 269 slsYtyrValAspTrpIleGlnGlnThrMetLysAsnAsn 282  
 Db 1114 CAAGTTTCAAGTGTGATCCAGAAACCATCCAGGCCAAC 1153

RESULT 15  
 US-09-210-084-2  
 ; Sequence 2, Application US/09210084  
 ; Patent No. 6197511  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Lal, Preeti  
 ; TITLE OF INVENTION: NOVEL KALLIKREIN  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/210,084  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/824,874  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0252 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-845-4166  
 ; TELEFAX: 415-855-0555  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1476 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: KERANOT02  
 ; CLONE: 820694  
 ; US-09-210-084-2

Alignment Scores:  
 Pred. No.: 9.65e-55 Length: 1476  
 Score: 637.50 Matches: 118  
 Percent Similarity: 67.95% Conservative: 41  
 Best Local Similarity: 50.43% Mismatches: 67  
 Query Match: 41.86% Indels: 8  
 DB: 3 Gaps: 4

US-09-856-320A-2 (1-282) x US-09-210-084-2 (1-1476)

OY 52 ThrAgtlletlelysglypHeGlucylsProhlsSerGlnProTrp-GlnAlaAla-- 70  
 Db 469 AGCGGCATCATCATGATCGACTGCGATGATGCACACCGCGTGGGAGCGCGCT 528  
 OY 71 -LeupheglulysThrArgleuLeuCyglAlaThrleuLeuAlaProAgtTPrleu 90  
 Db 529 GTTGCTAAGGCCCAACAGCTCTACTGCGGGCGGTGTGGTGCATCCAGTGGCTCT 588  
 OY 90 uThrAlaAlaHiscysleuysProAgtTylleValHlsleuglyGlnHlsasnleugl 110  
 Db 589 CACGCGCCCGCCACGAGAGAAAGTTTCAGAGTCGCTCCGCCACTCTCCCTGTC 648  
 OY 110 nlys---GluglucylsGlnGlnThrArgThrAlaThrGlsuSerPheProHlsProgl 129  
 Db 649 ACCAGTTTATGAACTGGGCGAGAGTGTCCAGGGGGTCAAAATCCATCCCGCCCTGG 708  
 OY 129 yPheasnAsnSerleuProAsnLysAspHlsArgAsnAspIleMetleuValLysMetAl 149

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QY      149 aSerProValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValTh 169
Db      757 CAGAGAAATTCGTCACCTTAAGATGTACAGACCATCAACGTCTCCCTCATGTGTCCCTC 816
QY      169 rAlaGlyThrSerCysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLe 189
Db      817 TGCTGGGACAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 876
QY      189 uProH1sthrLeuArgCysAlaAsnIleThrIleIleGlnH1sGlnLysCysGlnAsnAl 209
Db      877 CCCTAAGGTCCTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 936
QY      209 aTyrProGlyAsnIleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAs 229
Db      937 TTACCCGAGACAGATAGATGACACACATGTCTGTGCGCGGT---GACAAAGCAGGTAGAGA 993
QY      229 pSerCysGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleI 249
Db      994 CTCCTGCCAGGCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1053
QY      249 eSerTrpGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCy 269
Db      1054 GTCTGGGGAGATTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1113
QY      269 sLysTyrValAspTrpIleGlnGlnLysThrMetLysAsnAsn 282
Db      1114 CAAGTTCACCAAGTGGATCCAGAAACCATCCAGGCCAAC 1153
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Search completed: October 15, 2003, 21:09:00  
Job time : 84.364 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 15, 2003, 20:58:02 ; Search time 25.3855 Seconds

(without alignments)  
1789.927 Million cell updates/sec

Title: US-09-856-320A-2

Perfect score: 1523

Sequence: 1 MQRRLRMKSGSGRLTAA.....GVYTKCKYVDIQTAKNN 282

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*

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2: /cgn2\_6/ptodata/1/pubppa/PC1\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubppa/PC1US\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep:\*

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11: /cgn2\_6/ptodata/1/pubppa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubppa/US09C\_PUBCOMB.pep:\*

13: /cgn2\_6/ptodata/1/pubppa/US10C\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubppa/US10C\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/1/pubppa/US10C\_PUBCOMB.pep:\*

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17: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1355	89.0	250	12	US-10-137-870-506
4	1355	89.0	250	12	US-10-140-018-506
5	1355	89.0	250	12	US-10-140-021-506
6	1355	89.0	250	12	US-10-140-274-506
7	1355	89.0	250	12	US-10-140-471-506
8	1355	89.0	250	12	US-10-140-807-506
9	1355	89.0	250	12	US-10-140-822-506
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12	1355	89.0	250	12	US-10-141-698-506
13	1355	89.0	250	12	US-10-141-702-506
14	1355	89.0	250	12	US-10-141-704-506
15	1355	89.0	250	12	US-10-142-421-506

16	1355	89.0	250	12	US-10-142-432-506	Sequence 506, App
17	1355	89.0	250	12	US-10-142-767-506	Sequence 506, App
18	1355	89.0	250	12	US-10-143-033-506	Sequence 506, App
19	1355	89.0	250	12	US-10-144-994-506	Sequence 506, App
20	1355	89.0	250	12	US-10-145-628-506	Sequence 506, App
21	1355	89.0	250	12	US-10-145-631-506	Sequence 506, App
22	1355	89.0	250	12	US-10-145-633-506	Sequence 506, App
23	1355	89.0	250	12	US-10-145-746-506	Sequence 506, App
24	1355	89.0	250	12	US-10-145-823-506	Sequence 506, App
25	1355	89.0	250	12	US-10-145-828-506	Sequence 506, App
26	1355	89.0	250	12	US-10-145-826-506	Sequence 506, App
27	1355	89.0	250	12	US-10-145-870-506	Sequence 506, App
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32	1355	89.0	250	12	US-10-146-795-506	Sequence 506, App
33	1355	89.0	250	12	US-10-147-495-506	Sequence 506, App
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36	1355	89.0	250	12	US-10-147-509-506	Sequence 506, App
37	1355	89.0	250	12	US-10-147-509-506	Sequence 506, App
38	1355	89.0	250	12	US-10-147-510-506	Sequence 506, App
39	1355	89.0	250	12	US-10-147-511-506	Sequence 506, App
40	1355	89.0	250	12	US-10-147-529-506	Sequence 506, App
41	1355	89.0	250	12	US-10-152-397-506	Sequence 506, App
42	1355	89.0	250	12	US-10-153-586-506	Sequence 506, App
43	1355	89.0	250	12	US-10-158-783-506	Sequence 506, App
44	1355	89.0	250	12	US-10-158-786-506	Sequence 506, App
45	1355	89.0	250	12	US-10-006-130A-170	Sequence 170, App

#### ALIGNMENTS

RESULT 1

US-09-946-374-170

Sequence 170, Application US/09946374

Publication No. US20030073129A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2830P1C1

CURRENT APPLICATION NUMBER: US/09/946,374

CURRENT FILING DATE: 2001-09-04

PRIOR APPLICATION NUMBER: 60/098716

PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: 60/098723

PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: 60/098749

PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: 60/098750

1	PRIOR FILING DATE: 1998-09-01
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3	PRIOR FILING DATE: 1998-09-02
4	PRIOR APPLICATION NUMBER: 60/098821
5	PRIOR FILING DATE: 1998-09-02
6	PRIOR APPLICATION NUMBER: 60/098833
7	PRIOR FILING DATE: 1998-09-02
8	PRIOR APPLICATION NUMBER: 60/099536
9	PRIOR FILING DATE: 1998-09-09
10	PRIOR APPLICATION NUMBER: 60/099596
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12	PRIOR APPLICATION NUMBER: 60/099598
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14	PRIOR APPLICATION NUMBER: 60/099620
15	PRIOR FILING DATE: 1998-09-09
16	PRIOR APPLICATION NUMBER: 60/099642
17	PRIOR FILING DATE: 1998-09-09
18	PRIOR APPLICATION NUMBER: 60/099711
19	PRIOR FILING DATE: 1998-09-10
20	PRIOR APPLICATION NUMBER: 60/099722
21	PRIOR FILING DATE: 1998-09-10
22	PRIOR APPLICATION NUMBER: 60/099808
23	PRIOR FILING DATE: 1998-09-10
24	PRIOR APPLICATION NUMBER: 60/099812
25	PRIOR FILING DATE: 1998-09-10
26	PRIOR APPLICATION NUMBER: 60/099815
27	PRIOR FILING DATE: 1998-09-10
28	PRIOR APPLICATION NUMBER: 60/099816
29	PRIOR FILING DATE: 1998-09-10
30	PRIOR APPLICATION NUMBER: 60/100385
31	PRIOR FILING DATE: 1998-09-15
32	PRIOR APPLICATION NUMBER: 60/100388
33	PRIOR FILING DATE: 1998-09-15
34	PRIOR APPLICATION NUMBER: 60/100390
35	PRIOR FILING DATE: 1998-09-15
36	PRIOR APPLICATION NUMBER: 60/100584
37	PRIOR FILING DATE: 1998-09-16
38	PRIOR APPLICATION NUMBER: 60/100627
39	PRIOR FILING DATE: 1998-09-16
40	PRIOR APPLICATION NUMBER: 60/100651
41	PRIOR FILING DATE: 1998-09-16
42	PRIOR APPLICATION NUMBER: 60/100662
43	PRIOR FILING DATE: 1998-09-16
44	PRIOR APPLICATION NUMBER: 60/100664
45	PRIOR FILING DATE: 1998-09-16
46	PRIOR APPLICATION NUMBER: 60/100683
47	PRIOR FILING DATE: 1998-09-17
48	PRIOR APPLICATION NUMBER: 60/100684
49	PRIOR FILING DATE: 1998-09-18
50	PRIOR APPLICATION NUMBER: 60/100849
51	PRIOR FILING DATE: 1998-09-18
52	PRIOR APPLICATION NUMBER: 60/100919
53	PRIOR FILING DATE: 1998-09-17
54	PRIOR APPLICATION NUMBER: 60/100930
55	PRIOR FILING DATE: 1998-09-17
56	PRIOR APPLICATION NUMBER: 60/101014
57	PRIOR FILING DATE: 1998-09-18
58	PRIOR APPLICATION NUMBER: 60/101068
59	PRIOR FILING DATE: 1998-09-18
60	PRIOR APPLICATION NUMBER: 60/101071
61	PRIOR FILING DATE: 1998-09-18
62	PRIOR APPLICATION NUMBER: 60/101279
63	PRIOR FILING DATE: 1998-09-22

1	PRIOR APPLICATION NUMBER: 60/1014171
2	PRIOR FILING DATE: 1998-09-23
3	PRIOR APPLICATION NUMBER: 60/1014727
4	PRIOR FILING DATE: 1998-09-23
5	PRIOR APPLICATION NUMBER: 60/1014747
6	PRIOR FILING DATE: 1998-09-23
7	PRIOR APPLICATION NUMBER: 60/1014767
8	PRIOR FILING DATE: 1998-09-23
9	PRIOR APPLICATION NUMBER: 60/1014777
10	PRIOR FILING DATE: 1998-09-23
11	PRIOR APPLICATION NUMBER: 60/1014797
12	PRIOR FILING DATE: 1998-09-23
13	PRIOR APPLICATION NUMBER: 60/1017388
14	PRIOR FILING DATE: 1998-09-24
15	PRIOR APPLICATION NUMBER: 60/1017411
16	PRIOR FILING DATE: 1998-09-24
17	PRIOR APPLICATION NUMBER: 60/1017433
18	PRIOR FILING DATE: 1998-09-24
19	PRIOR APPLICATION NUMBER: 60/1019151
20	PRIOR FILING DATE: 1998-09-24
21	PRIOR APPLICATION NUMBER: 60/1019166
22	PRIOR FILING DATE: 1998-09-24
23	PRIOR APPLICATION NUMBER: 60/1020207
24	PRIOR FILING DATE: 1998-09-25
25	PRIOR APPLICATION NUMBER: 60/1020240
26	PRIOR FILING DATE: 1998-09-25
27	PRIOR APPLICATION NUMBER: 60/1023037
28	PRIOR FILING DATE: 1998-09-25
29	PRIOR APPLICATION NUMBER: 60/1023303
30	PRIOR FILING DATE: 1998-09-25
31	PRIOR APPLICATION NUMBER: 60/1023311
32	PRIOR FILING DATE: 1998-09-25
33	PRIOR APPLICATION NUMBER: 60/1024484
34	PRIOR FILING DATE: 1998-09-30
35	PRIOR APPLICATION NUMBER: 60/1024877
36	PRIOR FILING DATE: 1998-09-30
37	PRIOR APPLICATION NUMBER: 60/1025707
38	PRIOR FILING DATE: 1998-09-30
39	PRIOR APPLICATION NUMBER: 60/1025711
40	PRIOR FILING DATE: 1998-09-30
41	PRIOR APPLICATION NUMBER: 60/1026884
42	PRIOR FILING DATE: 1998-10-01
43	PRIOR APPLICATION NUMBER: 60/1026877
44	PRIOR FILING DATE: 1998-10-01
45	PRIOR APPLICATION NUMBER: 60/1029655
46	PRIOR FILING DATE: 1998-10-02
47	PRIOR APPLICATION NUMBER: 60/1032587
48	PRIOR FILING DATE: 1998-10-06
49	PRIOR APPLICATION NUMBER: 60/1033134
50	PRIOR FILING DATE: 1998-10-07
51	PRIOR APPLICATION NUMBER: 60/1033155
52	PRIOR FILING DATE: 1998-10-07
53	PRIOR APPLICATION NUMBER: 60/1033287
54	PRIOR FILING DATE: 1998-10-07
55	PRIOR APPLICATION NUMBER: 60/1033955
56	PRIOR FILING DATE: 1998-10-07
57	PRIOR APPLICATION NUMBER: 60/1033966
58	PRIOR FILING DATE: 1998-10-07
59	PRIOR APPLICATION NUMBER: 60/1034011
60	PRIOR FILING DATE: 1998-10-07
61	PRIOR APPLICATION NUMBER: 60/1034499
62	PRIOR FILING DATE: 1998-10-06
63	PRIOR APPLICATION NUMBER: 60/1036333
64	PRIOR FILING DATE: 1998-10-08
65	PRIOR APPLICATION NUMBER: 60/1036788
66	PRIOR FILING DATE: 1998-10-08
67	PRIOR APPLICATION NUMBER: 60/1036799
68	PRIOR FILING DATE: 1998-10-08
69	PRIOR APPLICATION NUMBER: 60/1037111
70	PRIOR FILING DATE: 1998-10-08
71	PRIOR APPLICATION NUMBER: 60/1042527

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; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
```

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Query Match      89.0%; Score 1355; DB 11; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 33 MRLIQLILALATGIVGETRIIKGFECCKPHSOPMOALFEKTRILCGATLIAPRWLTLTA 92
DB 1 MRLIQLILALATGIVGETRIIKGFECCKPHSOPMOALFEKTRILCGATLIAPRWLTLTA 60
OY 93 AHCLKPRIVHLGQHNLOKEBCEQOTRATESFPHPGFNNSLPNKDHRNDIMLYMASPV 152
DB 61 AHCLKPRIVHLGQHNLOKEBCEQOTRATESFPHPGFNNSLPNKDHRNDIMLYMASPV 120
OY 153 SITMAVRPLTSSRCVTAAGTSCILISGWSSTSPQLRLPHTRLCANITIIIEHOKCENAYPG 212
DB 121 SITMAVRPLTSSRCVTAAGTSCILISGWSSTSPQLRLPHTRLCANITIIIEHOKCENAYPG 180
OY 213 NITDTMVCASVOEGKDCSCQDSSGPLYCNSLOGIISMGODPCAITRRPGVYTRVCXYV 272
DB 181 NITDTMVCASVOEGKDCSCQDSSGPLYCNSLOGIISMGODPCAITRRPGVYTRVCXYV 240
OY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250
```

## RESULT 2

```
US-10-015-387A-170
; Sequence 170, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015.387A
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 170
; LENGTH: 250
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-015-387A-170
```

```
Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 33 MRLIQLILALATGIVGETRIIKGFECCKPHSOPMOALFEKTRILCGATLIAPRWLTLTA 92
DB 1 MRLIQLILALATGIVGETRIIKGFECCKPHSOPMOALFEKTRILCGATLIAPRWLTLTA 60
OY 93 AHCLKPRIVHLGQHNLOKEBCEQOTRATESFPHPGFNNSLPNKDHRNDIMLYMASPV 152
DB 61 AHCLKPRIVHLGQHNLOKEBCEQOTRATESFPHPGFNNSLPNKDHRNDIMLYMASPV 120
OY 153 SITMAVRPLTSSRCVTAAGTSCILISGWSSTSPQLRLPHTRLCANITIIIEHOKCENAYPG 212
DB 121 SITMAVRPLTSSRCVTAAGTSCILISGWSSTSPQLRLPHTRLCANITIIIEHOKCENAYPG 180
OY 213 NITDTMVCASVOEGKDCSCQDSSGPLYCNSLOGIISMGODPCAITRRPGVYTRVCXYV 272
DB 181 NITDTMVCASVOEGKDCSCQDSSGPLYCNSLOGIISMGODPCAITRRPGVYTRVCXYV 240
OY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250
```

## RESULT 3

```
US-10-137-870-506
; Sequence 506, Application US/10137870
; Publication No. US20030138883A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C155
; CURRENT APPLICATION NUMBER: US/10/137.870
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-870-506
```

```
Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 33 MRLIQLILALATGIVGETRIIKGFECCKPHSOPMOALFEKTRILCGATLIAPRWLTLTA 92
DB 1 MRLIQLILALATGIVGETRIIKGFECCKPHSOPMOALFEKTRILCGATLIAPRWLTLTA 60
OY 93 AHCLKPRIVHLGQHNLOKEBCEQOTRATESFPHPGFNNSLPNKDHRNDIMLYMASPV 152
```

```
Db      61  AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESPPHGFNNSLPNKDHNDIMLVKASPV 120
QY      153  SITWAVRPLTSSRCVYTAGTSCILISGWSSTSPOLRPHTLRCANITIIIEHOKCENAYPG 212
        |||||||
Db      121  SITWAVRPLTSSRCVYTAGTSCILISGWSSTSPOLRPHTLRCANITIIIEHOKCENAYPG 180
QY      213  NITDPMWCAVSGGKDCGSGGSPLYCNOSLQGIISWGODPCATIRKPGVYTKVKCY 272
        |||||||
Db      181  NITDPMWCAVSGGKDCGSGGSPLYCNOSLQGIISWGODPCATIRKPGVYTKVKCY 240
QY      273  DWIOETMKNN 282
        |||||||
Db      241  DWIOETMKNN 250

RESULT 4
US-10-140-018-506
; Sequence 506, Application US/10140018
; Publication No. US20030138865A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Saplen
US-10-140-018-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 5
US-10-140-021-506
; Sequence 506, Application US/10140021
; Publication No. US20030138866A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C167
; CURRENT APPLICATION NUMBER: US/10/140,021
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Saplen
US-10-140-021-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Query Match	89.0%;	Score 1355;	DB 12;	Length 250;
Best Local Similarity	100.0%;	Pred. No. 1.2e-126;		
Matches 250; Conservative	0;	Mismatches	0;	Indels 0;

RESULT 7  
US-10-140-471-506  
; Sequence 506, Application US/10140471  
Publ 4728444, US 7000001200071

```

      FILE REFERENCE: P3330R1C163
      CURRENT APPLICATION NUMBER: US/10/140,471
      CURRENT FILING DATE: 2002-05-06
      Prior Application removed - See file Wrapper or Palm
      NUMBER OF SEQ ID NOS: 550
      SEQ ID NO 506
      LENGTH: 250
      TYPE: PRT
      ORGANISM: Homo Sapien
      US-10-140-471-506

Query Match
Best Local Similarity 100.0%; Score 1355; DB 12; Length 250;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      33  MRLLQILLALATGLVGETRIIRKGECKPHSQPMQALFEKTRILLCGATIIAPRWLLTA  92
      1  MRLLQILLALATGLVGETRIIRKGECKPHSQPMQALFEKTRILLCGATIIAPRWLLTA  60
QY      93  AHCLKPRYIVHLGQHNLMQKEEGCEQTRTATESFPHPGNNSLPNKDRNDIMLVKMASPV  152
      61  AHCLKPRYIVHLGQHNLMQKEEGCEQTRTATESFPHPGNNSLPNKDRNDIMLVKMASPV  120
DB
QY      153  SITWAVRPLTSSRCYTAGTSCLISGWGSTSPQRLPHTLRKANITIIHQKCNAPG  212
      121  SITWAVRPLTSSRCYTAGTSCLISGWGSTSPQRLPHTLRKANITIIHQKCNAPG  180
QY      213  NITDFWVACVQEGKDCQGDSPGPIVNCOSLQIISWGDPCATIRKPGVYTKCKYV  272
      181  NITDFWVACVQEGKDCQGDSPGPIVNCOSLQIISWGDPCATIRKPGVYTKCKYV  240
QY      273  DWIQETMKNN 282
      DB      241  DWIQETMKNN 250

RESULT 8
US-10-140-807-506
; Sequence 506, Application US/10140807
; Publication No. US20030134354A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-140-807-506

Query Match
Best Local Similarity 100.0%; Score 1355; DB 12; Length 250;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

	Matches	Conservative	Mismatches	Indels	Gaps
QY	33	MRITLILATATGNGGETRIIRIGFECKRPSOPQALFEKTRLLCGATLIAPRWLT	92		
Dd	1	LILATATGTVGGETRIIRIGFECKRPSOPQALFEKTRLLCGATLIAPRWLT	60		
QY	93	AHCLKPRIVHAGHNHLQKEGCEBOTRTATSEFPHPGFNNSLPNKHNDNDIMLVMAASPV	152		
Dd	61	AHCLKPRIVHAGHNHLQKEGCEBOTRTATSEFPHPGFNNSLPNKHNDNDIMLVMAASPV	120		
QY	153	SITMAVRPLTSSRCVNAGSTCLISGMSTSPQLRLHTLRCAITITIIHQKCNAPG	212		
Dd	121	SITMAVRPLTSSRCVNAGSTCLISGMSTSPQLRLHTLRCAITITIIHQKCNAPG	180		
QY	213	NITDTMVCASVOEGSKDCQDGSGLPCVNCNLSGLIISMGODPCAITRPKPVTYTKVCXY	272		
Dd	181	NITDTMVCASVOEGSKDCQDGSGLPCVNCNLSGLIISMGODPCAITRPKPVTYTKVCXY	240		
QY	273	DMIOETMKNN	282		
Dd	241	DMIOETMKNN	250		

```

RESULT 9
US-10-140-922-506
; Sequence 506, Application US/10140922
; Publication No. US20030138869A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C1/9
; CURRENT APPLICATION NUMBER: US/10/140,922
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-140-922-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      33  MRILQILALATATGLVGETRIIRKFECKPSPQWALAEFKTILGATLLAPRWLLTA 92
Db      1  MRLIQILALATATGLVGETRIIRKFECKPSPQWALAEFKTILGATLLAPRWLLTA 60

QY      93  AHCLKRRYIVHLGQHNLDKEECGEQTRTATSPFHPGFGNNSLPKKDRNDIMLVKMASPV 152
Db      61  AHCLKRRYIVHLGQHNLDKEECGEQTRTATSPFHPGFGNNSLPKKDRNDIMLVKMASPV 120

QY      153 STTMAVRPLTSSRCVTAGTSCGISGWSSTSPQLRPLHTLRCAINTIIEHOCENAYPG 212
Db      121 STTMAVRPLTSSRCVTAGTSCGISGWSSTSPQLRPLHTLRCAINTIIEHOCENAYPG 180

```

QY	213	NINDFWACSVBEGGKDCSCGDSGGPLVNCNSLGGIISMGGDPCAIRFRKGVYTKVRY	272
Db	181	NINDFWACSVBEGGKDCSCGDSGGPLVNCNSLGGIISMGGDPCAIRFRKGVYTKVRY	240
QY	273	DWIQETRKNN	282
Db	241	DWIQETRKNN	250

```

RESULT 10
US-10-140-924-506
; Sequence 506, Application US/10140924
; Publication No. US20030134355A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Flivaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C177
CURRENT APPLICATION NUMBER: US/10/140,924
PRIORITY FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
; US-10-140-924-506

```

Query Match	99.0%;	Score 135;	DB 12;	Length 250;
Best Local Similarity	100.0%;	Pred. No. 1.2e-126;		
Matches 250;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	33	MRILQILILALATGIVGGETRIIKGFEECKPHSPQOALFEKTRILCGATLILAPRWLLTA	92	
Db	1	MRILQILILALATGIVGGETRIIKGFEECKPHSPQOALFEKTRILCGATLILAPRWLLTA	60	
QY	93	AHCLKPRIVHLGQHNLOKEEGCEQOTRTATESPPHGFNNSLPNKDRNDIMLVKMASPV	152	
Db	61	AHCLKPRIVHLGQHNLOKEEGCEQOTRTATESPPHGFNNSLPNKDRNDIMLVKMASPV	120	
QY	153	SITAAVAPRLTISSRCVTAAGTISCLISGWKSTSSPOLRLPHTLRCAITITIEHOKCENAYPG	212	
Db	121	SITAAVAPRLTISSRCVTAAGTISCLISGWKSTSSPOLRLPHTLRCAITITIEHOKCENAYPG	180	
QY	213	NITDTMVCASVQEGKDSQCGDSGGPLVCNCSLOGIISWGDDPCAITRKRPVYTVKCYV	272	
Db	181	NITDTMVCASVQEGKDSQCGDSGGPLVCNCSLOGIISWGDDPCAITRKRPVYTVKCYV	240	
QY	273	DWIOETMKN 282		
Db	241	DWIOETMKN 250		

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; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria A.
; APPLICANT: Stewart, Daniel
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C187
; CURRENT APPLICATION NUMBER: US/10/140,926
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-926-506
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Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 33 MRLIQLILALATGIVGETRIIKGFECCKPHSQPQALFEKTRLLCGATLIAPWMLTA 92
DB 1 MRLIQLILALATGIVGETRIIKGFECCKPHSQPQALFEKTRLLCGATLIAPWMLTA 60
QY 93 AHCLKPRYIVHGOHNLQKEGCEOTRTATESFPHPGFNNLSLPNDHRNDIMLVMA5PV 152
DB 61 AHCLKPRYIVHGOHNLQKEGCEOTRTATESFPHPGFNNLSLPNDHRNDIMLVMA5PV 120
QY 153 SITMAVRPLTSSRCVTAGTSCSLISGWSTSSPOLRLPHTLRCAITITIEHQKCNAYPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCSLISGWSTSSPOLRLPHTLRCAITITIEHQKCNAYPG 180
QY 213 NITDTMVCASVOEGKDCSQDGGSPLYCNSLOGIISWGDPACATITRKPGYTVCKYV 272
DB 181 NITDTMVCASVOEGKDCSQDGGSPLYCNSLOGIISWGDPACATITRKPGYTVCKYV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250
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RESULT 12  
US-10-141-698-506  
Sequence 506, Application US/10141698  
Publication No. US20030134357A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven

```
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C206
; CURRENT APPLICATION NUMBER: US/10/141,698
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-698-506
```

```
Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 33 MRLIQLILALATGIVGETRIIKGFECCKPHSQPQALFEKTRLLCGATLIAPWMLTA 92
DB 1 MRLIQLILALATGIVGETRIIKGFECCKPHSQPQALFEKTRLLCGATLIAPWMLTA 60
QY 93 AHCLKPRYIVHGOHNLQKEGCEOTRTATESFPHPGFNNLSLPNDHRNDIMLVMA5PV 152
DB 61 AHCLKPRYIVHGOHNLQKEGCEOTRTATESFPHPGFNNLSLPNDHRNDIMLVMA5PV 120
QY 153 SITMAVRPLTSSRCVTAGTSCSLISGWSTSSPOLRLPHTLRCAITITIEHQKCNAYPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCSLISGWSTSSPOLRLPHTLRCAITITIEHQKCNAYPG 180
QY 213 NITDTMVCASVOEGKDCSQDGGSPLYCNSLOGIISWGDPACATITRKPGYTVCKYV 272
DB 181 NITDTMVCASVOEGKDCSQDGGSPLYCNSLOGIISWGDPACATITRKPGYTVCKYV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250
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RESULT 13  
US-10-141-702-506  
Sequence 506, Application US/10141702  
Publication No. US20030134358A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Daniel  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C208  
CURRENT APPLICATION NUMBER: US/10/141,702  
CURRENT FILING DATE: 2002-05-08  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550



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; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Saplen
US-10-141-702-506

Query Match          89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRILQILALATGLVGGETRIIKGECKPHSOPMOALFEKTRLLCGATLAPRWLLTA 92
    |||||
Db 1 MRILQILALATGLVGGETRIIKGECKPHSOPMOALFEKTRLLCGATLAPRWLLTA 60

QY 93 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASPV 152
    |||||
Db 61 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASPV 120

QY 153 SITWAVRPLTSSRCVTAAGTSCGISGWSSTSPQLRPLPTLRCANTITIEHOKCENAYPG 212
    |||||
Db 121 SITWAVRPLTSSRCVTAAGTSCGISGWSSTSPQLRPLPTLRCANTITIEHOKCENAYPG 180

QY 213 NITDTWVCASVQEGKDSQCGDSGGLVNCNOSLOGIISWGODPCATITRRPGVYTKYCKYV 272
    |||||
Db 181 NITDTWVCASVQEGKDSQCGDSGGLVNCNOSLOGIISWGODPCATITRRPGVYTKYCKYV 240

QY 273 DWIOETMKNN 282
    |||||
Db 241 DWIOETMKNN 250

RESULT 14
US-10-141-704-506
; Sequence 506, Application US/10141704
; Publication No. US20030134359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C209
; CURRENT APPLICATION NUMBER: US/10/141,704
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Saplen
US-10-141-704-506

Query Match          89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRILQILALATGLVGGETRIIKGECKPHSOPMOALFEKTRLLCGATLAPRWLLTA 92
    |||||
Db 1 MRILQILALATGLVGGETRIIKGECKPHSOPMOALFEKTRLLCGATLAPRWLLTA 60
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QY 93 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASPV 152
    |||||
Db 61 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASPV 120

QY 153 SITWAVRPLTSSRCVTAAGTSCGISGWSSTSPQLRPLPTLRCANTITIEHOKCENAYPG 212
    |||||
Db 121 SITWAVRPLTSSRCVTAAGTSCGISGWSSTSPQLRPLPTLRCANTITIEHOKCENAYPG 180

QY 213 NITDTWVCASVQEGKDSQCGDSGGLVNCNOSLOGIISWGODPCATITRRPGVYTKYCKYV 272
    |||||
Db 181 NITDTWVCASVQEGKDSQCGDSGGLVNCNOSLOGIISWGODPCATITRRPGVYTKYCKYV 240

QY 273 DWIOETMKNN 282
    |||||
Db 241 DWIOETMKNN 250

RESULT 15
US-10-142-421-506
; Sequence 506, Application US/10142421
; Publication No. US20030134360A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C218
; CURRENT APPLICATION NUMBER: US/10/142,421
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Saplen
US-10-142-421-506

Query Match          89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRILQILALATGLVGGETRIIKGECKPHSOPMOALFEKTRLLCGATLAPRWLLTA 92
    |||||
Db 1 MRILQILALATGLVGGETRIIKGECKPHSOPMOALFEKTRLLCGATLAPRWLLTA 60

QY 93 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASPV 152
    |||||
Db 61 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASPV 120

QY 153 SITWAVRPLTSSRCVTAAGTSCGISGWSSTSPQLRPLPTLRCANTITIEHOKCENAYPG 212
    |||||
Db 121 SITWAVRPLTSSRCVTAAGTSCGISGWSSTSPQLRPLPTLRCANTITIEHOKCENAYPG 180

QY 213 NITDTWVCASVQEGKDSQCGDSGGLVNCNOSLOGIISWGODPCATITRRPGVYTKYCKYV 272
    |||||
Db 181 NITDTWVCASVQEGKDSQCGDSGGLVNCNOSLOGIISWGODPCATITRRPGVYTKYCKYV 240
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QY	273	DWIOETMKN	282
DB	241	DWIOETMKN	250

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job time : 25.3855 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 15, 2003, 20:55:12 ; Search time 16.0039 Seconds

(without alignments)  
745.546 Million cell updates/sec

Title: US-09-856-320A-2

Perfect score: 1523

Sequence: 1 MQRRLMDKSSGRGLTA.....GYTRKCKYVDWIGETKKN 282

Scoring table: BLOSUM62

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA.\*

1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*

2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*

3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*

4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*

5: /cgn2\_6/ptodata/2/1aa/PCrus.COMB.pep.\*

6: /cgn2\_6/ptodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1523	100.0	282	3	US-09-025-059-1
2	1355	89.0	250	4	US-09-205-258-427
3	1324	86.9	248	3	US-08-944-483-24
4	1227	80.6	289	4	US-09-386-642-14
5	748	49.1	246	4	US-09-205-258-1149
6	698.5	45.3	260	3	US-09-025-059-3
7	690	45.3	260	3	US-09-070-526-2
8	682	44.8	260	3	US-09-008-271A-7
9	679	44.6	288	4	US-09-386-642-13
10	666	43.7	228	4	US-09-205-258-1150
11	650.5	42.7	293	4	US-09-996-243-309
12	604.5	39.7	263	2	US-08-790-137-4
13	604.5	39.7	263	2	US-08-824-874-5
14	604.5	39.7	263	2	US-08-807-151-5
15	604.5	39.7	263	3	US-09-210-084-5
16	604.5	39.7	263	4	US-09-478-957-5
17	604.5	39.7	263	4	US-09-764-762-5
18	600.5	39.4	246	2	US-08-978-404B-44
19	600	39.4	268	2	US-08-824-874-1
20	600	39.4	268	3	US-09-210-084-1
21	600	39.4	268	4	US-09-764-762-1
22	596.5	39.2	261	3	US-08-768-859A-6
23	596.5	39.2	261	3	US-08-767-820A-6
24	596.5	39.2	261	3	US-08-622-046B-14
25	596.5	39.2	261	3	US-09-100-264-7
26	596.5	39.2	261	4	US-08-983-075D-7
27	596.5	39.2	261	4	US-08-843-076D-3

28	594	39.0	244	1	US-08-361-395-1	Sequence 1, Appli
29	593.5	39.0	261	3	US-08-768-859A-19	Sequence 19, Appli
30	593.5	39.0	261	3	US-08-767-820A-19	Sequence 19, Appli
31	593.5	39.0	261	3	US-08-622-046B-3	Sequence 3, Appli
32	592.5	38.9	261	5	PCT-US95-06157-6	Sequence 6, Appli
33	588	38.6	260	4	US-08-983-075D-9	Sequence 9, Appli
34	587	38.5	247	2	US-08-956-267A-2	Sequence 2, Appli
35	585.5	38.4	244	3	US-08-768-859A-10	Sequence 10, Appli
36	585.5	38.4	244	3	US-08-767-820A-10	Sequence 10, Appli
37	585.5	38.4	244	3	US-08-622-046B-16	Sequence 16, Appli
38	585.5	38.4	244	3	US-09-100-264-5	Sequence 5, Appli
39	585.5	38.4	244	4	US-08-843-076D-5	Sequence 5, Appli
40	582.5	38.2	244	3	US-08-622-046B-5	Sequence 5, Appli
41	581.5	38.2	244	5	PCT-US95-06157-10	Sequence 10, Appli
42	580	38.1	262	2	US-08-790-137-1	Sequence 1, Appli
43	580	38.1	262	2	US-08-790-137-3	Sequence 3, Appli
44	580	38.1	262	2	US-08-681-151-4	Sequence 4, Appli
45	580	38.1	262	2	US-08-824-874-4	Sequence 4, Appli

#### ALIGNMENTS

RESULT 1  
US-09-025-059-1  
; Sequence 1, Application US/09025059  
; Patent No. 6075136  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,059  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0481 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 282 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: LUNGDT110  
; CLONE: 2723646  
; US-09-025-059-1  
Query Match 100.0%; Score 1523; DB 3; Length 282;  
Best Local Similarity 100.0%; Pred. No. 1.9e-148;



RESULT 3  
US-08-944-483-24  
; Sequence 24, Application US/08944483  
; Patent No. 6232456  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPYTS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: GRANADOS, EDWARD N.  
; APPLICANT: KLAS, MICHAEL R.  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: STEWART, KENT D.  
; APPLICANT: STROPE, STEVEN D.  
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
; TITLE OF INVENTION: OF THE PROSTATE  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/944,483  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6183, US. 01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 248 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6232456e  
; US-08-944-483-24

Query Match 86.9%; Score 1324; DB 3; Length 248;  
Best Local Similarity 99.2%; Pred. No. 4.5e-128;  
Matches 248; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Db 33 MRILQLILALATGLVGEETRIIGFCKPSPOMALFEKTLGATLIARWLLTA 92  
1 MRILQLILALATGLVGEETRIIGFEC-PSOPMOLALF-KIRLLCGATLIARWLLTA 58

QY 93 AHCLKPRYIVHLGQHNLOKEGCEBOTRTATESFPHPGFNNSLPKDKHRNDIMLVKMA SPV 152  
Db 59 AHCLKPRYIVHLGQHNLOKEGCEQOTRTATESFPHPGFNNSLPKDKHRNDIMLVKMA SPV 118

QY 153 SITWAVRPLTLSSRCVTAGTISGLISGWSSTSSPOLRLPHTLRCANITIIIEHOKCENAYPG 212  
Db 119 SITWAVRPLTLSSRCVTAGTISGLISGWSSTSSPOLRLPHTLRCANITIIIEHOKCENAYPG 178

QY 213 NITDTMVCASVOEGSKSCGDSGGLVPCNOSLOGIISWGODPCATIRKPGVYTKVCKYV 272  
Db 179 NITDTMVCASVOEGSKSCGDSGGLVPCNOSLOGIISWGODPCATIRKPGVYTKVCKYV 238

QY 273 DWIOETMKN 282  
Db 239 DWIOETMKN 248

RESULT 4  
US-09-386-642-14  
; Sequence 14, Application US/09386642  
; Patent No. 6420157  
; GENERAL INFORMATION:  
; APPLICANT: Darrow, Andrew  
; APPLICANT: Q1, Jensen  
; APPLICANT: Andrade-Gordon, Patricia  
; TITLE OF INVENTION: Zymogen Activation System  
; FILE REFERENCE: ORT-1028  
; CURRENT APPLICATION NUMBER: US/09/386,642  
; CURRENT FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 289  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
; US-09-386-642-14

Query Match 80.6%; Score 1227; DB 4; Length 289;  
Best Local Similarity 84.3%; Pred. No. 5.1e-118;  
Matches 231; Conservative 9; Mismatches 12; Indels 22; Gaps 3;

QY 31 QAMRIQLIL--LALATGLV-----GETRIIGFEC-KRHSOPWQ 68  
Db 8 QKSRLLLVVSNLLCGVGVSDYKDDDDVAALAFDDDDKIVGGYNLEKHSOPWQ 67

QY 69 AALFEKTRLLCGATLIARWLLTAHCLKPRYIVHLGQHNLOKEGCEBOTRTATESFPHP 128  
Db 68 AALFEKTRLLCGATLIARWLLTAHCLKPRYIVHLGQHNLOKEGCEQOTRTATESFPHP 127

QY 129 GFNNSLPKDKHRNDIMLVKMA SPVSITWAVRPLTLSSRCVTAGTISGLISGWSSTSSPOLR 188  
Db 128 GFNNSLPKDKHRNDIMLVKMA SPVSITWAVRPLTLSSRCVTAGTISGLISGWSSTSSPOLR 187

QY 189 LPHTLRCANITIIIEHOKCENAYPGNITDTMVCASVOEGSKSCGDSGGLVPCNOSLOGI 248  
Db 188 LPHTLRCANITIIIEHOKCENAYPGNITDTMVCASVOEGSKSCGDSGGLVPCNOSLOGI 247

QY 249 ISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 282  
Db 248 ISWGODPCATIRKPGVYTKVCKYVDWIOETMKN 281

RESULT 5  
US-09-205-258-1149  
; Sequence 1149, Application US/09205258  
; Patent No. 6525174  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/09/205,258  
; CURRENT FILING DATE: 1998-12-04  
; EARLIER APPLICATION NUMBER: PCT/US98/11422  
; EARLIER FILING DATE: 1998-06-04  
; EARLIER APPLICATION NUMBER: 60/048,885  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,375  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,881  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,880  
; EARLIER FILING DATE: 1997-06-06

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EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
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EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1149

LENGTH: 246  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-1149  
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Best Local Similarity 92.8%; Score 748; DB 4; length 246;  
Matches 142; Conservative 1; Mismatches 10; Indels 0; Gaps 0;  
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QY 93 ARLKPRIVYHLCQNLQKEEGCEQTRTATESPPHGFNNSLPKDRNDIMLVKMASPV 152  
DB 61 ARLKPRIVYHLCQNLQKEEGCEQTRTATESPPHGFNNSLPKDRNDIMLVKMASPV 120  
QY 153 SITWAVPLTSSRCVYAGTSCFSGAGKPPD 185  
DB 121 SITWAVPLTSSRCVYAGTSCFSGAGKPPD 153  
RESULT 6  
US-09-025-059-3  
Sequence 3, Application US/09025059  
Patent No. 6075136  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,059  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0481 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1020091  
US-09-025-059-3  
Query Match  
Best Local Similarity 45.9%; Score 698.5; DB 3; length 260;  
Matches 129; Conservative 35; Mismatches 77; Indels 7; Gaps 3;



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QY      94  HCLAFRYIVHLGOHMLQKEBCEGQRTTATESPPHGEFNNSLPKNDHNDIMLVKMASPVs  153
Db      73  HCKMKQYSVRIGDHSILQSRDPEQETOVNOSTIOHPCYNNSNP-EDHSHTIMLIRLONSAN  131
QY      154  ITMAVRPELTLSRCYTAGTSCILISGMSGNSSPOLRLPHRLRCANITIEHOKENAYPGN  213
Db      132  LGDKYKRPQALMLCKRYGQKCLISGMYTTSQENFPNTLNCALVAYTYSQNKCERAYPGK  191
QY      214  ITDTWVCASVQEGKDSQGDSDSGGFLPVCNQLGIIISWGQDPCAITRRKPGVYTKVCKYYD  273
Db      192  ITEGVAVCAG-SSNGADTFCQGDSDGGFLVCGMLGQITSMGSDPCGRPEKPGVYTKICRYTT  250
QY      274  WIOETMKN 281
Db      251  WIKRTMDN 258

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1      RESULT 7
2      US-09-070-526-2
3      Sequence 2, Application US/09070526
4      Patent No. 6100059
5      GENERAL INFORMATION:
6      APPLICANT: SOUTHAN, CHRISTOPHER
7      APPLICANT: CLINKENBEARD, HELEN
8      APPLICANT: BURGESS, NICOLA
9      TITLE OF INVENTION: NO. 6100059e1 Compounds
10     NUMBER OF SEQUENCES: 4
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: RATNER & PRESTIA
13     STREET: P.O. BOX 980
14     CITY: VALLEY Forge
15     STATE: PA
16     COUNTRY: USA
17     ZIP: 19482
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: Diskette
20     COMPUTER: IBM Compatible
21     OPERATING SYSTEM: DOS
22     SOFTWARE: FASTSEQ for Windows Version 2.0
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/09/070,526
25     FILING DATE: 30-APR-1998
26     CLASSIFICATION:
27     PRIOR APPLICATION DATA:
28     APPLICATION NUMBER: GB 9711952.3
29     FILING DATE: 9-JUN-1997
30     APPLICATION NUMBER: EP 9730964.4
31     FILING DATE: 1-DEC-1997
32     ATTORNEY/AGENT INFORMATION:
33     NAME: PRESTIA, PAUL F
34     REGISTRATION NUMBER: 23,031
35     REFERENCE/DOCKET NUMBER: GH-30353
36     TELECOMMUNICATION INFORMATION:
37     TELEPHONE: 610-407-0700
38     TELEFAX: 610-407-0701
39     TELEX: 846169
40     INFORMATION FOR SEQ ID NO: 2:
41     SEQUENCE CHARACTERISTICS:
42     LENGTH: 260 amino acids
43     TYPE: amino acid
44     STRANDEDNESS: single
45     TOPOLOGY: linear
46     MOLECULE TYPE: protein
47     US-09-070-526-2
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49     Query Match          45.3%; Score 690; DB 3; Length 260;
50     Best Local Similarity 49.2%; Pred. No. 6.5e-63;
51     Matches 125; Conservative 45; Mismatches 80; Indels 4; Gaps 3;

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OY 144 MLVKNASVSTIMWAVRLPILSSRCYTAGTSCILSGMSGSSPOLRLPHILRCANITIIEN 203
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OY 204 QKCEANAYPGNITDTWYKASVQEGKSDSGDGGSLPYVNCOSLIGLIIISGCDPLPAITRIKPT 263
Db 182 KKCEDAYPGQITDGNVACGASSKGA--DTQGDGSGSLPYVCGALGISTSWSDPCGRSDRKE 240
OY 264 VYTKVCKRYVDNIOE 277
Db 241 VYTNICRYLDMWK 254

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RESULT 8
US-09-008-271A-7
Sequence 7, Application US/09008271A
Patent No. 6203979
GENERAL INFORMATION:
APPLICANT: Hildman, Olga
Hildman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Puvvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008.271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLN00T27
CLONE: 1798496
SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
US-09-008-271A-7

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EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1150  
LENGTH: 228  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-1150

Query Match 43.7%; Score 666; DB 4; Length 228;  
Best Local Similarity 91.9%; Pred. No. 1,6e-60;  
Matches 124; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

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DB 61 KEEOGEQRTATESFPHGFNNSLPNKDRNDIMLVKASPVSLTWAVRPLTSSRCVTA 120  
OY 171 GTCSLISGWSSTSSP 185  
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DB 121 GTCSFPAAGARPP 135

RESULT 11  
US-09-996-243-309  
Sequence 309, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kiljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
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PRIOR FILING DATE: 1998-02-25  
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PRIOR FILING DATE: 1998-06-03  
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PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11







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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1731049 seqs, 1297405648 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match length	DB ID	Description
1	1258	100.0	1186 14	US-10-205-823-211 Sequence 211, App

2	1258	100.0	1204	11	US-09-946-374-169	Sequence 169, App
3	1258	100.0	1204	12	US-10-015-387A-169	Sequence 169, App
4	1258	100.0	1204	12	US-10-137-870-505	Sequence 505, App
5	1258	100.0	1204	12	US-10-140-018-505	Sequence 505, App
6	1258	100.0	1204	12	US-10-140-021-505	Sequence 505, App
7	1258	100.0	1204	12	US-10-140-274-505	Sequence 505, App
8	1258	100.0	1204	12	US-10-140-471-505	Sequence 505, App
9	1258	100.0	1204	12	US-10-140-807-505	Sequence 505, App
10	1258	100.0	1204	12	US-10-140-922-505	Sequence 505, App
11	1258	100.0	1204	12	US-10-140-924-505	Sequence 505, App
12	1258	100.0	1204	12	US-10-140-926-505	Sequence 505, App
13	1258	100.0	1204	12	US-10-141-688-505	Sequence 505, App
14	1258	100.0	1204	12	US-10-141-702-505	Sequence 505, App
15	1258	100.0	1204	12	US-10-141-704-505	Sequence 505, App
16	1258	100.0	1204	12	US-10-142-421-505	Sequence 505, App
17	1258	100.0	1204	12	US-10-142-432-505	Sequence 505, App
18	1258	100.0	1204	12	US-10-142-767-505	Sequence 505, App
19	1258	100.0	1204	12	US-10-143-033-505	Sequence 505, App
20	1258	100.0	1204	12	US-10-144-994-505	Sequence 505, App
21	1258	100.0	1204	12	US-10-145-628-505	Sequence 505, App
22	1258	100.0	1204	12	US-10-145-631-505	Sequence 505, App
23	1258	100.0	1204	12	US-10-145-633-505	Sequence 505, App
24	1258	100.0	1204	12	US-10-145-746-505	Sequence 505, App
25	1258	100.0	1204	12	US-10-145-748-505	Sequence 505, App
26	1258	100.0	1204	12	US-10-145-823-505	Sequence 505, App
27	1258	100.0	1204	12	US-10-145-826-505	Sequence 505, App
28	1258	100.0	1204	12	US-10-145-870-505	Sequence 505, App
29	1258	100.0	1204	12	US-10-145-876-505	Sequence 505, App
30	1258	100.0	1204	12	US-10-145-895-505	Sequence 505, App
31	1258	100.0	1204	12	US-10-146-724-505	Sequence 505, App
32	1258	100.0	1204	12	US-10-146-725-505	Sequence 505, App
33	1258	100.0	1204	12	US-10-146-795-505	Sequence 505, App
34	1258	100.0	1204	12	US-10-147-495-505	Sequence 505, App
35	1258	100.0	1204	12	US-10-147-501-505	Sequence 505, App
36	1258	100.0	1204	12	US-10-147-504-505	Sequence 505, App
37	1258	100.0	1204	12	US-10-147-506-505	Sequence 505, App
38	1258	100.0	1204	12	US-10-147-509-505	Sequence 505, App
39	1258	100.0	1204	12	US-10-147-510-505	Sequence 505, App
40	1258	100.0	1204	12	US-10-147-511-505	Sequence 505, App
41	1258	100.0	1204	12	US-10-147-529-505	Sequence 505, App
42	1258	100.0	1204	12	US-10-147-397-505	Sequence 505, App
43	1258	100.0	1204	12	US-10-153-566-505	Sequence 505, App
44	1258	100.0	1204	12	US-10-158-783-505	Sequence 505, App
45	1258	100.0	1204	12	US-10-158-786-505	Sequence 505, App

## ALIGNMENTS

RESULT 1  
US-10-205-823-211  
; Sequence 211, Application US/10205823  
; Publication No. US20030108963A1  
GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John E.  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Gannavarapu, Manjula  
; APPLICANT: Gorbatcheva, Bella  
; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Wansley, Angela M.  
; APPLICANT: Glat, Xumel  
; APPLICANT: Zhao, Xumel  
; APPLICANT: Anderson, Dustin  
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER  
FILE REFERENCE: MRI-044  
CURRENT APPLICATION NUMBER: US/10/205,823  
CURRENT FILING DATE: 2002-07-25  
PRIOR APPLICATION NUMBER: 60/307,982  
PRIOR FILING DATE: 2001-07-25  
PRIOR APPLICATION NUMBER: 60/314,356



;; PRIOR FILING DATE: 2001-08-22  
;; PRIOR APPLICATION NUMBER: 60/325,020  
;; PRIOR FILING DATE: 2001-09-25  
;; PRIOR APPLICATION NUMBER: 60/341,746  
;; PRIOR FILING DATE: 2001-12-12  
;; PRIOR APPLICATION NUMBER: 60/362,158  
;; PRIOR FILING DATE: 2002-03-05  
;; NUMBER OF SEQ ID NOS: 455  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 211  
;; LENGTH: 1186  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-203-823-211

Alignment Scores:  
Pred. No.: 1,2e-134 Length: 1186  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-09-856-320a-2\_COPY\_54\_282 (1-229) x US-10-203-823-211 (1-1186)

QY 1 ILeIIeIySgLyPhgIuCySlySPROHISerGlnProTrrpGlnAlaAlaIeupheglu 20  
DB 185 ATCATCAAGGGGTTGAGTGCACAGCCCTCACTCCAGCCCGGAGCGCAGCCCTGTGCAG 244  
QY 21 LyeThrArgLeuLeuCySGIyAlaThrLeuIleAlaProArgrTrpLeuThAlaAla 40  
DB 245 AAGAGCGGGCTACTCTGTGGGGGACCCCTCATGCCCGCCAGATGGCTGTGACGAGCC 304  
QY 41 HISCysLeuysPROArgrTrIleValHISleuGlyGlnHISasnLeuGlnIySGluGlu 60  
DB 305 CACTGCCTCAAGCCCGGCTACATAGTTCACCTGGGGAGACACAACCTCGAAGGAGAG 364  
QY 61 GLyCysgluGlnThrArgTrpAlaThrGluSerPheProHISProGlyPheAsnAsnSer 80  
DB 365 GGCTGTGAGAGAGAGCCGAGCAGCCAGTCTCTCCCGACCCCGCTTCAACACAGC 424  
QY 81 LeuProHISlySPHISArGAsnAspIleMetIleuValIySMetaIAserProvalSer 100  
DB 425 CTGCCCAAGAAAGCCAGCCCAATGACATATGCTGTGAGATGGCATGCCAGTCTCC 484  
QY 101 ILeThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThralaGlyThrSer 120  
DB 485 ATCACTGGGGCTGTGGCAGCCCTCACCTCTCTGACGCTGTGCACACTGTGGGACAGC 544  
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHISThrLeu 140  
DB 545 TGCCTCAATTCGCGCTGGGACACCTCCAGCCCGGAGTTCAGCCCTGCACACCTTG 604  
QY 141 ArgCysAlaAsnIleThrIleIleGlnHISGlnIySCysGlnuAsnAlaTrpProGlyAsn 160  
DB 605 CGATGCGCCAAATCATCATCATTTGACACAGAGAGGTGAGAACGGCTTACCCCGGAGC 664  
QY 161 ILeThrAspThrMetValCysAlaSerValGlnIyGlnIyLysAspSerCysGlnIy 180  
DB 665 ATCAAGACAGACATGGTGTGCCAGGCTCAGAAAGGGGGAAGAGACTCTGCGCAGGT 724  
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnIyIleIleSerTrpGlyGln 200  
DB 725 GACTCGGGGGCCCTCGTCTGTAAACCACTCTTCAGAGCATTAATCTCGGGGCGAG 784  
QY 201 AspProCysAlaIleThrArgLysProGlyValIyThrIyValCysIyTyValAsp 220  
DB 785 GATCGGTGTGCGATCACCCGAAAGCCGTGGTGTCTACAGAAAGTGTGCAATATGTGGAC 844  
QY 221 TrpIleGlnIyThrMetLysAsn 229  
DB 845 TGGATCCAGAGAGAGATGAAGAACAT 871

RESULT 2  
US-09-946-374-169  
;; Sequence 169, Application US/09946374  
;; Publication No. US20030073129A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Bolstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, Christopher J.  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Hillan, Kenneth J.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Smith, Victoria  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2830P1c1  
;; CURRENT APPLICATION NUMBER: US/09/946,374  
;; PRIOR FILING DATE: 2001-09-04  
;; PRIOR APPLICATION NUMBER: 60/098716  
;; PRIOR FILING DATE: 1998-09-01  
;; PRIOR APPLICATION NUMBER: 60/098723  
;; PRIOR FILING DATE: 1998-09-01  
;; PRIOR APPLICATION NUMBER: 60/098749  
;; PRIOR FILING DATE: 1998-09-01  
;; PRIOR APPLICATION NUMBER: 60/098750  
;; PRIOR FILING DATE: 1998-09-01  
;; PRIOR APPLICATION NUMBER: 60/098803  
;; PRIOR FILING DATE: 1998-09-02  
;; PRIOR APPLICATION NUMBER: 60/098821  
;; PRIOR FILING DATE: 1998-09-02  
;; PRIOR APPLICATION NUMBER: 60/098843  
;; PRIOR FILING DATE: 1998-09-02  
;; PRIOR APPLICATION NUMBER: 60/099536  
;; PRIOR FILING DATE: 1998-09-09  
;; PRIOR APPLICATION NUMBER: 60/099596  
;; PRIOR FILING DATE: 1998-09-09  
;; PRIOR APPLICATION NUMBER: 60/099598  
;; PRIOR FILING DATE: 1998-09-09  
;; PRIOR APPLICATION NUMBER: 60/099602  
;; PRIOR FILING DATE: 1998-09-09  
;; PRIOR APPLICATION NUMBER: 60/099642  
;; PRIOR FILING DATE: 1998-09-09  
;; PRIOR APPLICATION NUMBER: 60/099741  
;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: 60/099754  
;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: 60/099763  
;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: 60/099792  
;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: 60/099808  
;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: 60/099812  
;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: 60/099815  
;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: 60/099816  
;; PRIOR FILING DATE: 1998-09-10  
;; PRIOR APPLICATION NUMBER: 60/100385  
;; PRIOR FILING DATE: 1998-09-15

PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
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PRIOR FILING DATE: 1998-09-17  
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PRIOR FILING DATE: 1998-09-17  
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PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
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PRIOR FILING DATE: 1998-09-18  
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PRIOR FILING DATE: 1998-09-17  
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PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101068  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101071  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101471  
PRIOR FILING DATE: 1998-09-23  
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PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101475  
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PRIOR FILING DATE: 1998-09-29  
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PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102307  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102330  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484

PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102487  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102571  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102684  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102687  
PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102965  
PRIOR FILING DATE: 1998-10-02  
PRIOR APPLICATION NUMBER: 60/103258  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103314  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103315  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103328  
PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103395  
PRIOR FILING DATE: 1998-10-07  
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PRIOR FILING DATE: 1998-10-07  
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PRIOR FILING DATE: 1998-10-07  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103633  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103678  
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PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
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PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/104257  
PRIOR FILING DATE: 1998-10-14  
PRIOR APPLICATION NUMBER: 60/104987  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105002  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105104  
PRIOR FILING DATE: 1998-10-21  
PRIOR APPLICATION NUMBER: 60/105169  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105266  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105693  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105694  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105807

## Alignment Scores:

Pred. No.:	1,23e-134	Length:	1204
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-09-856-320a-2\_COPY\_54\_282 (1-229) x US-09-946-374-169 (1-1204)

QY 1 llellysglypneglucyslysfrohisserglnptpglnalalaLeupheglu 20  
|||||  
DB 169 ATCATCAGGGGTTGAGTGCAGGCTCCTGAGCCCTGAGGAGCCCTGTGAG 228  
QY 21 llystratgleuleucysglyalathreullealepfoadgtrpleuleuthAlala 40  
|||||

```

Db      229  AAGACGGGCTACTCTGTGGGGGAGCGCTATCGCCCCCGAGATGGCTCTGACAGCAGCC 288
QY      41  HiscysleuylsProArGlyrIleValHiscysleuylsGlnHiscysleuylsGlnGlu 60
      |||
Db      289  CACTGGCTCAAGGCCGCTACATAGTTACCTGGGGGAGCACAACCTCCAGAGGAGAG 348
QY      61  GLYCysgluInThrArGThrAlaThrGluSerPheProHispGlyPheAsnAsnSer 80
      |||
Db      349  GGCTGTGAGCAGACCGCGAGCGACACGAGTCTCTCCCGACCCCGGCTTCAACACAGC 408
QY      81  LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
      |||
Db      409  CTCCCAACAAGACCAACCCCAATGACATATGCTGTGTAAGATGGCATGCGACAGTCC 468
QY      101  IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
      |||
Db      469  ATACACGGGCTGTGGACCCCTCACCCCTCTCCACGCTGTGTCACTGTGGCACCAGC 528
QY      121  CysLeuIleSerGlyrTrpGlySerThrSerSerProGlnLeuArgLeuProHispThrLeu 140
      |||
Db      529  TGCCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCGAGTTACGCTGCTCACACCTTG 588
QY      141  ArgCysAlaAsnIleThrIleIleGlnHiscysGlnAsnAlaTrpProGlyAsn 160
      |||
Db      589  CGATGGCCCAACATCAACATCATTTGAGCACCAAGTGTAGAAAGCCCTTACCCGGCAGC 648
QY      161  IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
      |||
Db      649  ATCACAGACACCATGGTGTGTGCCACGCTCAGAGAAAGGGGCAAGGACTCTCCGCAAGGT 708
QY      181  AspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
      |||
Db      709  GACTCCGGGGGCCCTGTGGTCTTAACCACTCTTCAAGGCAATTAATCTCTGGGGCAG 768
QY      201  AspProCysAlaIleThrArGlySerProGlyValIleThrLysValCysLysTrpValAsp 220
      |||
Db      769  GATCCGCTGTCGATCAACCCGAAAGCCGTGTGTCTACACGAAAGTCTGCAAAATATGTGGAC 828
QY      221  TrpIleGlnGluThrMetLysAsnAsn 229
Db      829  TGGATCCAGGAGAGATGAAGAACAAT 855

RESULT 3
US-10-015-387A-169
; Sequence 169, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 169
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-387A-169

```

```

Alignment Scores:
Pred. No.: 1,236-134 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.008 Conservative: 0
Best Local Similarity: 100.008 Mismatches: 0
Query Match: 100.008 Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x US-10-015-387A-169 (1-1204)

QY      1  IleIleLysGlyTheGluCysLysProHisSerGlnProTrpGlnAlaLeuPheGlu 20
      |||
Db      169  ATCATCAAGGGGGTTCAGATGCAAGCTCATCTCCAGCCCTGGAGGACAGCCGCTTCCGAG 228
QY      21  LysThrArgLeuLeuCysGlyAlaThrLeuAlaProArgThrLeuThrAlaAla 40
      |||
Db      229  AAGACGGGCTACTCTGTGGGGGAGCGCTATATGCCCCCGAGATGGCTCTGACAGCAGCC 288
QY      41  HiscysleuylsProArGlyrIleValHiscysleuylsGlnHiscysleuylsGlnGlu 60
      |||
Db      289  CACTGGCTCAAGGCCGCTACATAGTTACCTGGGGGAGCACAACCTCCAGAGGAGAG 348
QY      61  GLYCysgluInThrArGThrAlaThrGluSerPheProHispGlyPheAsnAsnSer 80
      |||
Db      349  GGCTGTGAGCAGACCGCGAGCGACCTGAGTCTCTCCCGACCCCGGCTTCAACACAGC 408
QY      81  LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
      |||
Db      409  CTCCCAACAAGACCAACCCCAATGACATATGCTGTGTAAGATGGCATGCGACAGTCC 468
QY      101  IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
      |||
Db      469  ATCACCGGGCTGTGGACCCCTCACCCCTCTCCACGCTGTGTCACTGTGGCACCAGC 528
QY      121  CysLeuIleSerGlyrTrpGlySerThrSerSerProGlnLeuArgLeuProHispThrLeu 140
      |||
Db      529  TGCCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCGAGTTACGCTGCTCACACCTTG 588
QY      141  ArgCysAlaAsnIleThrIleIleGlnHiscysGlnAsnAlaTrpProGlyAsn 160
      |||
Db      589  CGATGGCCCAACATCAACATCATTTGAGCACCAAGTGTAGAAAGCCCTTACCCGGCAGC 648
QY      161  IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
      |||
Db      649  ATCACAGACACCATGGTGTGTGCCACGCTCAGAGAAAGGGGCAAGGACTCTCCGCAAGGT 708
QY      181  AspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
      |||
Db      709  GACTCCGGGGGCCCTGTGGTCTTAACCACTCTTCAAGGCAATTAATCTCTGGGGCAG 768
QY      201  AspProCysAlaIleThrArGlySerProGlyValIleThrLysValCysLysTrpValAsp 220
      |||
Db      769  GATCCGCTGTCGATCAACCCGAAAGCCGTGTGTCTACACGAAAGTCTGCAAAATATGTGGAC 828
QY      221  TrpIleGlnGluThrMetLysAsnAsn 229
Db      829  TGGATCCAGGAGAGATGAAGAACAAT 855

RESULT 4
US-10-137-870-505
; Sequence 505, Application US/10137870
; Publication No. US20030138883A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```

APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C155  
CURRENT APPLICATION NUMBER: US/10/137,870  
CURRENT FILING DATE: 2002-05-03  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 505  
LENGTH: 1204  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-137-870-505

Alignment Scores:  
Pred. No.: 1,236-134 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-856-320a-2\_copy\_54\_282 (1-229) x US-10-137-870-505 (1-1204)

OY 1 ILeIlelySGlyPheGluCysAlaProHisSerGlnProTyrGlnAlaAlaLeuPheGlu 20  
DB 169 ATCATCAAGGGGTTGAGTGCAGAGCTCATCCAGCCCTGGCAGGAGCCCTGTTCCAG 228  
OY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeaProArgTyrPheLeuThrAlaAla 40  
DB 229 AAGAGCGCGTACTCTGTGGGCGAGCTCATGCCCGCAGATGGCTCTCGACACACACC 288  
OY 41 HisCysLeuLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLysGlu 60  
DB 289 CACTGCGTCAGACCCCGCTACATAGTTCACCGGGGCGAGCAACCTCCAGAGAGAGAG 348  
OY 61 GlyCysGlnGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
DB 349 GCGTGTGAGCAGACCCGCGAGCCAGCTGATCTCCCGCCAGCCGCTTCAACACAGC 408  
OY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
DB 409 CTCCCAACAAAGACACCGCAATGACATGCTGGTGAAGATGGCATCGCCAGCTCC 468  
OY 101 ILeThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 469 ATCAAGCTGGGTGTGGCGAGCCCTCAGCTCTCCAGCTGTGTACGTGGCGACAGC 528  
OY 121 CysLeuLeuSerGlyTyrPheGlySerThrSerSerProGlnLeuAlaGluProHisThrLeu 140  
DB 529 TGCTCATATTCGGCTGGGCGAGCAGTCACGCCCGCTTACAGGCTCTCCACACCTTG 588  
OY 141 ArgCysAlaAsnIleThrIleGlnHisGlnLysCysGlnLysAsnAlaTyrProGlyLys 160  
DB 589 CGATGCCGCAACATCACCATATTGAGACACAGAGTGTGAAGAGCGCTACCCCGGACAC 648  
OY 161 ILeThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180  
DB 649 ATCAAGACACACATGGTGTGGCAGGCTGCAGAGAGGGGCGAGAGATCTCTGCAGAGGT 708  
OY 181 AsperGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrPheGln 200  
DB 709 GACTCCGGGGGCGCTGTGGTGTGAACAGTCTTCAAGGCAATTATCTCTGGGGCCAG 768  
OY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220

DB 769 GATCCGTGTGCATACACCGAAAGCCGTGTGTCTACACGAAAGTCTGCAAAATATGTGAC 828  
OY 221 TrpIleGlnGluThrMetLysAsnAsn 229  
DB 829 TGGATCCAGAGACGATGAGAAACAT 855

RESULT 5  
US-10-140-018-505  
Sequence 505, Application US/10140018  
Publication No. US20030138885A1  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C158  
CURRENT APPLICATION NUMBER: US/10/140,018  
CURRENT FILING DATE: 2002-05-06  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 505  
LENGTH: 1204  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-140-018-505

Alignment Scores:  
Pred. No.: 1,236-134 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-856-320a-2\_copy\_54\_282 (1-229) x US-10-140-018-505 (1-1204)

OY 1 ILeIlelySGlyPheGluCysAlaProHisSerGlnProTyrGlnAlaAlaLeuPheGlu 20  
DB 169 ATCATCAAGGGGTTGAGTGCAGAGCTCATCCAGCCCTGGCAGGAGCCCTGTTCCAG 228  
OY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeaProArgTyrPheLeuThrAlaAla 40  
DB 229 AAGAGCGCGTACTCTGTGGGCGAGCTCATGCCCGCAGATGGCTCTCGACACAGC 288  
OY 41 HisCysLeuLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLysGlu 60  
DB 289 CACTGCGTCAGACCCCGCTACATAGTTCACCTGGGGCGAGCAACCTCCAGAGAGAGAG 348  
OY 61 GlyCysGlnGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80  
DB 349 GCGTGTGAGCAGACCCGCGAGCCAGCTGATCTCCCGCCAGCCGCTTCAACACAGC 408  
OY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
DB 409 CTCCCAACAAAGACACCGCAATGACATGCTGGTGAAGATGGCATCGCCAGGTCTCC 468  
OY 101 ILeThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120



Prior Application removed - See File Wrapper or Palm  
 : NUMBER OF SEQ ID NOS: 550  
 : SEQ ID NO 505  
 : LENGTH: 1204  
 : TYPE: DNA  
 : ORGANISM: Homo Sapien  
 US-10-140-274-505

Alignment Scores:  
 Pred. No.: 1,236-134 Length: 1204  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 12 Gaps: 0

US-09-856-320a-2\_copy\_54\_282 (1-229) x US-10-140-274-505 (1-1204)

QY 1 llellelysglypnehlucyslyspromhisserginprotpglnalalauepneclu 20  
 DB 169 ATCATCAAGGGGTTGAGTGCAGAGCTCCAGCCCTGGCAGGAGCCCTGTTCCAG 228  
 QY 21 lysthrarqluenucysglaalathrleuilealaproatgtrpleuenuThralaia 40  
 DB 229 AAGAGCGCGCTACTCTGTGGGGCAGCGCTCATCGCCCAATGAGTCTCTGACAGCACC 288  
 QY 41 HiscysleuylsProatgTyrIleValHiscleuglylnhisasnleuglnlysglu 60  
 DB 289 CACTGCCCTCAAGCCCCGCTACATAGTTCACTGGGGCAGCAACCTCCAGAGAGAGAG 348  
 QY 61 glycysgluglnthrarqThralathrgluserpheprohissprogllypheasnanser 80  
 DB 349 GCGGTGAGCAGACCCGAGCAGCACTGATCTTCCGCCACCCGCGCTCAACACAGC 408  
 QY 81 leuproasnlysaaphisargasnaspillemetleuValysmetalaSerProvalser 100  
 DB 409 CTCCCAACAAAGACACCCGAGATGACATCATGCTGGAGAGATGGCATCCGCACTGCC 468  
 QY 101 llethrrpalaValargProleuthrleuSerSerargCysValThralaglYthrser 120  
 DB 469 ATCACAGCGGCTGTGGCAGCCCTCACTCCCTGACCTGTGACAGCAGC 528  
 QY 121 cystleuileserglYtrpGlySerThrserserProglneuValgleuProhithreu 140  
 DB 529 TGCCCTCAATTCGGGCTGGGGCAGCAGCTCCAGCCCTGCTCCACACCTTGG 588  
 QY 141 ArgCysalaasnillethrllelelgluhisglnlyscysgluasnalatyrProglYasn 160  
 DB 589 CGATGCGCCACATCACCATCATTTGAGCAGCAGAAAGTGTGAAGACGCTTACCCGGCAGC 648  
 QY 161 llethraspthrmetValCysalaSerValglnlglYlyAspSerCysglnly 180  
 DB 649 ATCACAGACACCATGAGTGTGGCCAGCGCTGCAAGAGGGGGCAGAGGACTCTGCCAGGCT 708  
 QY 181 AspergilyglYProleuValCysasnGlnserleuGlnlylleSerTrpGlyln 200  
 DB 709 GACTCCGGGGGCGCTGTGGTCTGTACACAGCTCTTCAAGGCAATTAATCTGGGGCCAG 768  
 QY 201 AsprProCysalailethrarqlyspromhissproglYValYthrlyrsValCyslystyValasp 220  
 DB 769 GATCGCGTGTGAGTACACCCGAAAGCCTGGTGTCTACAGAAAGTCTGCAATATGTGGAC 828  
 QY 221 TrpilleglnlunthrmetyAsnasn 229  
 DB 829 TGGATCCAGAGAGATGAAGAACAT 855

RESULT 8  
 US-10-140-471-505  
 : Sequence 505, Application US/10140471  
 : Publication No. US2003013887A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Baker, Kevin P.  
 : APPLICANT: BetesIntl, Maureen

: APPLICANT: DeForge, Laura  
 : APPLICANT: Desnoyers, Luc  
 : APPLICANT: Filvaroff, Ellen  
 : APPLICANT: Gao, Wei-Qiang  
 : APPLICANT: Gerritsen, Mary E.  
 : APPLICANT: Goddard, Audrey  
 : APPLICANT: Godowski, Paul J.  
 : APPLICANT: Gurney, Austin L.  
 : APPLICANT: Sherwood, Steven  
 : APPLICANT: Smith, Victoria  
 : APPLICANT: Stewart, Timothy A.  
 : APPLICANT: Tumas, Daniel  
 : APPLICANT: Watanabe, Colin K  
 : APPLICANT: Wood, William  
 : APPLICANT: Zhang, Zemin  
 : TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 : FILE OF INVENTION: ACTS ENCODING THE SAME  
 : FILE REFERENCE: P3330R1C13  
 : CURRENT APPLICATION NUMBER: US/10/140,471  
 : PRIOR FILING DATE: 2002-05-06  
 : PRIOR APPLICATION removed - See File Wrapper or Palm  
 : NUMBER OF SEQ ID NOS: 550  
 : SEQ ID NO 505  
 : LENGTH: 1204  
 : TYPE: DNA  
 : ORGANISM: Homo Sapien  
 US-10-140-471-505

Alignment Scores:  
 Pred. No.: 1,236-134 Length: 1204  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 12 Gaps: 0

US-09-856-320a-2\_copy\_54\_282 (1-229) x US-10-140-471-505 (1-1204)

QY 1 llellelysglypnehlucyslyspromhisserginprotpglnalalauepneclu 20  
 DB 169 ATCATCAAGGGGTTGAGTGCAGAGCTCCAGCCCTGGCAGGAGCCCTGTTCCAG 228  
 QY 21 lysthrarqluenucysglaalathrleuilealaproatgtrpleuenuThralaia 40  
 DB 229 AAGAGCGCGCTACTCTGTGGGGCAGCGCTCATCGCCCAATGAGTCTCTGACAGCACC 288  
 QY 41 HiscysleuylsProatgTyrIleValHiscleuglylnhisasnleuglnlysglu 60  
 DB 289 CACTGCCCTCAAGCCCCGCTACATAGTTCACTGGGGCAGCAACCTCCAGAGAGAGAG 348  
 QY 61 glycysgluglnthrarqThralathrgluserpheprohissprogllypheasnanser 80  
 DB 349 GCGGTGAGCAGACCCGAGCAGCACTGATCTTCCGCCACCCGCGCTCAACACAGC 408  
 QY 81 leuproasnlysaaphisargasnaspillemetleuValysmetalaSerProvalser 100  
 DB 409 CTCCCAACAAAGACACCCGAGATGACATCATGCTGGAGAGATGGCATCCGCACTGCC 468  
 QY 101 llethrrpalaValargProleuthrleuSerSerargCysValThralaglYthrser 120  
 DB 469 ATCACAGCGGCTGTGGCAGCCCTCACTCCCTGACCTGTGACAGCAGC 528  
 QY 121 cystleuileserglYtrpGlySerThrserserProglneuValgleuProhithreu 140  
 DB 529 TGCCCTCAATTCGGGCTGGGGCAGCAGCTCCAGCCCTGATACGCTCTCCACACCTTGG 588  
 QY 141 ArgCysalaasnillethrllelelgluhisglnlyscysgluasnalatyrProglYasn 160  
 DB 589 CGATGCGCCACATCACCATCATTTGAGCAGCAGAAAGTGTGAAGACGCTTACCCGGCAGC 648  
 QY 161 llethraspthrmetValCysalaSerValglnlglYlyAspSerCysglnly 180  
 DB 649 ATCACAGACACCATGAGTGTGGCCAGCGTGCAGAGAGGGGGCAGAGGACTCTGCCAGGCT 708

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OY 181 AspSerGlyProLeuValCysAsnGlnSerLeuGlnIleIleSerTrpGlyGln 200
DB 709 GACTCCGGGGCCCTCTGGTCTGTAACCACTCTTCAAGCAATTAATCTCTGGGGCCAG 768
OY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
DB 769 GATCCGCGTGCATCACCCCAAGCCGCTGTCTACAGAAAGTGTGCAATAATATGTGGAC 828
OY 221 TrpIleGlnIuThrMetLysAsnAsn 229
DB 829 TGGATCCAGCAGACGATGAAGAACAAAT 855

RESULT 9
US-10-140-807-505
; Sequence 505, Application US/10140807
; Publication No. US20030134354A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Saplen
US-10-140-807-505

Alignment Scores:
Pred. No.: 1,23e-134 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-2_COPY_54_282 (1-229) x US-10-140-807-505 (1-1204)
OY 1 IleIleLysGlyheGlyCysLysProHisSerGlnProTrpGlnAlaIleAlaLeuPheGlu 20
DB 169 ATCATCAAGGGGTTCAGTCTCAAGCCCTCACTCCAGCCCTGGAGGAGAGCCCTGTTCGAG 228
OY 21 LysThrArgLeuLeuCysGlyAlaThrIleAlaProArgTrpLeuLeuThrAlaAla 40
DB 229 AAGACGGGCTACTCTGTGGGGGAGCGCTCATCGCCCGCCAGATGGCTCTCGAAGCAGACC 288
OY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
DB 289 CACTGCGCTCAAGCCCGGCTACATAGTTCACCTGGGCGACAGCAACCTCCAGAGAGAGAG 348
OY 61 GlyCysGlnGlnThrArgThrArgThrArgLysSerPheProHisProGlyPheAsnAsnSer 80
DB 349 GGCTGTGAGCAGACCCGGACGCCACTGAGTCTTCCGCCACCCCGGCTTCAACACAGC 408
```

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OY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 409 CTCGCCAACAAGACCAACCGCATATCATATCATCTGTGTGAATGGATGGCCAGTCTCC 468
OY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 469 ATACCTGGGCTGTGGCAGCCCTCACCTCTCTCACAGCTGTGTCACTGTCTGGCACCAGC 528
OY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
DB 529 TGGCTATTTCCGGCTGGGGCAGCAGCTCCAGGCCCACTAGCCCTGCTCACACTTG 568
OY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
DB 589 CGATGGCGCCAAATACCATCATATTAAGACACAGAGTGTGAGAAGCGCTACCCGGGCAAC 648
OY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
DB 649 ATCACAGACACCATGTGTGTGCAGGCTCAGAGAGGGGGCAAGGACTCTCCAGGGGT 708
OY 181 AspSerGlyProLeuValCysAsnGlnSerLeuGlnIleIleSerTrpGlyGln 200
DB 709 GACTCCGGGGCCCTCTGGTCTGTAACCACTCTTCAAGCAATTAATCTCTGGGGCCAG 768
OY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
DB 769 GATCCGCGTGCATCACCCCAAGCCGCTGTCTACAGAAAGTGTGCAATAATATGTGGAC 828
OY 221 TrpIleGlnIuThrMetLysAsnAsn 229
DB 829 TGGATCCAGCAGACGATGAAGAACAAAT 855

RESULT 10
US-10-140-922-505
; Sequence 505, Application US/10140922
; Publication No. US20030138889A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C179
; CURRENT APPLICATION NUMBER: US/10/140,922
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Saplen
US-10-140-922-505

Alignment Scores:
Pred. No.: 1,23e-134 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-856-320a-2\_copy\_54\_282 (1-229) x US-10-140-924-505 (1-1204)

```
QY 1 llellelysglypHegluCyslySProHISserGlnProTrpGlnAlaAlaLeuPheGlu 20
DB 169 ATCATCAAGGGGTGGAGTGAAGCCTCACTCCCAAGCCTGGCAGGACAGCCCTGTTCCGAG 228
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 40
DB 229 AAGACGGCGGTACTGTGTGGGGCGACGCTCATCGCCCAAGTGGCTCTCTGACAGCAGCC 288
QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60
DB 289 CACTGCTCAAGCCCCCGGTACTAGTTCACCTGGGGGCGACACACTCCAGAAAGAGGAGAG 348
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHISProGlyPheAsnAsnSer 80
DB 349 GGCTGTGAGCAGACCCGGGACAGCAGCTGACTCTTCCCAACCCGGCTTCAACACAGC 408
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 409 CTCCCCAACAAGACACCGCAATGACATGATGCTGTGAAGATGGCATCGGCAGTCTCC 468
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 469 ATCACCCTGGGCTGTGAGACCCCTCACTCTCTCACTGCTGCTGCTGCTGCTGCTGCTG 528
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHISThrLeu 140
DB 529 TGCCCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCAAGTACGCTGCTTCAACCTTG 588
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaArgProGlyAsn 160
DB 589 CGATCGCGCAACATACCATCATTTGAGCAGCAGAAAGTGTGAGAACGCCCTACCCCGGCAAC 648
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
DB 649 ATCAGACAGACCATGTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
DB 709 GACTCGGGGGGCGCTGTGTGTGAACAGTCTCTTCAAGCATTAATATCTCGGGGGCAG 768
QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysIleValAsp 220
DB 769 GATCCGTGTGGGATCAACCGAAAGCCTGTGTCTACAGAAAGTCTGCAAAATATGTGGAC 828
QY 221 TrpIleGlnGluThrMetLysAsnAsn 229
DB 829 TGGATCCAGAGACGATGAAGAACAT 855
```

RESULT 11  
US-10-140-924-505

; Sequence 505, Application US/10140924  
; Publication No. US20030134355A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DePorge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Collin K

; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C17  
; CURRENT APPLICATION NUMBER: US/10/140,924  
; CURRENT FILING DATE: 2002-05-07  
; PRIOR APPLICATION removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 505  
; LENGTH: 1204  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; US-10-140-924-505

Alignment Scores:

Pred. No.:	1,23e-134	Length:	1204
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-856-320a-2\_copy\_54\_282 (1-229) x US-10-140-924-505 (1-1204)

```
QY 1 llellelysglypHegluCyslySProHISserGlnProTrpGlnAlaAlaLeuPheGlu 20
DB 169 ATCATCAAGGGGTGGAGTGAAGCCTCACTCCCAAGCCTGGCAGGACAGCCCTGTTCCGAG 228
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 40
DB 229 AAGACGGCGGTACTGTGTGGGGCGACGCTCATCGCCCAAGTGGCTCTCTGACAGCAGCC 288
QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60
DB 289 CACTGCTCAAGCCCCCGGTACTAGTTCACCTGGGGGCGACACACTCCAGAAAGAGGAGAG 348
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHISProGlyPheAsnAsnSer 80
DB 349 GGCTGTGAGCAGACCCGGGACAGCAGCTGACTCTTCCCAACCCGGCTTCAACACAGC 408
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 409 CTCCCCAACAAGACACCGCAATGACATGATGCTGTGAAGATGGCATCGGCAGTCTCC 468
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 469 ATCACCCTGGGCTGTGAGACCCCTCACTCTCTCACTGCTGCTGCTGCTGCTGCTGCTG 528
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHISThrLeu 140
DB 529 TGCCCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCAAGTACGCTGCTGCTGCTGCTGCTG 588
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGluAsnAlaArgProGlyAsn 160
DB 589 CGATCGCGCAACATACCATCATTTGAGCAGCAGAAAGTGTGAGAACGCCCTACCCCGGCAAC 648
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
DB 649 ATCAGACAGACCATGTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
DB 709 GACTCGGGGGGCGCTGTGTGTGAACAGTCTCTTCAAGCATTAATATCTCGGGGGCAG 768
QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysIleValAsp 220
DB 769 GATCCGTGTGGGATCAACCGAAAGCCTGTGTCTACAGAAAGTCTGCAAAATATGTGGAC 828
QY 221 TrpIleGlnGluThrMetLysAsnAsn 229
DB 829 TGGATCCAGAGACGATGAAGAACAT 855
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RESULT 12
US-10-140-926-505
; Sequence 505, Application US/10140926
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Zhang, Zemin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; FILE REFERENCE: P3330R1C187
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/140,926
; PRIOR APPLICATION DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-926-505

Alignment Scores:
Pred. No.: 1,23e-134 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-856-320a-2_COPY_54_282 (1-229) x US-10-140-926-505 (1-1204)
QY 1 llellelsglypnehegucyslyspromhsserglnprotfplnaalaaleupheglu 20
DB 169 ATCATCAAGGGGTTTCAGAGTCCAGCTCACTCCAGCCCTGGCAGGAGCCCTGTCGAG 228
QY 21 lvsfthargleuencysgylalathrlleuillaalaprargtrpleuethrallaala 40
DB 229 AAGACCGGCTACTGTGTGGGGCGAGCGCTCATCGCCCGCCAGATGGCTCTCGACAGAGCC 288
QY 41 HlsCysleuysfrolargtryrlllevalhlsleuiglhlhlsanleuignlsglu 60
DB 289 CACTGCTCAAGCCCGGCTACATAGTTCACCTGGGCGACACAACTCCAGAAAGAGAG 348
QY 61 gLyCysgluglnthrarqthralarhrgluserPheProHisProGlyPheAsnAsnSer 80
DB 349 GGCTGTGAGCAGACCCGAGCAGCAGTCTCTCCCGCCCGCTTCAACAAACAGC 408
QY 81 leuPAsnlysaPhisArGAsnAspIleMetleuVallysmetAlaserProvalSer 100
DB 409 CTCGCCAACAAGAACCCAGCCCAATGACATCATCTGTGTAAGTGCATCGCAGTCTCC 468
QY 101 llelthralalalargproleuethrluserSerArgCysValhralaaglythrser 120
DB 469 ATACCTGGGGCTGTGGACCCCTCACCTCTCTCTCCAGCTGTGTCTACCTGTGGACACAGC 528
QY 121 CysleuileserglytrpglserthrserserProGlnleuargleuProHisThrleu 140
DB 529 TGGCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCGCCAGTTACGCTTGCCTCACACCTTG 568
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RESULT 13
US-10-141-698-505
; Sequence 505, Application US/10141698
; Publication No. US20030134357A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C206
; CURRENT APPLICATION NUMBER: US/10/141,698
; PRIOR APPLICATION DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-698-505

Alignment Scores:
Pred. No.: 1,23e-134 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-856-320a-2_COPY_54_282 (1-229) x US-10-141-698-505 (1-1204)
QY 1 llellelsglypnehegucyslyspromhsserglnprotfplnaalaaleupheglu 20
DB 169 ATCATCAAGGGGTTTCAGAGTCCAGCTCACTCCAGCCCTGGCAGGAGCCCTGTCGAG 228
QY 21 lvsfthargleuencysgylalathrlleuillaalaprargtrpleuethrallaala 40
DB 229 AAGACCGGCTACTGTGTGGGGCGAGCGCTCATCGCCCGCCAGATGGCTCTCGACAGAGCC 288
```

QY 41 H1SCYLEUYSProArGTyrIleValH1SLenUG1nH1SAsnLeuG1nLysG1nU 60  
DB 289 CACTGCCCAAGCCCCGCTACATAGTTCACCTGGGGGAGCAACCTCCAGAAAGAGAG 348  
QY 61 GLYCYSGLUG1nThrArgThrAlaThrG1nSerPheProH1SProG1LPheAsnAsnSer 80  
DB 349 GCGCTGTAGCAGACCCGGAGACGCCCTGAGTCTTCCCCCAGCCGGCTTCAACAAAC 408  
QY 81 LeuProAsnLysAspH1SArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
DB 409 CTCGCCCAAAAGACCCAGCAATGACATGCTGTGGAAGATGGATCGCCAGCTGCC 468  
QY 101 IleThrTPAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaG1yThrSer 120  
DB 469 ATCACTGGGTGTGTCGAGACCCCTCCCTCCACCTGTCTACCTGTCTGGCCAGC 528  
QY 121 CysLeuIleSerG1YTrpG1YSerThrSerSerProG1nLeuArgLeuProH1SThrLeu 140  
DB 529 TGCCCATTTCCGGCTGGGGGAGCACGTCACGCCCTTACGCTTGCCTCAGACCTTG 588  
QY 141 ArgCysAlaAsnIleThrIleIleG1nH1SGLnLysCysG1nAsnAlaTyPProG1YAsn 160  
DB 589 CGATCGCCCAACATCACCATTGATGAGCAGCAGAAAGTGAGAAAGCGCTACCCGGCAAC 648  
QY 161 IleThrAspThrMetValCysAlaSerValG1nG1nLysG1nLysAspSerCysG1nG1y 180  
DB 649 ATCAAGACACCATGTGTGTGTCGCGAGCGTGCAGAAAGGGGGGAGACCTCTCCAGG 708  
QY 181 AspSerG1Yg1YProLeuValCysAsnG1nSerLeuG1nG1yIleIleSerTrpG1Yg1n 200  
DB 709 GACTCGGGGGGCGCTGTGTGTGTAACCAAGTCTTCAAGGCAATATCTCTCGGGGGCAG 768  
QY 201 AspProCysAlaIleThrArgLysProG1YValTYrThrLysValCysLysTyPValAsp 220  
DB 769 GATCGGTGGGATCACCAGAAAGCGCTGTGTCTACAGAAAGTGTGCAAAATATGTGAG 828  
QY 221 TrpIleG1nG1nThrMetLysAsnAsn 229  
DB 829 TGGATCCAGAGACGATGAGAAACAAT 855

RESULT 14  
US-10-141-702-505  
; Sequence 505, Application US/10141702  
; Publication No. US20030134358A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C208  
; CURRENT APPLICATION NUMBER: US/10-141,702  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 505  
; LENGTH: 1204  
; TYPE: DNA  
; ORGANISM: Homo Sapien

US-10-141-702-505  
Alignment Scores:  
Pred. No.: 1,23e-134 Length: 1204  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-10-141-702-505 (1-1204)

QY 1 IleIleLysG1YPhcG1nUcysLysProH1SArgG1nProTrpG1nAlaAlaLeuPheG1n 20  
DB 169 ATCATCAAGAGGGGTGTGAGTGCAGAGCTCACCAGCCCTGGCAGGAGCCCTGTTCGAG 228  
QY 21 LysThrArgLeuLeuCysG1YAlaThrIleuIleAlaProArgTrpLeuThrAlaAla 40  
DB 229 AAGACGGGCTACTGTGTGGGGGAGCGCTCATCGCCCCAGATGGCTCTCGACAGCAGCC 288  
QY 41 H1SCYLEUYSProArGTyrIleValH1SLenUG1nH1SAsnLeuG1nLysG1nU 60  
DB 289 CACTGCCCAAGCCCCGCTACATAGTTCACCTGGGGGAGCAACCTCCAGAAAGAGAG 348  
QY 61 GLYCYSGLUG1nThrArgThrAlaThrG1nSerPheProH1SProG1LPheAsnAsnSer 80  
DB 349 GCGCTGTAGCAGACCCGGAGACGCCCTGAGTCTTCCCCCAGCCGGCTTCAACAAAC 408  
QY 81 LeuProAsnLysAspH1SArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
DB 409 CTCGCCCAAAAGACCCAGCAATGACATGCTGTGGAAGATGGATCGCCAGCTGCC 468  
QY 101 IleThrTPAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaG1yThrSer 120  
DB 469 ATCACTGGGTGTGTCGAGACCCCTCCCTCCACCTGTCTACCTGTGTCTGGCCAGC 528  
QY 121 CysLeuIleSerG1YTrpG1YSerThrSerSerProG1nLeuArgLeuProH1SThrLeu 140  
DB 529 TGCCCATTTCCGGCTGGGGGAGCACGTCACGCCCTTACGCTTGCCTCAGACCTTG 588  
QY 141 ArgCysAlaAsnIleThrIleIleG1nH1SGLnLysCysG1nAsnAlaTyPProG1YAsn 160  
DB 589 CGATCGCCCAACATCACCATTGATGAGCAGCAGAAAGTGAGAAAGCGCTACCCGGCAAC 648  
QY 161 IleThrAspThrMetValCysAlaSerValG1nG1nLysG1nLysAspSerCysG1nG1y 180  
DB 649 ATCAAGACACCATGTGTGTGTCGCGAGCGTGCAGAAAGGGGGGAGACCTCTCCAGG 708  
QY 181 AspSerG1Yg1YProLeuValCysAsnG1nSerLeuG1nG1yIleIleSerTrpG1Yg1n 200  
DB 709 GACTCGGGGGGCGCTGTGTGTGTAACCAAGTCTTCAAGGCAATATCTCTCGGGGGCAG 768  
QY 201 AspProCysAlaIleThrArgLysProG1YValTYrThrLysValCysLysTyPValAsp 220  
DB 769 GATCGGTGGGATCACCAGAAAGCGCTGTGTCTACAGAAAGTGTGCAAAATATGTGAG 828  
QY 221 TrpIleG1nG1nThrMetLysAsnAsn 229  
DB 829 TGGATCCAGAGACGATGAGAAACAAT 855

RESULT 15  
US-10-141-704-505  
; Sequence 505, Application US/10141704  
; Publication No. US20030134359A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P330R1C209  
 ; CURRENT APPLICATION NUMBER: US/10/141,704  
 ; PRIOR APPLICATION REMOVED - See Palm or File Wrapper  
 ; SEQ ID NO 505  
 ; LENGTH: 1204  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-141-704-505

Alignment Scores:  
 Pred. No.: 1,23e-134 Length: 1204  
 Score: 1258.00 Matches: 229  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 12 Gaps: 0

US-09-856-320a-2\_copy\_54\_282 (1-229) x US-10-141-704-505 (1-1204)

QY 1 ILEILEYSGLYPHEGLUCYLSYSPROHISERGLINPROTRPGINALAIALEUPHEGLU 20  
 DB 169 ATCATCAAGGGGTTGCGAGTCAAGCCCTCCAGCCCTGGCAGGCGCCCTGTTCGAG 228  
 QY 21 LYSTHRTGLEUUCYSGLYAIAIATHRLEUILLALAPROARGTTRPLEUETHRALAIA 40  
 DB 229 AAGACGGGCTACTGTGTGGGCGACGCTCATCGCCCAAGATGGCTCTGACACGAGCC 288  
 QY 41 HISCYSLLEULYSPROARGTTRILEVALHISLEUGLYGINHISASNLEUGLINSGLU 60  
 DB 289 CACTGGCTCAAGCCCGCTCATATAGTTCACCTGGGGCAGCACAACCTCCAGAGAGAG 348  
 QY 61 GLYCYSGLUGLINTHRTARTRHIALATHRGILUSERPHEPROHISPROGLYPHEASN 80  
 DB 349 GGGTGTGACGACGCCGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 408  
 QY 81 LEUPROASNLYSAPHISARGASNAPRIEMETLEUVALYLSMETALASERPROVALSER 100  
 DB 409 CTCGCCCAACAAAGCCACCCCAATGACATGCTGGTGAAGATGGCATGCCAGTCTCC 468  
 QY 101 ILETHRPAIAVALARGPROLEUTHRLEUSERARGCYSAVALTHRALAGLYTHRSER 120  
 DB 469 ATCAACCTGGGCTGTGGGACCCCTCACCCCTCTCTCACGCTGTGTCTACTGTGGAC 528  
 QY 121 CYSLEULLESERGLYTRPGIYSETRHISERSETPROGLINLEUARGLEUPROHIS 140  
 DB 529 TGCCTCATTTCCGGCTGGGCGACAGCTCCAGCCCGCAGTTACGCTGCCCTCACAC 588  
 QY 141 ARGCYALASANTLEHTRILLEGLINHISGLINYSGLIUSNAIATYRPROGLYASN 160  
 DB 589 CGATGGCCCAACATCATTCATTTGACACACAGAAAGTGTAGAAGCGCTTACCCCGCAC 648  
 QY 161 ILETHRAPHTRMETVALCYSAISERVAIGLUGLYLYLSASPSERCYSGLINGLY 180  
 DB 649 ATCAACAGACACCATGTGTGTGTGCCAGCGTCCAGAAAGGGGCAAGGACTCTGCCAG 708  
 QY 181 ASPSERGLYGLIPROLEUVALCYASNGINSETRLEUGLINSGLYILELESERTPGI 200  
 DB 709 GACTCCGGGGGCGCTGT 768  
 QY 201 ASPPROCYSALAIETHRTARGLYSPROGLYVALTYRTHLYSVALCYLSYSTYRVALASP 220

DB 769 GATCCGTGTGATCACCCGAAAGCTGTGTCTACACGAAAGTCTGCAAAATATGTGAC 828  
 QY 221 TRPILLEGGLINTHRTMETLYSASN 229  
 DB 829 TGGATCCAGAGACGATGAAAGAACAT 855

Search completed: October 15, 2003, 23:04:22  
 Job time: 258.648 secs

GenCore version 5.1.6  
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Run on: October 15, 2003, 20:58:42 ; Search time 63.636 Seconds  
(without alignments)  
1588.358 Million cells updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282  
Perfect score: 1258  
Sequence: 1 IIRGECKPHSQPMQALFE.....GVYIKVKYVMIQETMKN 229

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cgn2.1/USPTO\_SPOOL\_P/US09856320/rn1at\_15102003.105826.10042/app.query.fasta\_1.846  
-DB-Issued Patents\_NA -OEWTF-fastap -SUFFIT-rn1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUEFT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09856320.ecgn.1.1.133-efrnat\_15102003.105826.10042 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6  
-FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*

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2: /cgn2.6/ptodata/2/ina/5B.COMB.seq:\*  
3: /cgn2.6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgn2.6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgn2.6/ptodata/2/ina/PCUUS.COMB.seq:\*  
6: /cgn2.6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1258	100.0	1192	3	US-08-944-483-8
2	1258	100.0	1292	4	US-09-205-258-189
3	1258	100.0	1314	4	US-09-025-059-2
4	1248	99.2	1146	4	US-09-205-258-247
5	1246	99.0	1166	3	US-08-944-483-7
6	1219.5	96.9	1052	4	US-09-386-642-10
7	1213	96.4	833	2	US-08-790-137-2
8	916.5	72.9	618	4	US-09-280-116-3
9	681	54.1	944	3	US-09-070-526-1
10	673	53.5	994	4	US-09-008-271A-19
11	671.5	53.4	1049	4	US-09-386-642-9
12	644.5	51.2	1570	4	US-09-996-243-308

C	13	634.5	50.4	1364	4	US-09-280-116-20	Sequence 20, Appl
	14	631.5	50.2	1476	2	US-08-824-874-2	Sequence 2, Appl1
	15	631.5	50.2	1476	3	US-09-210-084-2	Sequence 2, Appl1
	16	631.5	50.2	1476	4	US-09-764-762-2	Sequence 2, Appl1
	17	577.5	45.9	711	3	US-08-622-046B-13	Sequence 13, Appl
	18	577.5	45.9	711	3	US-09-100-264-2	Sequence 2, Appl1
	19	577.5	45.9	711	4	US-08-843-076D-2	Sequence 2, Appl1
	20	577.5	45.9	760	3	US-08-768-859A-7	Sequence 7, Appl1
	21	577.5	45.9	760	3	US-08-768-859A-7	Sequence 7, Appl1
	22	577.5	45.9	766	3	US-08-768-859A-9	Sequence 9, Appl1
	23	577.5	45.9	766	3	US-08-767-820A-9	Sequence 9, Appl1
	24	577.5	45.9	766	3	US-08-622-046B-17	Sequence 17, Appl
	25	577.5	45.9	766	3	US-09-100-264-6	Sequence 6, Appl1
	26	577.5	45.9	766	4	US-08-843-076D-6	Sequence 6, Appl1
	27	577.5	45.9	822	3	US-09-100-264-8	Sequence 8, Appl1
	28	577.5	45.9	832	3	US-08-768-859A-5	Sequence 5, Appl1
	29	577.5	45.9	832	3	US-08-767-820A-5	Sequence 5, Appl1
	30	577.5	45.9	832	3	US-08-622-046B-15	Sequence 15, Appl
	31	577.5	45.9	832	4	US-08-843-076D-4	Sequence 4, Appl1
	32	577.5	45.9	1341	4	US-08-983-075D-6	Sequence 6, Appl1
	33	577.5	45.9	1358	4	US-08-983-075D-8	Sequence 8, Appl1
	34	577	45.9	732	1	US-08-361-395-2	Sequence 2, Appl1
	35	577	45.9	897	2	US-08-956-267A-1	Sequence 1, Appl1
	36	574.5	45.7	711	3	US-08-622-046B-2	Sequence 2, Appl1
	37	574.5	45.7	766	3	US-08-622-046B-6	Sequence 6, Appl1
	38	574.5	45.7	832	3	US-08-768-859A-20	Sequence 20, Appl
	39	574.5	45.7	832	3	US-08-767-820A-20	Sequence 20, Appl
	40	574.5	45.7	832	3	US-08-622-046B-4	Sequence 4, Appl1
	41	573.5	45.6	760	5	PCT-US95-06157-7	Sequence 7, Appl1
	42	573.5	45.6	766	5	PCT-US95-06157-9	Sequence 9, Appl1
	43	573.5	45.6	832	5	PCT-US95-06157-5	Sequence 5, Appl1
	44	570	45.3	1504	4	US-09-280-116-1	Sequence 1, Appl1
	45	564	44.8	825	3	US-09-120-582-1	Sequence 1, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-944-483-8  
; Sequence 8, Application US/08944483  
; Patent No. 6232456  
GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLASS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROUPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: PASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

```
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1192 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-944-483-8

Alignment Scores:
Pred. NO.: 1.85e-123 Length: 1192
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-856-320a-2_COPY_54_282 (1-229) x US-08-944-483-8 (1-1192)
QY 1 llellelysglypnehlucylsProHisSerGlnProTrpGlnAlaIalaLeuPheGlu 20
Db 170 ATCATCAAGGGGTTGAGTGCAGTGCACCTCCAGCCCTGGCAGGAGCCCTTTGAG 229
QY 21 LysThrArgLeuLeuCySGlyAlaThrLeuIleAlaProArgTrpLeuThrAlaAla 40
Db 230 AAGACGGCGGTACTCTGTGGGCGACGCTCATCCGCCAGATGGCTCTGACAGCAGCC 289
QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyLinhIsanLeuGlnLysGluGlu 60
Db 290 CACTGCCTCAAGCCCGCTACATAGTTCACCTGGGCGACACAACCTCCAGAAAGAGAG 349
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
Db 350 GCGGTGAGCAGACCGGACAGCAGTCCCTCCGCCACCCGGGCTTCAACAAAGC 409
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 410 CTCGCCAACAAGACACCCCAATGACATCATGCTGTGAAGATGGCATGCCAGTCTCC 469
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db 470 ATCACTGGGCTGGCACCCTCACCCTCTCCACAGCTGTGTCACTGCTGGCACCAGC 529
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
Db 530 TGCCTATTTCGGGCTGGGCGACAGCTCCAGCCCCAGTTAGCGCTGCACACCTTG 589
QY 141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTrpProGlyAsn 160
Db 590 CGATGGCCCAACATCAACATCATTTGACACACAGAAAGTGAAGCGCTACCCGGGAC 649
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
Db 650 ATCACAACACCAATGGGTGTGCCAGGTGCAGAAAGGGGCAAGGACCTCGCAGGGT 709
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
Db 710 GACTCCGGGGCCCTCTGGTCTGTAACTCTCTTCAAGCATTAATCTCTGGGGCAG 769
QY 201 AspProCysAlaIleThrArgLysProGlyValTrpThrLysValCysLysTrpValAsp 220
Db 770 GATCCGGGTGCGATCAACCCGAAAGCGGTGTCTACACGAAAGTGTGCAAAATATGTGAC 829
QY 221 TrpIleGlnIuThrMetLysAsnAsn 229
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Db 830 TGCATCCAGGAGACGATGAAGAACAT 856
RESULT 2
US-09-205-258-189
Sequence 189, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
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EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 189  
LENGTH: 1292  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-205-258-189

Alignment Scores:  
Pred. No.: 2,096-123 Length: 1292  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-856-320a-2\_COPY\_54\_282 (1-229) x US-09-205-258-189 (1-1292)

QY 1 llellelysglyphglucyslyspromhsSerGlnProTTPGlnAlaAlaLeuPheGlu 20  
DB 270 ATCATCAAGGGGTTGAGTGCAGAGCTCACCACCCCTGCGAGGAGCCCTGTTCGAG 329  
QY 21 lvsThrArgLeuLeuGlyAlaThrLeuIleAlaProArgTTPLeuLeuThrAla 40  
DB 330 AAGAGCGGCTACTCTGTGGGCGAGGCTCATCGCCCGAGTGGCTCTGTACACAGCC 389  
QY 41 HsCysLeuLysProArgTyrIleValHsLeuGlyGlnHsAsnLeuGlnLysGlu 60  
DB 390 CACTGCCCTCAAGCCCCGCTACTAGTTCACCTGGGGCGACACACTCCAGAGAGGAG 449  
QY 61 GlyCysGluGlnThrArgThrAlaThrGlnSerPheProHsProGlyPheAsnAsnSer 80  
DB 450 GGCTGTGAGCAGACCCGGAGACAGCCACTGAGTCTCCCGACCCCGGCTTCAACAGAGC 509  
QY 81 LeuProAsnLysAspHsIleArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
DB 510 CTCCCAACAAAGACACCGCAGATGATCATGTGGTGAAGATGGCATCGGCACTTCC 569  
QY 101 lIeThrTPAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 570 ATCACTGGGCTGTGCGACCCCTCCTCCTCCTACGCTGTGTACTGTGCGACCGAC 629  
QY 121 CysLeuIleSerGlyTTPGlySerThrSerSerProGlnLeuArgLeuProHsThrLeu 140  
DB 630 TGYCTCATTTCCGGCTGGGGCGAGCAGTCACAGCCCGAGTTACGGCTGCATCACCTTG 689  
QY 141 ArgCysAlaAsnIleThrIleIleGlnHsGlnLysCysGluAsnAlaIleTyrProGlyAsn 160  
DB 690 CGATCGCCACATCATCATCATATGAGCAGCAAGAGTGTGAAGAGCGCTACCCCGGCAAC 749  
QY 161 lIeThrAspThrMetValCysAlaSerValGlnGluGlyGlyAspSerCysGlnGly 180  
DB 750 ATCAAGACACCATGTGTGTGCGCAGCTGCAGAGAGGGGGGAGGACTCTCTGCGAGGT 809

QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTTPGlyGln 200  
DB 810 GACTCCGGGGCCCTGTGTGTGTACAGATCTTCAAGGCAATATCTCGGGCCAG 869  
QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220  
DB 870 GATCGGTGTGCATTCACCCGAAAGCCTGTGTCTACAGAAAGTGTCAAAATGTGTGAG 929  
QY 221 TTPGlnGlnLThrMetLysAsn 229  
DB 930 TGATCCAGAGACGATGAGAACAAAT 956

RESULT 3  
US-09-025-059-2  
Sequence 2, Application US/09025059  
Patent No. 6075136  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA

COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,059  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0481 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1314 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGUT10  
CLONE: 2723646  
US-09-025-059-2

Alignment Scores:  
Pred. No.: 2,146-123 Length: 1314  
Score: 1258.00 Matches: 229  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-09-856-320a-2\_COPY\_54\_282 (1-229) x US-09-025-059-2 (1-1314)

QY 1 llellelysglyphglucyslyspromhsSerGlnProTTPGlnAlaAlaLeuPheGlu 20  
DB 287 ATCATCAAGGGGTTGAGTGCAGAGCTCACCACCCCTGCGAGGAGCCCTGTTCGAG 346





NAME/KEY: SITE  
LOCATION: (35)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (36)  
OTHER INFORMATION: n equals a,t,g, or c  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (37)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-205-258-247

Alignment Scores:  
Pred. No.: 1.98e-122 Length: 1146  
Score: 1248.00 Matches: 227  
Percent Similarity: 99.13% Conservative: 0  
Best Local Similarity: 99.13% Mismatches: 2  
Query Match: 99.21% Indels: 0  
Gaps: 4

US-09-856-320a-2\_COPY\_54\_282 (1-229) x US-09-205-258-247 (1-1146)

OY 1 llellelysglypneglucyslyspnohisserginprotrpglnalaleupheglu 20  
DB 124 ATCATCAAGGGGTTGAGTGCAGAGCTCCTCCAGCCCTGGCAGGAGCCCTGTTGAG 183  
OY 21 lvsftrargleuLeucysglyAlaThrleuilealaproargtrpleuLeuThrala 40  
DB 184 AAGACGGCGCTACTCTGTGGGGCGAGCTCATCGCCCAAGATGGCTCTGCACAGCACC 243  
OY 41 HiscysleuLysProargTyrIleValHisleuglylnHlsasnleuglnLysglu 60  
DB 244 CACTGCTCAAGCCCGCTGATAGTTCACCTGGGGCAGCAGCCTCCAGAGAGAGAG 303  
OY 61 GlycysgluInthrargThralaThrIuSerPheProHisProGlyPheasnanser 80  
DB 304 GCGTGTGAGCAGACCCGAGCAGCCCTGAGTCTTCCCCACCCCGGCTTCAACACAGC 363  
OY 81 LeuproasnLysAspHisArgAsnAspIleMetleuValLysMetAlaSerProvalSer 100  
DB 364 CTCCCAACAAAGACACACCGCATGATGATGCTGGAGAGATGGATCGCAGTCTCC 423  
OY 101 IlerhtrpAlaValArgProleuThleuserSerArgCysValThAlaGlyThrser 120  
DB 424 ATCACTGGGCTGTGGCAGCCCTCCTCTCCACCTGTGTCACCTGTGGCAGCAGC 483  
OY 121 CysleuileSerGlyTTPGlySerThrSerSerProginleuArgleuProHisThrleu 140  
DB 484 TGCTCATTTCCGGCTGGGGCGAGGCTCAGCCCGCTTACGCTCTCCACACCTTG 543  
OY 141 ArgCysAlaAsnIleThrIleIleIuHiscLysCysgluAsnAlaTyrProglyasn 160  
DB 544 SGATGGCGCAACATCAGCATCTGAGCAGCAGAGTGTGAAGCGCTTACCCCGCAGC 603  
OY 161 IlerhtrpIleMetValCysAlaSerValGlnGlyLysAspSerCysGlnGly 180  
DB 604 ATCAAGAGACCAATGTTGTGTCCAGCTGAGAGAGGGCGCAAGAGATCTCTGCAAGGGT 663  
OY 181 AspergilyglyProleuValCysasnGlnSerleuglnGlyIleIleSerTTPGlyln 200  
DB 664 GACTCGGGGGCCCTGTGTGTGTAACAGTCTTCAAGGCAATTAATCTCTGGGGCAG 723  
OY 201 AspProCysAlaIleThrArgLysProglyValTyrThrLysValCysLysTyrValasp 220  
DB 724 GATCGGTGTGGATCAGCAGCCGAAAGCTGTCTACAGAAAGTCTGCAATATCTGAC 783  
OY 221 TTPleuglnIuThrMetLysasn 229  
DB 784 TGGATCCAGAGAGATGAGAGACAT 810

RESULT 5  
US-08-944-483-7

Sequence 7, Application US/08944483  
Patent No. 6232456  
GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLASS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STEWART, KENT D.  
APPLICANT: STROUPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
NUMBER OF INVENTION: OF THE PROSTATE  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESS: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183-US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1166 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-944-483-7

Alignment Scores:  
Pred. No.: 3.31e-122 Length: 1166  
Score: 1246.00 Matches: 227  
Percent Similarity: 99.13% Conservative: 0  
Best Local Similarity: 99.13% Mismatches: 2  
Query Match: 99.05% Indels: 0  
Gaps: 3

US-09-856-320a-2\_COPY\_54\_282 (1-229) x US-08-944-483-7 (1-1166)

OY 1 llellelysglypneglucyslyspnohisserginprotrpglnalaleupheglu 20  
DB 166 ATCATCAAGGGGTTGAGTGCAGAGCTCCTCCAGCCCTGGCAGGAGCCCTGTTGAG 225  
OY 21 lvsftrargleuLeucysglyAlaThrleuilealaproargtrpleuLeuThrala 40  
DB 226 AAGACGGCGCTACTCTGTGGGGCGAGCTCATCGCCCAAGATGGCTCTGCACAGCACC 285  
OY 41 HiscysleuLysProargTyrIleValHisleuglylnHlsasnleuglnLysglu 60  
DB 286 CACTGCTCAAGCCCGCTGATAGTTCACCTGGGGCGAGCAGCAGCTCCAGAGAGAG 345  
OY 61 GlycysgluInthrargThralaThrIuSerPheProHisProGlyPheasnanser 80

Db	346	GGCGTGTGAGCAGACCCGGACAGCAGCATGTAGTCTTCCGCCACCCGGCTTCAACACAGC	405
Qy	81	LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer	100
Db	406	CTCCCCACAAACACACCCGCCAATGCATCATCTGTGTGAGATGGCATTCGCCAGTCTCC	465
Qy	101	IleThrTrpAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer	120
Db	466	ATACACCTGGGCTGTGGACCCCTCAACCCCTCTCTACCGCTGTGCATCTGGGACACAGC	522
Qy	121	CysLeuLeuSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu	140
Db	526	TGCTCATTTCCGGCTGGGGGACAGCTACACCCCACTTACGCTCTCTCAACACTTG	585
Qy	141	ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn	160
Db	586	CGATGGCCCAATCATCATATTGTGAGCCACGAAGTGTGAGAACGCTTACCCCGGCACAC	645
Qy	161	IleThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAspSerCysGlnGly	180
Db	646	ATCACACACACATGTGTGTGTGTGCCACGCTGCACGACGAAGGGGCGAAGACTCTCTCCACGGT	705
Qy	181	AspSerGlyGlyProLeuValLysAsnGlnSerLeuGlnGlyIleLeuSerTrpGlyGln	200
Db	706	GACTCGGGGGCCCTTGGTCTGTGAACCACTCTTCAAGGCAATATATCTCTGGGGCCAG	765
Qy	201	AspProCysAlaIleThrArgLysProGlyValIleTyrThrLysValCysLysTyrValAsp	220
Db	766	GATCCGCGTGCATACACCCGAAGACCTGGTGTCTACACGAAGAAGTCTGCATAATATGTGGAC	825
Qy	221	TrpIleGlnGluThrMetLysAsnAsn	229
Db	826	TGGATCCAGGACGATGAAGAACAT	852

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RESULT 6
US-09-386-642-10
; Sequence 10, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: OMT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1052
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: With homo sapien serine protease catalytic domain
US-09-386-642-10

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Alignment Scores:	
Pred. No.:	1,78e-119
Score:	1219, 50
Percent Similarity:	98/268
Best Local Similarity:	96,968
Query Match:	96,94%
DB:	4
	Gaps: 1
	Length: 1055
	Matches: 223
	Conservative: 3
	Mismatches: 3
	Indels: 1
	Gaps: 1

US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-09-386-642-10 (1-1052)

QY 1 HlellellyGlyphelulucys---LysProHissSerGlnProTTPGlnAlaAlaLeuPhe 19  
 166 ATCGTTGGGGGGGACACACTGCTCTACAAAAAGCACTCCAGCCCTGGACAGCCCTGTTC 225  
 QY 20 GlnUlyThrArgleuLeuCySclYalathrIleuIlealProAlqTTPleuLeuThrAla 39

Db	226	GAGAAAGACGGGGCTACTGTGTGGGGGAGACGCTCATCGCCGCCAGATGGCTCTGACAGCA	285
Qy	40	AlAHIScysLeuLysProArgTyrIleValHISLeuGIyGINHISAsnLeuGINLysGIu	59
Db	286	GCCCACTGCTCTCAAGCCCGCTACATAGTCAACCTGGGGGAGCAACCTCCGAAAGGAG	345
Qy	60	GIuGIcysseGIuGINHrArgrHrIaThrGusErPheProHISProGIyPheAsn	79
Db	346	GAGGGCTGTGAGAGACCGCGACACCACTAGTGTCTTCCCCACCCCGGCTTCACAC	405
Qy	80	SerLeuProAsnLysAspHISArgAsnSPIIeMetLeuValLysMetIaSerProVal	99
Db	406	AGCCTCCCAACAAACACCCGCAATGCATCAAGCTGTGGAAGATGGCATGCGCCAGTC	465
Qy	100	SerIleThrTryAlaValArgProLeuHrLeuSerSerArgCysValIThrAlaGIYThr	119
Db	466	TTCATCACTGGGCTGTGGACCCCTCAACCTCTCTCTACCTGTGTACCTGTGGACCC	525
Qy	120	SerCysLeuIleSerGIYTrpGIYSerThrSerSerProGlnLeuArgLeuProHISThr	139
Db	526	AGCTGCTCAATWTCGGGCTGTGGGGGAGCACTCCAGCCCGCCAGTACCCCTGCACACCC	585
Qy	140	LeuArgCysAlaAsnIleHrIleIleGINHISGINLysCysGIuAsnAlaIYTrpProGIy	159
Db	586	TTTCGATGGCCCAATCACTCACTATTAGACCAAGAAAGTGTGAAGACGCTTACCCGGG	645
Qy	160	AsnIleThrAspThrMetValCysAlaSerValGINLugINLysGIYLysAspSerCysGIN	179
Db	646	AMCATACAGACACCCTATGGTGTGTGTCCAGCGGCGAGAAAGGGGGCAAGACTCTGCCAG	705
Qy	180	GIYAspSerGIYGIYProLeuValCysAsnGINserLeuGINLysIleIleSerTrpGIy	199
Db	706	GGGACTCCGGGGGCCCTCTGGTCTGTAAACAGTCTCTTCAGGCAATTATCTCTGGGGC	765
Qy	200	GlnAspProCysAlaIleThrArgLysProGIYAlaYTrpLysValCysLysYVal	219
Db	766	CAGGATCTCGTGTGCATCAACCGAAGAGCTGGTGTCTACAGAAAGTCTCAATATATGTC	825
Qy	220	AspTrpIleGlnGIuThrMetLysAsn	229
Db	826	GACTGGATCCAGAGACGATGAAGAACAT	855

RESULT 7  
 US-08-790-137-2  
 : Sequence 2, Application US/08790137  
 : Patent No. 5840871  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Hillman, Jennifer L.  
 : APPLICANT: Goll, Surya K.  
 : TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED  
 : TITLE OF INVENTION: KALLIKREIN  
 : NUMBER OF SEQUENCES: 4  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 31/4 Porter Drive  
CITY: Palo Alto  
STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE  
MEDIUM

MEDIUM TYPE:

COMPUTER: IBM

OPERATING SITS  
SOFTWARE: Fa

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CURRENT ADPTICA

CONSENT HEREIN  
APPLICATION N

ESTIMATING DATE:

CLASSIFICATIO

PRIOR APPLICATI

## APPLICATION N

FILING DATE:

ATTORNEY/AGENT

NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0195 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 833 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-790-137-2

## Alignment Scores:

Pred. No.:	6,09e-119	Length:	833
Score:	1213.00	Matches:	219
Percent Similarity:	97.82%	Conservative:	5
Best Local Similarity:	95.63%	Mismatches:	5
Query Match:	96.42%	Indels:	0
DB:	2	Gaps:	0

US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-08-790-137-2 (1-833)

QY 1 llelelelysglypnehlucyslypProhisSerGlnProTTPGlnAlaAlaLeupheglu 20  
DB 99 ATTTGGGGAGGCTGGAGTGTGAGCAGCATTCGCCGCTGGAGGGCTGTGTACAG 158  
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTTPLeuThrAlaAla 40  
DB 159 AAGACGGCGCTACTCTGTGGGGCGACGTCATNGCCCCACAGTGGTCTTGAACAGCACCC 218  
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLysGlnlu 60  
DB 219 CACTGACCTNAGACCCCGCTACATAGTTCACTGGGGCGACAACTCAGAGAGAGAG 278  
QY 61 GlyysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 80  
DB 279 GGGCTGTGAGACCCCGACAGCCACTGAGTCTTCCCCACCCGGCTTCAACMAACAGC 338  
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100  
DB 339 CTCCCAACAAAGACACCCGCAATGACATGCTGGTGAAGATGGCATGCCAGCTTCC 398  
QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120  
DB 399 ATCACTGGGCTGTGCGACCCCTCACCTCTCCACGCTGTGTACACTGGCGACACAGC 458  
QY 121 CysLeuIleSerGlyTTPGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140  
DB 459 TGCTTCATTTCCGGCTGGGCGACAGCTCCAGCCCCAGTTACGCTCTCACACACTTG 518  
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnuAsnAlaTyrProGlyLysn 160  
DB 519 CGATGGCCCAACATCACCATCATTTGACACCAAGATGTGAAAGCGCTTACCCGGCGAC 578  
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180  
DB 579 ATCACAAGACACCATGATGTGTGCGACGCTGCAGAAAGGGGCGCAAGGACTCTGCAGAGGT 638  
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTTPGlyGln 200  
DB 639 GACTTCGGGGGCGCTGTGTGTGTACAGTCTTCAAGGCAATATCTCTGGGGCGAG 698  
QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220  
DB 699 GATCCGCTGTGATCACCCGAAAGCTGTGTCTTACACGAAAGTCTGCAAAATATGTGGAC 758  
QY 221 TTPleGlnGlnThrMetLysAsnAsn 229  
DB 759 TGGATCCAGAGAGCATGAAGAACAT 785

RESULT 8

US-09-280-116-3  
; Sequence 3, Application US/09280116A  
; Patent No. 6331427  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs  
; FILE REFERENCE: 5800-24, 035800/176965  
; CURRENT APPLICATION NUMBER: US/09/280,116A  
; CURRENT FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 268  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 618  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: trypsin-like serine proteases  
US-09-280-116-3

## Alignment Scores:

Pred. No.:	7.8e-88	Length:	618
Score:	916.50	Matches:	184
Percent Similarity:	90.78%	Conservative:	3
Best Local Similarity:	89.32%	Mismatches:	4
Query Match:	72.85%	Indels:	16
DB:	4	Gaps:	2

US-09-856-320A-2\_COPY\_54\_282 (1-229) x US-09-280-116-3 (1-618)

QY 23 ArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTTPLeuThrAlaAlaHisCys 42  
DB 2 CGGCTACTCTGTGGGGCGACCC---TCATCGCTCTGAGATGGCTCCGACAGCCACCTG 58  
QY 42 sLeuLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLysGlnGlnGlyCys 62  
DB 59 CCTCAAGCCCGCTTCAATAGTTCACTGGGGCGACCAACCTCCAGAAAGAGAGAGGCTG 118  
QY 62 sGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuPr 82  
DB 119 TGAGCAGACCCGGACAGCCACTGAGTCTTCCCCACCCGGCTTCAACMAACAGCTTCC 178  
QY 82 ObsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProVal-SerIleT 102  
DB 179 CAACAAAGACACCGCAATGACATGCTGTGTAAGATGGCATGCCAGTGTCTCATCA 238  
QY 102 hTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysL 122  
DB 239 CTTGGGCTGTGCGACCCCTCACCTCTCTCATGCTGTGTACACTGGCGACACAGCTGCC 298  
QY 122 euIleSerGlyTTPGlySerThrSerSerProGlnLeuArgLeuProHisThrLeuArgC 142  
DB 299 TCATTTCGGCTGGGGCGACAGCTCCAGCCCACTTACGCTGTGTACACCTTGGCAT 358  
QY 142 ysaAlaAsnIleThrIleIleGlnHisGlnLysCysGlnuAsnAlaTyrProGlyLysnIleT 162  
DB 359 GCGCCAAACATCACCATCATTTGACACCAAGATGTGAAAGCGCTTACCCGGCGACATCA 418  
QY 162 hAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGlyLys 182  
DB 419 CAGAACCATGATGTGTGCGACGCTGAAGAGAGGGGCGCAAGACTCTGCCAA----- 471  
QY 182 erGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTTPGlyGln 201  
DB 472 -----GCTCTTC-AAAGCATATATCTCTGGGGCGCAAGAC 507  
QY 202 -ProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAspTr 221  
DB 508 TCCGTGTGCGATCACCCGAAAGCTGTGTCTTACACGAAAGTCTGCAAAATATGTGGACTG 567  
QY 221 PileGlnGln 224  
DB 568 GATCCAGGAA 577



```

;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 994 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;     LIBRARY: COLANOT27
;     CLONE: 1798496
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 19 :
US-09-008-271A-19

Alignment Scores:
Pred. No.:      8,1e-62      Length:      994
Score:          673.00      Matches:      115
Percent Similarity: 70.09%   Conservative: 42
Best Local Similarity: 51.34% Mismatches:    65
Query Match:     53.50%     Indels:        2
DB:              3          Gaps:          2

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-008-271A-19 (1-994)

QY      1  l l e l l e l y s g l y p h e g l u c y s l y s p r o h i s s e r g i n p r o t r p g l a l a l a l e u p h e g l u
Db      251  G T G C T G G G G G C A T G A G T G C C A A C C C A T T G C A G C C T T G G C A G G C G C C T T G T G C C A G
QY      21  l y s t h r a t g l e u l e u c y s g l y a l a t h r l e u l e a l a p r o a r g t r p l e u l e u t h r l a a l a
Db      311  G G C C A G C A A C T A C T C T G T G C G T G C C T G T A G G T G G C A A C T G G G C C T T A C A C A C T G C C
QY      41  h i s c y s l e u l y s p r o a r g t y r l l e v a l h i s l e u g l y g i n h i s a s n l e u g l i n l y s g l u
Db      371  C A C T G T A A A A A A C C G A A A T A C A C A G T A C C C T G G A G C A C C A C C C T G T A C A A C A G A A T A A A T
QY      61  g l y c y s g l u g i n t h r a r g t h r a l a t h r g l u s e r p h e p r o h i s p r o g l y p h e a s n a n s e r
Db      431  G G C C C A G A G A A A A T A C C T G T G T C A G T C C A T C C C A C A C C C C T G T A C A A C A G C A G C
QY      81  l e u p r o a n l y s a s p h i s a r g a s n a s p i l e m e t l e u a l l y s m e t a l a s e r p r o v a l s e r
Db      491  - - - G A T G T G A G G A C C A C C A M C C A G A N C T G A T G C T T T C A A C T G C C T G A C C A G G C A T C C
QY      101  l l e t h r t r p a l a v a l a r g p r o l e u t h r l e u s e r s e r a r g y s v a l t h r a l a g l y t h r s e r
Db      548  C T G G G G T C C A A G A G A A A T A C C T G T G C A G C A G A T C T T C A C C C A C C C T G G C C A G A G
QY      121  c y s l e u l e s e r g l y t r p g l y s e r t h r s e r s e r p r o g l i n l e u a r g l e u p r o h i s t h r l e u
Db      608  T G C A C C G T C A G G C T G G G C A C T G T C A C C A G T C C C C G A G A A T T T T C C T G A C A C T G T C
QY      141  a r g y s a l a s n i l e t h r l l e i l e g l u h i s g l i n l y s c y s g l u a s n a l a t y r p r o g l y a s n
Db      668  A A C T G T C A G A A G T A A A A A T C T T T C C C A G A A A G T G A G A T G C T T A C C C G G G C A G
QY      161  l l e t h r a s p t h r m e t v a l c y s a l a s e r v a l g i n g l y g l y l y s a s e r c y s g l i n g l y
Db      728  A T C A C A G A T G C A G G T C T G T G C A G C A G C A G C A A A G G G C T - - - G A C A C T G C C A G G C
QY      181  a s p s e r g l y g l y p r o l e u a l c y s a n g l i n s e r l e u g l i n g l y l l e i l e s e r t r p g l y g l n
Db      785  G A T T C T G A G G C C C C C T G T G T G A T G T C A C T C C A G G G C A T C A C A T C C T G G G G C A
QY      201  a s p r o c y s a l a l e t h r a r g l y s p r o g l y a l t y r t h r l y s v a l c y s l y s t y r v a l a s p
Db      845  G A C C C T G T G G A G A G T C C G A C A A C C T G G G T A T A C C A A C A T C G C C G T A C T G A C
QY      221  t r p l l e g l i n l u 224
Db      905  T G G A T C A A G A A G 916

RESULT 11
US-09-386-642-9
; Sequence 9, Application US/09386642
; Patent No. 6420157
```

```

;
; GENERAL INFORMATION:
;   APPLICANT: Darrow, Andrew
;   APPLICANT: Qi, Jensen
;   APPLICANT: Andrade-Gordon, Patricia
;   TITLE OF INVENTION: Zymogen Activation System
;   FILE REFERENCE: ORT-1028
;   CURRENT APPLICATION NUMBER: US/09/386,642
;   NUMBER OF SEQ ID NOS: 60
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO: 9
;   LENGTH: 1049
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
;   OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-9

Alignment Scores:
Pred. No.:      1,26e-61      Length:      1049
Score:          671.50      Matches:      116
Percent Similarity: 70.22%   Conservative: 42
Best Local Similarity: 51.56% Mismatches:    64
Query Match:     53.38%     Indels:        3
DB:              4          Gaps:          3

US-09-856-320A-2_COPY_54_282 (1-229) x US-09-386-642-9 (1-1049)

QY      1  l l e l l e l y s g l y p h e g l u c y s - - - l y s p r o h i s s e r g i n p r o t r p g l a l a l a l e u p h e
Db      166  A T C G T T G G G C C T A C A C T G T C T A G A C C C A T T G C A G C C C T T G G C A G G C G C C T T G T C
QY      20  g l u y s t h r a r g l e u l e u c y s g l y a l a t h r l e u l e a l a p r o a r g t r p l e u l e u t h r l a
Db      226  C A G G C C A G C A A C T A C T G T G C G G T C C T T G A G G T G C A A C T G G G C C T T A C A C C T
QY      40  a l a h i s c y s l e u l y s p r o a r g t y r l l e v a l h i s l e u g l y g i n h i s a s n l e u g l i n l y s g l u
Db      286  G C C C A C T G T A A A A A C C G A A A T A C A C A G T A G C C C T G G A G A C A C A C C C T A C A G A T A A A
QY      60  g l u g l y c y s g l u g i n t h r a r g t h r a l a t h r g l u s e r p h e p r o h i s p r o g l y p h e a s n a n
Db      346  G A T G C C C A G A G A A A A T A C C T G T G T T A C C A C C C A C A C C C C T G T A C A A C A G C
QY      80  s e r l e u p r o a n l y s a s p h i s a r g a s n a s p i l e m e t l e u a l l y s m e t a l a s e r p r o v a l
Db      406  A G C - - - G A T G T G A G A G A C C A C A C A C A T G A T G A T G C T T T C A A C T G C T G A C C A G G C A
QY      100  s e r l e t h r t r p a l a v a l a r g p r o l e u t h r l e u s e r s e r a r g y s v a l t h r a l a g l y t h r
Db      463  T C C C T G G G G T C C A A A G T A G A C C C A T C A G C T G G A G A T C A T T G A C C C A C C C T G G C C A G
QY      120  s e r c y s l e u l e s e r g l y t r p g l y s e r t h r s e r s e r p r o g l i n l e u a r g l e u p r o h i s t h r
Db      523  A A G T G A C C G T C A G G C T G G G C A C T G T C A C A G T C C C C A G A G A A T T T T C C T G A C A C T
QY      140  l e u a r g y s a l a s n i l e t h r l l e i l e g l u h i s g l i n l y s c y s g l u a s n a l a t y r p r o g l y
Db      583  C T A C A C T G C A G A A G T A A A A T C T T T C C C A G A A G A G T G A G A T G C T T A C C C G G G C
QY      160  a s n i l e t h r a s p t h r m e t v a l c y s a l a s e r v a l g i n g l y g l y l y s a s e r c y s g l i n
Db      643  C A G A T C A C A G A T G C A G G T C T G T G C A G C A G C A G A A A G G G C T - - - G A C A C T G C C A G
QY      180  g l y s p s e r g l y g l y p r o l e u a l c y s a n g l i n s e r l e u g l i n g l y l l e i l e s e r t r p g l y
Db      700  G C C A T T C T G A G G C C C C C T G T G T G A T G T C A C T C C A G G G C A T C A C A T C C T G G G G C
QY      200  g l i n a s p p r o c y s a l a l e t h r a r g l y s p r o g l y a l t y r t h r l y s v a l c y s l y s t y r v a l
Db      760  T C A G A C C C C T G T G G A G A G T C C G A C A A C C T G G C C T T A T A C A A C A T C T G C C G T A C C T G

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OY 220 AsptfplecInclu 224  
Db 820 GACTGATCAAGAAG 834  
RESULT 12  
US-09-996-243-308  
Sequence 308, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028

PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22



Percent Similarity: 64.82% Conservative: 41  
 Best Local Similarity: 48.62% Mismatches: 60  
 Query Match: 50.44% Indels: 29  
 DB: 4 Gaps: 3

US-09-856-320a-2\_COPY\_54\_282 (1-229) x US-09-280-116-20 (1-1364)

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QY      4  GlyPheGluCysLysProHisSerGlnProTyrGlnAlaAlaLeuPheGluCysThrArg 23
      828 GGGTACACCTGGCTCCCTCCACTCTCACCCCTGGAGGCTGCTCTACTAGTGAAGGCGG 769
      24  LeuLeuCysGlyAlaThr-LeuIleAlaProArgTyrPheLeuThrAlaHisCysLe 43
      768 CTACTCTGTGGGGAATCTCTGGTCCACCCCAATGGGCTCTCTGCTCCGACCTGTCT 709
      43  uLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLysGluGluCysG1 63
      708 AAAGGAGGCGCTCAAGATTACTAGGCAAGCAAGCCCTAGGGGCTGTGAAGCTGTGCA 649
      63  uGlnThrArgTyrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAs 83
      648 GCAGGTGAGGGAAGTTGTCCACTCTATCCCTCCGTAATACCGAGAGACCCACCA 589
      83  nLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTr 103
      588 CCGAACACCAACACCATACATCATGCTGTGGAGCTGACAGTCCCGGCTCCAGCTCACAG 529
      103  palValAlaArgProLeuThrLeuSer---SerArgCysValThrAlaGlyThrSerCysLe 122
      528 CTACATCCAAACCTGCGCTTCCCAACAACACCGCTTAACCGCTGGACACACCTGTGC 469
      122  uLieserGlyTyrGlySerThrSerSerProGln-----LeuArg 135
      468 GGTGTCTGGCTGGGACACACACACCGGATGATCCACACACAGTGTGCTGAG 409
      135  g-----Le 136
      408 GCCCATAGAGAGTGGCTGGGGAACAGGCGGACAGATGGAGGGAAGTCTGATGTAAT 349
      136  uProHis-ThrLeuAlaGlyAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsn 156
      348 ACCCCAAACCTCATCATGTCGCAACATCCACTGCTCAGATGAGAGAGTGTGTCGACAG 289
      156  LatyrProGlyAsnIleThrAspThrMetValLysAlaSerValGlnGluGlyLysA 176
      288 TCTACCCGAGGAAGATCATGACACACATGTTGTGTGCGGCAACAAAGAGGCTGGCAAG 229
      176  spSerCysGlnGlyAspSerGlyLysProLeuValCysAsnGlnSerLeuGlnGlyTyr 196
      228 ACTCTGTGAGGCTGACTCTGGGGGCGCCCTGCTGTAAACACACACTGTATGGCATCG 169
      196  LeSerTyrPheGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValC 216
      168 TCTCTGGGAGAGACTTCCCATGTGGGCAACCTGACCGGCTGTGTCTACACCGGTGTCT 109
      216  yslYsTyrValAspTyrPheGlnGlnGlnThrMetLys 227
      108 CAAGATACGTCGTGTGATCCGTGAACAATCCGA 74
  
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# RESULT 14

US-08-824-874-2  
 ; Sequence 2, Application US/08824874  
 ; Patent No. 5962300  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Lal, Preeti  
 ; TITLE OF INVENTION: NOVEL KALLIKREIN  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Inocyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA

```

: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/824,874
: FILING DATE: Filed Herewith
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0252 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1476 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: KERN40702
: CLONE: 820694
  
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## Alignment Scores:

Score: 3,53e-57 Length: 1476  
 Pred. No.: 631.50 Matches: 117  
 Percent Similarity: 67.67% Conservative: 40  
 Best Local Similarity: 50.43% Mismatches: 67  
 Query Match: 50.20% Indels: 8  
 DB: 2 Gaps: 4

US-09-856-320a-2\_COPY\_54\_282 (1-229) x US-08-824-874-2 (1-1476)

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QY      1  IleIleLysGlyPheGluCysLysProHisSerGlnProTyr-GlnAlaAla---LeuPh 19
      475 ATCATCAATGGAATCCAGCTGCGATATGACACCCAGCGGCGGACAGGCGCTGTGCT 534
      19  eGluLysThrArgLeuLeuGlnGlyAlaThrIleAlaProArgTyrPheLeuThrAl 39
      535 AAGGCCCAACCACTTACTGCGGGCGGCTGTGTGTCATCCACAGTGGCTGTCCAGCG 594
      39  aAlaHisCysLeuLysProArgTyrIleValHisLeuGlnHisAsnLeuGlnLys-- 58
      595 CGCCCACTGGAGGAAGATTCTCAGAGTCGCTCGGCACTACTCCCTGTCCACAT 654
      59  -GluGluGlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAs 78
      655 TTAATGATCTGGGACACAGATGTTCCAGGGGGTCAATATCCATCCCGCTGGTACTTC 714
      78  nAsnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerPr 98
      715  C-----CACCTGGCCACTCTTAACGACTCATGCTCATTAACAACTGAACAGAG 762
      98  oValSerIleThrTyrPheValAlaArgProLeuThrLeuSerSerArgCysValThrAlaG1 118
      763 AATTCGTCACCAATGAAGATGTAGACCAATCAACGCTCTCTCATATGCTCCCTGTGCTG 822
      118  yThrSerCysLeuIleSerGlyTyrPheLysThrSerSerProGlnLeuArgLeuProH1 138
      823 GACAAAGTCTTGTGCTCGGCTGGGGAACACCAAGACCCCAAGTGCATCTCCCTTA 882
      138  sThrLeuArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrPr 158
      883 GGTCTCCAGTCTTGAATATCATGCGTGTGAAGTGAAGAAAGTGGAGATGCTTACCC 942
  
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QY 158 oGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyAspSerCy 178  
 Db 943 GAGACAGATGATGACACCATGTTCTGCGCCGGT---GACAAAGCAGGTAGACTCTCG 999  
 QY 178 sGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleLeuSerTr 198  
 Db 1000 CCAGGATGATCTGGGGGCGCTGTGCTGCATAGCTCCCTGCGAGGAGCTGCTGCTG 1059  
 QY 198 pGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTy 218  
 Db 1060 GGGAGATTACCTTGTGCGCGGCCCAACAGACCGGGGTGTCTACAGGAACCTCTGCAAGTT 1119  
 QY 218 rValAspTrpIleGlnGluThrMetLysAsnAsn 229  
 Db 1120 CACCAAGTGATCCAGAAACCATCCAGGCCAAC 1153

## RESULT 15

US-09-210-084-2  
 ; Sequence 2, Application US/09210084  
 ; Patent No. 6197511  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Lal, Preeti  
 ; TITLE OF INVENTION: NOVEL KALLIKREIN  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/210,084  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/824,874  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; TELEPHONE: 415-855-0555  
 ; TELEFAX: 415-845-4166  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1476 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: KERANOT02  
 ; CLONE: 820694  
 ; US-09-210-084-2

Alignment Scores:  
 Pred. No.: 3.53e-57 Length: 1476  
 Score: 631.50 Matches: 117  
 Percent Similarity: 67.67% Conservative: 40  
 Best Local Similarity: 50.43% Mismatches: 67  
 Query Match: 50.20% Indels: 8  
 DB: 3 Gaps: 4

US-09-856-320a-2\_COPY\_54\_282 (1-229) x US-09-210-084-2 (1-1476)

QY 1 IleIleGlyGlyPheGluCysLysProHisSerGlnProTrp-GlnAlaAla---LeuPh 19  
 Db 475 ATCATCAATGATCCGACTGATATGACACCCAGCCGTGGGAGCGCCGTGTGCT 534  
 QY 19 eGluLysThrArgLeuLeuCysGlyAlaLeuIleAlaProArgTrpLeuThrAl 39  
 Db 535 AAGGCCCAACAGCTCTTACTGCGGGGGGTGTGTGGTCATCCACAGTGGCTCTCAGCGC 594  
 QY 39 AlaHisCysLeuLysProArgTrpIleValHisLeuGlnHisAsnLeuGlnLys-- 58  
 Db 595 CGCCACATCAGAGAAAGTTTCAGACTCCGTCTCGGCCACTACTCCCTTCAACACT 654  
 QY 59 -GluGluGlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAs 78  
 Db 655 TTATGATCTGGGAGACAGATGTTCCAGGGGGTCAAAATCCATCCACCCCGCTGTACTC 714  
 QY 78 nasnSerLeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerP 98  
 Db 715 C-----CACCTGGCCACTTACACGACTCATGCTCATCAACCTGAACAGAAAG 762  
 QY 98 oValSerIleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGl 118  
 Db 763 AATTGTCCTCACTAAAGATGTCAGACCCATCAAGCTCTCTCATTTGTCCCTGTGCTG 822  
 QY 118 yThrSerCysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProH 138  
 Db 823 GACAAAGTCTTGCTGGCTCGCGCTGGGGGACAAAGACCCCAAGTGCACCTTCCCTTA 882  
 QY 138 sThrLeuArgCysAlaAsnIleThrIleLeuHisGlnLysCysGlnAsnAlaTyrPr 158  
 Db 883 GGTCTCTCACTGCTGAATATCAGCGTGTAACTCAGAAAGTGTGAGATGCTTACCC 942  
 QY 158 oGlyAsnIleThrAspThrMetValCysAlaSerValGlnGluGlyGlyAspSerCy 178  
 Db 943 GAGACAGATGATGACACCATGTTCTGCGCCGGT---GACAAAGCAGGTAGACTCTCG 999  
 QY 178 sGlnGlyAspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleLeuSerTr 198  
 Db 1000 CCAGGATGATCTGGGGGCGCTGTGCTGCATAGCTCCCTGCGAGGAGCTGCTGCTG 1059  
 QY 198 pGlyGlnAspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTy 218  
 Db 1060 GGGAGATTACCTTGTGCGCGGCCCAACAGACCGGGGTGTCTACAGGAACCTCTGCAAGTT 1119  
 QY 218 rValAspTrpIleGlnGluThrMetLysAsnAsn 229  
 Db 1120 CACCAAGTGATCCAGAAACCATCCAGGCCAAC 1153

Search completed: October 15, 2003, 21:09:06  
 Job time : 69.636 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OK protein - protein search, using sw model

Run on: October 15, 2003, 20:58:02 ; Search time 20.6145 Seconds  
(without alignments)  
1789.927 Million cell updates/sec

Title: US-09-856-320A-2\_COPY\_54\_282

Perfect score: 1258  
Sequence: 1 IIRGECKPHSQPWQALFE.....GVYTKCKYVDIQTNN 229

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/PCR\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/1/pubppaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	100.0	250	11	US-09-946-374-170
2	1258	100.0	250	12	US-10-015-387A-170
3	1258	100.0	250	12	US-10-137-870-506
4	1258	100.0	250	12	US-10-140-018-506
5	1258	100.0	250	12	US-10-140-021-506
6	1258	100.0	250	12	US-10-140-274-506
7	1258	100.0	250	12	US-10-140-471-506
8	1258	100.0	250	12	US-10-140-807-506
9	1258	100.0	250	12	US-10-140-822-506
10	1258	100.0	250	12	US-10-140-924-506
11	1258	100.0	250	12	US-10-140-926-506
12	1258	100.0	250	12	US-10-141-698-506
13	1258	100.0	250	12	US-10-141-702-506
14	1258	100.0	250	12	US-10-141-704-506
15	1258	100.0	250	12	US-10-142-421-506

16	1258	100.0	250	12	US-10-142-432-506
17	1258	100.0	250	12	US-10-142-767-506
18	1258	100.0	250	12	US-10-143-033-506
19	1258	100.0	250	12	US-10-144-994-506
20	1258	100.0	250	12	US-10-145-628-506
21	1258	100.0	250	12	US-10-145-631-506
22	1258	100.0	250	12	US-10-145-633-506
23	1258	100.0	250	12	US-10-145-746-506
24	1258	100.0	250	12	US-10-145-748-506
25	1258	100.0	250	12	US-10-145-823-506
26	1258	100.0	250	12	US-10-145-826-506
27	1258	100.0	250	12	US-10-145-870-506
28	1258	100.0	250	12	US-10-145-876-506
29	1258	100.0	250	12	US-10-145-959-506
30	1258	100.0	250	12	US-10-146-724-506
31	1258	100.0	250	12	US-10-146-725-506
32	1258	100.0	250	12	US-10-146-795-506
33	1258	100.0	250	12	US-10-147-495-506
34	1258	100.0	250	12	US-10-147-501-506
35	1258	100.0	250	12	US-10-147-504-506
36	1258	100.0	250	12	US-10-147-506-506
37	1258	100.0	250	12	US-10-147-509-506
38	1258	100.0	250	12	US-10-147-510-506
39	1258	100.0	250	12	US-10-147-511-506
40	1258	100.0	250	12	US-10-147-529-506
41	1258	100.0	250	12	US-10-152-397-506
42	1258	100.0	250	12	US-10-153-586-506
43	1258	100.0	250	12	US-10-158-783-506
44	1258	100.0	250	12	US-10-158-786-506
45	1258	100.0	250	12	US-10-006-130A-170

#### ALIGNMENTS

RESULT 1  
US-09-946-374-170  
; Sequence 170, Application US/09946374  
; Publication No. US20030073129A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Collin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C1  
; CURRENT APPLICATION NUMBER: US/09/946,374  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750



PRIOR FILING DATE: 1998-10-14  
PRIOR APPLICATION NUMBER: 60/104987  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105002  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105104  
PRIOR FILING DATE: 1998-10-21  
PRIOR APPLICATION NUMBER: 60/105169  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105266  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105693  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105694  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1258; DB 11; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1.3e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECKPHSOPWQALFEKTRLCGATLLAPRMLTAAHCKRRTYVHLGQHNLOKEE 60  
DB 22 IIKGECKPHSOPWQALFEKTRLCGATLLAPRMLTAAHCKRRTYVHLGQHNLOKEE 81  
QY 61 GCEOTRTATESPFPHPGFNNSLPNKDRNDIMLVKASVSTWAVRPLTSSRCVTAGTS 120  
DB 82 GCEOTRTATESPFPHPGFNNSLPNKDRNDIMLVKASVSTWAVRPLTSSRCVTAGTS 141  
QY 121 CLISGWSTSSPOLRPLPTLRCANITTIHOKCENAYPGNITDVMWCVASVDEGGKDSGCG 180  
DB 142 CLISGWSTSSPOLRPLPTLRCANITTIHOKCENAYPGNITDVMWCVASVDEGGKDSGCG 201  
QY 181 DSGGPLVCNOSLOGIISWGQDPCAITRKPGYTYTKYCKVDMIOETMKN 229  
DB 202 DSGGPLVCNOSLOGIISWGQDPCAITRKPGYTYTKYCKVDMIOETMKN 250

RESULT 2  
US-10-015-387A-170  
Sequence 170, Application US/10015387A  
Publication No. US20030135034A1

GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Boistein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830P1C54  
CURRENT APPLICATION NUMBER: US/10/015,387A  
PRIOR FILING DATE: 2001-12-12  
PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 170  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-015-387A-170

Query Match 100.0%; Score 1258; DB 12; Length 250;

Best Local Similarity 100.0%; Pred. No. 1.3e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 IIKGECKPHSOPWQALFEKTRLCGATLLAPRMLTAAHCKRRTYVHLGQHNLOKEE 60  
DB 22 IIKGECKPHSOPWQALFEKTRLCGATLLAPRMLTAAHCKRRTYVHLGQHNLOKEE 81  
QY 61 GCEOTRTATESPFPHPGFNNSLPNKDRNDIMLVKASVSTWAVRPLTSSRCVTAGTS 120  
DB 82 GCEOTRTATESPFPHPGFNNSLPNKDRNDIMLVKASVSTWAVRPLTSSRCVTAGTS 141  
QY 121 CLISGWSTSSPOLRPLPTLRCANITTIHOKCENAYPGNITDVMWCVASVDEGGKDSGCG 180  
DB 142 CLISGWSTSSPOLRPLPTLRCANITTIHOKCENAYPGNITDVMWCVASVDEGGKDSGCG 201  
QY 181 DSGGPLVCNOSLOGIISWGQDPCAITRKPGYTYTKYCKVDMIOETMKN 229  
DB 202 DSGGPLVCNOSLOGIISWGQDPCAITRKPGYTYTKYCKVDMIOETMKN 250

RESULT 3  
US-10-137-870-506  
Sequence 506, Application US/10137870  
Publication No. US20030138883A1

GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zhen  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C155  
CURRENT APPLICATION NUMBER: US/10/137,870  
CURRENT FILING DATE: 2002-05-03  
PRIOR APPLICATION REMOVED - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 506  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-137-870-506

Query Match 100.0%; Score 1258; DB 12; Length 250;  
Best Local Similarity 100.0%; Pred. No. 1.3e-118;  
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECKPHSOPWQALFEKTRLCGATLLAPRMLTAAHCKRRTYVHLGQHNLOKEE 60  
DB 22 IIKGECKPHSOPWQALFEKTRLCGATLLAPRMLTAAHCKRRTYVHLGQHNLOKEE 81  
QY 61 GCEOTRTATESPFPHPGFNNSLPNKDRNDIMLVKASVSTWAVRPLTSSRCVTAGTS 120  
DB 82 GCEOTRTATESPFPHPGFNNSLPNKDRNDIMLVKASVSTWAVRPLTSSRCVTAGTS 141  
QY 121 CLISGWSTSSPOLRPLPTLRCANITTIHOKCENAYPGNITDVMWCVASVDEGGKDSGCG 180  
DB 142 CLISGWSTSSPOLRPLPTLRCANITTIHOKCENAYPGNITDVMWCVASVDEGGKDSGCG 201  
QY 181 DSGGPLVCNOSLOGIISWGQDPCAITRKPGYTYTKYCKVDMIOETMKN 229  
DB 202 DSGGPLVCNOSLOGIISWGQDPCAITRKPGYTYTKYCKVDMIOETMKN 250

```
Db      202 DSGGPLVNCNOSLOGIISWGDPCATITRKPGVYTKVCKYVDIOETMKN 250

RESULT 4
US-10-140-018-506
; Sequence 506, Application US/10140018
; Publication No. US2003013885A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Daniel
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-018-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IIKGFCKRPHSQWQAALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKBE 60
        |||||||
Db      22 IIKGFCKRPHSQWQAALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKBE 81
        |||||||

QY      61 GCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKASPSITWAVRPLTSSRCYTAGTS 120
        |||||||
Db      82 GCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKASPSITWAVRPLTSSRCYTAGTS 141
        |||||||

QY      121 CLISGWGSTSSPOLRLPHTLRKANITIIHOKCENAYPGNITDTWVCASVQEGKSDSCG 180
        |||||||
Db      142 CLISGWGSTSSPOLRLPHTLRKANITIIHOKCENAYPGNITDTWVCASVQEGKSDSCG 201
        |||||||

QY      181 DSGGPLVNCNOSLOGIISWGDPCATITRKPGVYTKVCKYVDIOETMKN 229
        |||||||
Db      202 DSGGPLVNCNOSLOGIISWGDPCATITRKPGVYTKVCKYVDIOETMKN 250
        |||||||

RESULT 5
US-10-140-021-506
; Sequence 506, Application US/10140021
; Publication No. US2003013886A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Daniel
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C161
; CURRENT APPLICATION NUMBER: US/10/140,021
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-021-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IIKGFCKRPHSQWQAALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKBE 60
        |||||||
Db      22 IIKGFCKRPHSQWQAALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKBE 81
        |||||||

QY      61 GCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKASPSITWAVRPLTSSRCYTAGTS 120
        |||||||
Db      82 GCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKASPSITWAVRPLTSSRCYTAGTS 141
        |||||||

QY      121 CLISGWGSTSSPOLRLPHTLRKANITIIHOKCENAYPGNITDTWVCASVQEGKSDSCG 180
        |||||||
Db      142 CLISGWGSTSSPOLRLPHTLRKANITIIHOKCENAYPGNITDTWVCASVQEGKSDSCG 201
        |||||||

QY      181 DSGGPLVNCNOSLOGIISWGDPCATITRKPGVYTKVCKYVDIOETMKN 229
        |||||||
Db      202 DSGGPLVNCNOSLOGIISWGDPCATITRKPGVYTKVCKYVDIOETMKN 250
        |||||||

RESULT 6
US-10-140-274-506
; Sequence 506, Application US/10140274
; Publication No. US20030143674A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Daniel
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C161
; CURRENT APPLICATION NUMBER: US/10/140,274
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-274-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IIKGFCKRPHSQWQAALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKBE 60
        |||||||
Db      22 IIKGFCKRPHSQWQAALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKBE 81
        |||||||

QY      61 GCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKASPSITWAVRPLTSSRCYTAGTS 120
        |||||||
Db      82 GCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKASPSITWAVRPLTSSRCYTAGTS 141
        |||||||

QY      121 CLISGWGSTSSPOLRLPHTLRKANITIIHOKCENAYPGNITDTWVCASVQEGKSDSCG 180
        |||||||
Db      142 CLISGWGSTSSPOLRLPHTLRKANITIIHOKCENAYPGNITDTWVCASVQEGKSDSCG 201
        |||||||

QY      181 DSGGPLVNCNOSLOGIISWGDPCATITRKPGVYTKVCKYVDIOETMKN 229
        |||||||
Db      202 DSGGPLVNCNOSLOGIISWGDPCATITRKPGVYTKVCKYVDIOETMKN 250
        |||||||
```

```
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-274-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCKPHSQPQWALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
    |||
DB 22 IIKGFCKPHSQPQWALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81
    |||

QY 61 GCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASVSTTMAVRPLTSSRCVTAGTS 120
    |||
DB 82 GCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASVSTTMAVRPLTSSRCVTAGTS 141
    |||

QY 121 CLISGWSSTSSPOLRPLPTLRCANITIIHOKCENAYGNTIDTWVCASVDEGGKDSGCG 180
    |||
DB 142 CLISGWSSTSSPOLRPLPTLRCANITIIHOKCENAYGNTIDTWVCASVDEGGKDSGCG 201
    |||

QY 181 DSGGPLVNCNOSLQGIISWGODPCATRRKPGYTKVCKYVDWIOETMKN 229
    |||
DB 202 DSGGPLVNCNOSLQGIISWGODPCATRRKPGYTKVCKYVDWIOETMKN 250
    |||

RESULT 7
US-10-140-471-506
; Sequence 506, Application US/10140471
; Publication No. US20030138887A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C163
; CURRENT APPLICATION NUMBER: US/10/140,471
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-471-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCKPHSQPQWALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
    |||
DB 22 IIKGFCKPHSQPQWALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81
    |||

QY 61 GCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASVSTTMAVRPLTSSRCVTAGTS 120
    |||
DB 82 GCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASVSTTMAVRPLTSSRCVTAGTS 141
    |||

QY 121 CLISGWSSTSSPOLRPLPTLRCANITIIHOKCENAYGNTIDTWVCASVDEGGKDSGCG 180
    |||
DB 142 CLISGWSSTSSPOLRPLPTLRCANITIIHOKCENAYGNTIDTWVCASVDEGGKDSGCG 201
    |||

QY 181 DSGGPLVNCNOSLQGIISWGODPCATRRKPGYTKVCKYVDWIOETMKN 229
    |||
DB 202 DSGGPLVNCNOSLQGIISWGODPCATRRKPGYTKVCKYVDWIOETMKN 250
    |||
```

```
DB 142 CLISGWSSTSSPOLRPLPTLRCANITIIHOKCENAYGNTIDTWVCASVDEGGKDSGCG 201
    |||

QY 181 DSGGPLVNCNOSLQGIISWGODPCATRRKPGYTKVCKYVDWIOETMKN 229
    |||
DB 202 DSGGPLVNCNOSLQGIISWGODPCATRRKPGYTKVCKYVDWIOETMKN 250
    |||

RESULT 8
US-10-140-807-506
; Sequence 506, Application US/10140807
; Publication No. US20030134354A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-807-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFCKPHSQPQWALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
    |||
DB 22 IIKGFCKPHSQPQWALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81
    |||

QY 61 GCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASVSTTMAVRPLTSSRCVTAGTS 120
    |||
DB 82 GCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASVSTTMAVRPLTSSRCVTAGTS 141
    |||

QY 121 CLISGWSSTSSPOLRPLPTLRCANITIIHOKCENAYGNTIDTWVCASVDEGGKDSGCG 180
    |||
DB 142 CLISGWSSTSSPOLRPLPTLRCANITIIHOKCENAYGNTIDTWVCASVDEGGKDSGCG 201
    |||

QY 181 DSGGPLVNCNOSLQGIISWGODPCATRRKPGYTKVCKYVDWIOETMKN 229
    |||
DB 202 DSGGPLVNCNOSLQGIISWGODPCATRRKPGYTKVCKYVDWIOETMKN 250
    |||

RESULT 9
US-10-140-922-506
; Sequence 506, Application US/10140922
; Publication No. US20030138889A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
```

```
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C179
; CURRENT APPLICATION NUMBER: US/10/140,922
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Saplen
US-10-140-922-506
```

```
Query Match          100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 IIRGFCKRHSQWQALFEKTRILCGATLIARWMLTAHCKPRIVYHVGHNLOKEE 60
   |||||||
DB 22 IIRGFCKRHSQWQALFEKTRILCGATLIARWMLTAHCKPRIVYHVGHNLOKEE 81
   |||||||
QY 61 GCEQTRATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSIYAVRPLTSSRCVYAGTS 120
   |||||||
DB 82 GCEQTRATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSIYAVRPLTSSRCVYAGTS 141
   |||||||
QY 121 CLISGSGTSSPOLRLPHTLRKANITIIHQKCNAYPGNITDTMVCASVQEGKDSGCG 180
   |||||||
DB 142 CLISGSGTSSPOLRLPHTLRKANITIIHQKCNAYPGNITDTMVCASVQEGKDSGCG 201
   |||||||
QY 181 DSGGPLVCNOSLOGIISWGDDPCATIRKPGVYTRKCKYVDWIDETMKN 229
   |||||||
DB 202 DSGGPLVCNOSLOGIISWGDDPCATIRKPGVYTRKCKYVDWIDETMKN 250
   |||||||
```

## RESULT 10

```
US-10-140-924-506
; Sequence 506, Application US/10140924
; Publication No. US20030134355A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Beresini, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C177
; CURRENT APPLICATION NUMBER: US/10/140,924
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; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Saplen
US-10-140-924-506
```

```
Query Match          100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 IIRGFCKRHSQWQALFEKTRILCGATLIARWMLTAHCKPRIVYHVGHNLOKEE 60
   |||||||
DB 22 IIRGFCKRHSQWQALFEKTRILCGATLIARWMLTAHCKPRIVYHVGHNLOKEE 81
   |||||||
QY 61 GCEQTRATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSIYAVRPLTSSRCVYAGTS 120
   |||||||
DB 82 GCEQTRATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSIYAVRPLTSSRCVYAGTS 141
   |||||||
QY 121 CLISGSGTSSPOLRLPHTLRKANITIIHQKCNAYPGNITDTMVCASVQEGKDSGCG 180
   |||||||
DB 142 CLISGSGTSSPOLRLPHTLRKANITIIHQKCNAYPGNITDTMVCASVQEGKDSGCG 201
   |||||||
QY 181 DSGGPLVCNOSLOGIISWGDDPCATIRKPGVYTRKCKYVDWIDETMKN 229
   |||||||
DB 202 DSGGPLVCNOSLOGIISWGDDPCATIRKPGVYTRKCKYVDWIDETMKN 250
   |||||||
```

## RESULT 11

```
US-10-140-926-506
; Sequence 506, Application US/10140926
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C187
; CURRENT APPLICATION NUMBER: US/10/140,926
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Saplen
US-10-140-926-506
```

```
Query Match          100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 IIRGFCKRHSQWQALFEKTRILCGATLIARWMLTAHCKPRIVYHVGHNLOKEE 60
   |||||||
DB 22 IIRGFCKRHSQWQALFEKTRILCGATLIARWMLTAHCKPRIVYHVGHNLOKEE 81
   |||||||
```



```
QY 61 GCEQRTATSESPHGFNNSLPNKRNDIMLVKMASPVSTWAVRPLTSSRCTYAGTS 120
    |||
DB 82 GCEQRTATSESPHGFNNSLPNKRNDIMLVKMASPVSTWAVRPLTSSRCTYAGTS 141
QY 121 CLISGWSSTSPQRLPHTLRCAANTITIEHOKCENAYPGNTIDTMVCAVQEGKDSGCG 180
    |||
DB 142 CLISGWSSTSPQRLPHTLRCAANTITIEHOKCENAYPGNTIDTMVCAVQEGKDSGCG 201
QY 181 DSGGPLVCNOSLOGIISWGODPCAITRRPGVYTKVKYVDWIQETMKN 229
    |||
DB 202 DSGGPLVCNOSLOGIISWGODPCAITRRPGVYTKVKYVDWIQETMKN 250
```

## RESULT 12

```
US-10-141-698-506
; Sequence 506, Application US/10141698
; Publication No. US20030134357A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACTS ENCODING THE SAME
; FILE REFERENCE: P3330R1C206
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-698-506
```

```
Query Match 100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 IIRGFECKPHSQPMQALFEKTRLLCGATLAPRMLTFAHCLKPRYVHIGOHNLQKEE 60
    |||
DB 22 IIRGFECKPHSQPMQALFEKTRLLCGATLAPRMLTFAHCLKPRYVHIGOHNLQKEE 81
QY 61 GCEQRTATSESPHGFNNSLPNKRNDIMLVKMASPVSTWAVRPLTSSRCTYAGTS 120
    |||
DB 82 GCEQRTATSESPHGFNNSLPNKRNDIMLVKMASPVSTWAVRPLTSSRCTYAGTS 141
QY 121 CLISGWSSTSPQRLPHTLRCAANTITIEHOKCENAYPGNTIDTMVCAVQEGKDSGCG 180
    |||
DB 142 CLISGWSSTSPQRLPHTLRCAANTITIEHOKCENAYPGNTIDTMVCAVQEGKDSGCG 201
QY 181 DSGGPLVCNOSLOGIISWGODPCAITRRPGVYTKVKYVDWIQETMKN 229
    |||
DB 202 DSGGPLVCNOSLOGIISWGODPCAITRRPGVYTKVKYVDWIQETMKN 250
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## RESULT 13

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US-10-141-702-506
; Sequence 506, Application US/10141702
; Publication No. US20030134358A1
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACTS ENCODING THE SAME
; FILE REFERENCE: P3330R1C208
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-702-506
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Query Match 100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 IIRGFECKPHSQPMQALFEKTRLLCGATLAPRMLTFAHCLKPRYVHIGOHNLQKEE 60
    |||
DB 22 IIRGFECKPHSQPMQALFEKTRLLCGATLAPRMLTFAHCLKPRYVHIGOHNLQKEE 81
QY 61 GCEQRTATSESPHGFNNSLPNKRNDIMLVKMASPVSTWAVRPLTSSRCTYAGTS 120
    |||
DB 82 GCEQRTATSESPHGFNNSLPNKRNDIMLVKMASPVSTWAVRPLTSSRCTYAGTS 141
QY 121 CLISGWSSTSPQRLPHTLRCAANTITIEHOKCENAYPGNTIDTMVCAVQEGKDSGCG 180
    |||
DB 142 CLISGWSSTSPQRLPHTLRCAANTITIEHOKCENAYPGNTIDTMVCAVQEGKDSGCG 201
QY 181 DSGGPLVCNOSLOGIISWGODPCAITRRPGVYTKVKYVDWIQETMKN 229
    |||
DB 202 DSGGPLVCNOSLOGIISWGODPCAITRRPGVYTKVKYVDWIQETMKN 250
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## RESULT 14

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US-10-141-704-506
; Sequence 506, Application US/10141704
; Publication No. US20030134359A1
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
```

```

: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3330R1C209
: CURRENT APPLICATION NUMBER: US/10/141,704
: CURRENT FILING DATE: 2002-05-08
: Prior Application removed - See Palm or File Wrapper
: NUMBER OF SEQ ID NOS: 350
: SEQ ID NO 506
: LENGTH: 250
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-141-704-506

Query Match          100.0%; Score 1258; DB 12; length 250;
Best local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIGFECKPHSQWQAALFEKTRILCGATLIAPRWILTAHCLKPRYIVHLGQHNLOKEE 60
   |||
Db 22 IIGFECKPHSQWQAALFEKTRILCGATLIAPRWILTAHCLKPRYIVHLGQHNLOKEE 81
   |||

QY 61 GCEOTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
   |||
Db 82 GCEOTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 141
   |||

QY 121 CLISGWSSTSSPOLRLPHTLRCAANTITIEHQKCNAPGNITDPMWCASVQEGKDSGCG 180
   |||
Db 142 CLISGWSSTSSPOLRLPHTLRCAANTITIEHQKCNAPGNITDPMWCASVQEGKDSGCG 201
   |||

QY 181 DSGGPLVCNOSLOGIISWGDDPCAITRKPGVYTKCKYVDWIOETMKN 229
   |||
Db 202 DSGGPLVCNOSLOGIISWGDDPCAITRKPGVYTKCKYVDWIOETMKN 250
   |||

RESULT 15
US-10-142-421-506
: Sequence 506, Application US/10142421
: Publication No. US20030134360A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Geriltsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3330R1C218
: CURRENT APPLICATION NUMBER: US/10/142,421
: CURRENT FILING DATE: 2002-05-09
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 506
: LENGTH: 250
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-142-421-506

Query Match          100.0%; Score 1258; DB 12; length 250;
Best local Similarity 100.0%; Pred. No. 1.3e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 1 IIGFECKPHSQWQAALFEKTRILCGATLIAPRWILTAHCLKPRYIVHLGQHNLOKEE 60
   |||
Db 22 IIGFECKPHSQWQAALFEKTRILCGATLIAPRWILTAHCLKPRYIVHLGQHNLOKEE 81
   |||

QY 61 GCEOTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
   |||
Db 82 GCEOTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 141
   |||

QY 121 CLISGWSSTSSPOLRLPHTLRCAANTITIEHQKCNAPGNITDPMWCASVQEGKDSGCG 180
   |||
Db 142 CLISGWSSTSSPOLRLPHTLRCAANTITIEHQKCNAPGNITDPMWCASVQEGKDSGCG 201
   |||

QY 181 DSGGPLVCNOSLOGIISWGDDPCAITRKPGVYTKCKYVDWIOETMKN 229
   |||
Db 202 DSGGPLVCNOSLOGIISWGDDPCAITRKPGVYTKCKYVDWIOETMKN 250
   |||

Search completed: October 15, 2003, 21:06:23
Job time : 21.6145 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 15, 2003, 20:55:12 ; Search time 12.9961 Seconds  
(without alignments)  
745.546 Million cell updates/sec

Title: US-09-856-320a-2\_COPY\_54\_282

Perfect score: 1258  
Sequence: 1 LIKFECKPHSQPMQALFE.....GVYTKVCKYVDIETMKN 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/CTRUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/Backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	100.0	250	4	US-09-205-258-427 Sequence 427, App
2	1258	100.0	282	3	US-09-025-059-1 Sequence 1, Appl
3	1227	97.5	248	3	US-08-944-483-24 Sequence 24, Appl
4	1219.5	96.9	289	4	US-09-386-642-14 Sequence 14, Appl
5	684	54.4	260	3	US-09-025-059-3 Sequence 3, Appl
6	681	54.1	260	3	US-09-070-526-2 Sequence 2, Appl
7	673	53.5	260	3	US-09-008-271A-7 Sequence 7, Appl
8	671.5	53.4	288	4	US-09-386-642-13 Sequence 13, Appl
9	651	51.7	228	4	US-09-203-258-1150 Sequence 1150, Ap
10	651	51.7	246	4	US-09-205-258-1149 Sequence 309, App
11	644.5	51.2	293	4	US-09-996-243-309 Sequence 1, Appl
12	597.5	47.5	268	2	US-08-824-874-1 Sequence 1, Appl
13	597.5	47.5	268	4	US-09-210-084-1 Sequence 1, Appl
14	597.5	47.5	268	4	US-09-764-762-1 Sequence 1, Appl
15	591.5	47.0	263	2	US-08-790-137-4 Sequence 4, Appl
16	591.5	47.0	263	2	US-08-824-874-5 Sequence 5, Appl
17	591.5	47.0	263	3	US-08-807-151-5 Sequence 5, Appl
18	591.5	47.0	263	3	US-09-210-084-5 Sequence 5, Appl
19	591.5	47.0	263	4	US-09-478-957-5 Sequence 5, Appl
20	591.5	47.0	263	4	US-09-764-762-5 Sequence 5, Appl
21	587	46.7	246	2	US-08-978-404B-44 Sequence 44, Appl
22	578	45.9	232	2	US-08-978-404B-45 Sequence 45, Appl
23	577.5	45.9	237	3	US-08-768-859A-16 Sequence 16, Appl
24	577.5	45.9	237	3	US-08-767-820A-16 Sequence 16, Appl
25	577.5	45.9	237	3	US-08-622-046B-12 Sequence 12, Appl
26	577.5	45.9	237	3	US-08-944-483-37 Sequence 37, Appl
27	577.5	45.9	237	3	US-09-100-264-1 Sequence 1, Appl

28	577.5	45.9	237	4	US-08-843-076D-1	Sequence 1, Appl
29	577.5	45.9	238	3	US-08-768-859A-8	Sequence 8, Appl
30	577.5	45.9	238	3	US-08-767-820A-8	Sequence 8, Appl
31	577.5	45.9	244	3	US-08-768-859A-10	Sequence 10, Appl
32	577.5	45.9	244	3	US-08-767-820A-10	Sequence 10, Appl
33	577.5	45.9	244	3	US-08-622-046B-16	Sequence 16, Appl
34	577.5	45.9	244	3	US-09-100-264-5	Sequence 5, Appl
35	577.5	45.9	244	4	US-08-843-076D-5	Sequence 5, Appl
36	577.5	45.9	261	3	US-08-768-859A-6	Sequence 6, Appl
37	577.5	45.9	261	3	US-08-767-820A-6	Sequence 6, Appl
38	577.5	45.9	261	3	US-08-622-046B-14	Sequence 14, Appl
39	577.5	45.9	261	3	US-09-100-264-7	Sequence 7, Appl
40	577.5	45.9	261	4	US-08-983-075D-7	Sequence 7, Appl
41	577.5	45.9	261	4	US-08-843-076D-3	Sequence 3, Appl
42	577	45.9	228	1	US-08-278-091-7	Sequence 7, Appl
43	577	45.9	228	1	US-08-483-859-7	Sequence 7, Appl
44	577	45.9	228	1	US-08-472-173-7	Sequence 7, Appl
45	577	45.9	228	2	US-08-487-167-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-09-205-258-427  
; Sequence 427, Application US/09205258  
; Patent No. 6525174  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/09/205,258  
; CURRENT FILING DATE: 1998-12-04  
; EARLIER APPLICATION NUMBER: PCT/US98/11422  
; EARLIER FILING DATE: 1998-06-04  
; EARLIER APPLICATION NUMBER: 60/048, 885  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049, 375  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 881  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 880  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 876  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 896  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049, 020  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 876  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 895  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 884  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 894  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 971  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 882  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 899  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 893  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 900  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 901  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 892  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 915  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048, 915  
; EARLIER FILING DATE: 1997-06-06

9  
10  
12  
14  
15

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; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 427
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-427

Query Match      100.0%; Score 1258; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 9, 6e-126;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IINGFECKPHSOPWQALFEKTRILCGATLIAFRWLLTAHCLKPRYIVHLGQHNLOKEE 60
DB 22 IINGFECKPHSOPWQALFEKTRILCGATLIAFRWLLTAHCLKPRYIVHLGQHNLOKEE 81
QY 61 GCQOTRATESFPHGFNNSLPKNDHNDIMLVKMA SPVITVAVPLTSSRCVYAGTS 120
DB 82 GCQOTRATESFPHGFNNSLPKNDHNDIMLVKMA SPVITVAVPLTSSRCVYAGTS 141
QY 121 CLISGSGTSSPOLRLPHTRLCANITIIHOKCENAYPGNITDTMVCASVQEGGKDCSCG 180
DB 142 CLISGSGTSSPOLRLPHTRLCANITIIHOKCENAYPGNITDTMVCASVQEGGKDCSCG 201
QY 181 DSGGPLVNCNSLOGIISWGDDPCATIRKPGVYTKVKCYVWIOETMKN 229
DB 202 DSGGPLVNCNSLOGIISWGDDPCATIRKPGVYTKVKCYVWIOETMKN 250
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RESULT 2
US-09-025-059-1
; Sequence 1, Application US/09025059
; Patent No. 6075136
```

```

; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0481 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 282 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGCTUT10
; CLONE: 2723646
US-09-025-059-1

Query Match      100.0%; Score 1258; DB 3; Length 282;
Best Local Similarity 100.0%; Pred. No. 1, 1e-125;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IINGFECKPHSOPWQALFEKTRILCGATLIAFRWLLTAHCLKPRYIVHLGQHNLOKEE 60
DB 54 IINGFECKPHSOPWQALFEKTRILCGATLIAFRWLLTAHCLKPRYIVHLGQHNLOKEE 113
QY 61 GCQOTRATESFPHGFNNSLPKNDHNDIMLVKMA SPVITVAVPLTSSRCVYAGTS 120
DB 114 GCQOTRATESFPHGFNNSLPKNDHNDIMLVKMA SPVITVAVPLTSSRCVYAGTS 173
QY 121 CLISGSGTSSPOLRLPHTRLCANITIIHOKCENAYPGNITDTMVCASVQEGGKDCSCG 180
DB 174 CLISGSGTSSPOLRLPHTRLCANITIIHOKCENAYPGNITDTMVCASVQEGGKDCSCG 233
QY 181 DSGGPLVNCNSLOGIISWGDDPCATIRKPGVYTKVKCYVWIOETMKN 229
DB 234 DSGGPLVNCNSLOGIISWGDDPCATIRKPGVYTKVKCYVWIOETMKN 282
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RESULT 3
US-08-944-483-24
; Sequence 24, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
```

```

; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLAUS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; TITLE OF INVENTION: OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183 .US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
; US-08-944-483-24

Query Match          97.5%; Score 1227; DB 3; Length 248;
Best Local Similarity 99.1%; Pred. No. 1.9e-122;
Matches 227; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 IIKGFEC-PHSQPMQALFEKTRILCGATLTAAPRWLTAAHCLPRTYIVHLGQHNLOKEE 60
    |||
DB 22 IIKGFEC-PHSQPMQALF-KTRLICGATLTAAPRWLTAAHCLKPKRYIVHLGQHNLOKEE 79
    |||
QY 61 GCEQRTATESPPHGFENSLPNKDRNDIMLVKASPVSTTMAVRPLTSSRCVTAGT 120
    |||
DB 80 GCEQRTATESPPHGFENSLPNKDRNDIMLVKASPVSTTMAVRPLTSSRCVTAGT 139
    |||
QY 121 CLISGWSSTSPQRLPRTLTCANITTEHOKCENAYPGNTIDTVMCASVQEGKDSQCG 180
    |||
DB 140 CLISGWSSTSPQRLPRTLTCANITTEHOKCENAYPGNTIDTVMCASVQEGKDSQCG 199
    |||
QY 181 DSGGPLVNCNOSLOGIISWGQDPCATITRKPGYTVCKYVDMIOETMKN 229
    |||
DB 200 DSGGPLVNCNOSLOGIISWGQDPCATITRKPGYTVCKYVDMIOETMKN 248
    |||

RESULT 4
US-09-386-642-14
; Sequence 14, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Ol, Jensen

```

```

; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-14

Query Match          96.9%; Score 1219.5; DB 4; Length 289;
Best Local Similarity 97.0%; Pred. No. 1.5e-121;
Matches 223; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 IIKGFEC-KPHSQPMQALFEKTRILCGATLTAAPRWLTAAHCLPRTYIVHLGQHNLOKEE 59
    |||
DB 52 IYGVNCLKHSQPMQALFEKTRILCGATLTAAPRWLTAAHCLPRTYIVHLGQHNLOKEE 111
    |||
QY 60 ECEQRTATESPPHGFENSLPNKDRNDIMLVKASPVSTTMAVRPLTSSRCVTAGT 119
    |||
DB 112 ECEQRTATESPPHGFENSLPNKDRNDIMLVKASPVSTTMAVRPLTSSRCVTAGT 171
    |||
QY 120 SCLISGWSSTSPQRLPRTLTCANITTEHOKCENAYPGNTIDTVMCASVQEGKDSQCG 179
    |||
DB 172 SCLISGWSSTSPQRLPRTLTCANITTEHOKCENAYPGNTIDTVMCASVQEGKDSQCG 231
    |||
QY 180 GDSGPLVNCNOSLOGIISWGQDPCATITRKPGYTVCKYVDMIOETMKN 229
    |||
DB 232 GDSGPLVNCNOSLOGIISWGQDPCATITRKPGYTVCKYVDMIOETMKN 281
    |||

RESULT 5
US-09-025-059-3
; Sequence 3, Application US/09025059
; Patent No. 6075136
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0481 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166

```

TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1020091  
US-09-025-059-3

Query Match 54.4%; Score 684; DB 3; Length 260;  
Best Local Similarity 53.1%; Pred. No. 1e-64;  
Matches 121; Conservative 35; Mismatches 70; Indels 2; Gaps 2;

QY 1 IINGFECKPHSQWQALAEKTRLLCGATLIAPRWLITAAHCLPKRYIHLGQHNLOKEE 60  
DB 33 ILERECIPHSQWQALAEKTRLLCGATLIAPRWLITAAHCLPKRYIHLGQHNLOKEE 92  
QY 61 GCEOTRATESFPHGFNNSLPKNDHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120  
DB 93 QPEDEIQVAOSIHPHCYNNSNP-EDHSHDMLIRLQNSANLGDVKFVQLANLCPKVGOK 151  
QY 121 CLISGWTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVOEGKDCSCG 180  
DB 152 CIIISGWTYVSPRENPDITLNCALVKIIFPKKCEDAYPGQITDGMVCAGSSKGA-DTCG 210  
QY 181 DSGGPLVNCNLSGIIISWGDPICATIRKPGVYTRKVCYVWIOETMKN 228  
DB 211 DSGGPLVCDGLGIIISWGSDPCGKPEKPGVYTRKVCYVWIOETMKN 258

RESULT 6  
US-09-070-526-2  
Sequence 2, Application US/09070526  
Patent No. 6100059  
GENERAL INFORMATION:  
APPLICANT: SOUTHAN, CHRISTOPHER  
APPLICANT: CLINKENBEARD, HELEN  
APPLICANT: BURGESS, NICOLA  
TITLE OF INVENTION: No. 6100059e1 Compounds  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: RATHER & PRESTIA  
STREET: P.O. BOX 980  
CITY: VALLEY FORGE  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,526  
FILING DATE: 30-APR-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9711952.3  
FILING DATE: 9-JUN-1997  
APPLICATION NUMBER: EP 97309646.4  
FILING DATE: 1-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: PRESTIA, PAUL F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GH-30353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-070-526-2

Query Match 54.1%; Score 681; DB 3; Length 260;  
Best Local Similarity 51.8%; Pred. No. 2.2e-64;  
Matches 116; Conservative 42; Mismatches 64; Indels 2; Gaps 2;

QY 1 IINGFECKPHSQWQALAEKTRLLCGATLIAPRWLITAAHCLPKRYIHLGQHNLOKEE 60  
DB 33 ILERECIPHSQWQALAEKTRLLCGATLIAPRWLITAAHCLPKRYIHLGQHNLOKEE 92  
QY 61 GCEOTRATESFPHGFNNSLPKNDHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120  
DB 93 QPEDEIPVOSIHPHCYNNS-DVEDHNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 151  
QY 121 CLISGWTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVOEGKDCSCG 180  
DB 152 CIIISGWTYVSPRENPDITLNCALVKIIFPKKCEDAYPGQITDGMVCAGSSKGA-DTCG 210  
QY 181 DSGGPLVNCNLSGIIISWGDPICATIRKPGVYTRKVCYVWIOE 224  
DB 211 DSGGPLVCDGLGIIISWGSDPCGKPEKPGVYTRKVCYVWIOE 254

RESULT 7  
US-09-008-271A-7  
Sequence 7, Application US/09008271A  
Patent No. 6203979  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
Hillman, Jennifer L.  
Yue, Henry  
Guegler, Karl J.  
Corley, Neil C.  
Tang, Tom Y.  
Shah, Purvi  
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/008,271A  
FILING DATE: 16-Jan-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mohan-Peterson, Sheela  
REGISTRATION NUMBER: 41,201  
REFERENCE/DOCKET NUMBER: PF-0458 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

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?      TOPOLOGY: linear
?
?      IMMEDIATE SOURCE:
?
?      LIBRARY: COLNOT27
?      CLONE: 1798496
?
?      SEQUENCE DESCRIPTION: SEQ ID NO: 7
?
US-09-008-271A-7

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Query Match	53.5%;	Score 673;	DB 3;	Length 260;
Best Local Similarity	51.3%;	Pred. No. 1.5e-63;		
Matches 115;	Conservative 42;	Mismatches 65;	Indels 2;	Gaps 2

QY	1	IIKFEPCFHPQPMOALFFERTKRLGATVILAPRLLTAAHLCJKRYIVLHCOHNIQJEE	60
		:: ::	
Db	33	VLGHECPHPQPMOALSGOQQLCGGVLVGNNVLTAAHCKKRYIVRLGDSHLQNDK	92
QY	61	GCEOTRATESPHEPFENNSLPNTDRNDIMLVKMAFSVITWAVRPLTSSRCTYAGTS	120
		:: ::	
Db	93	GPEDEIPVQSIGPHPCVYSS - DVEDHNNDIMLQDRDQASGSKVKPLSLDHCHQPPQK	151
QY	121	CLISGWSTSSPOLRPLHTLPCANITIIIEHOKENAYGNTITDIWVCASVOEGGDSQCG	180
		:: ::	
Db	152	CTVSGWGVTVPRENFPEPTLNCIAEYKILPQKKCEDAYGQITDGMVACAGSSKGA - DFCQG	210
QY	181	DSGGPILVNCNLSGIIISWGDPCLATKRPQYTVYTKVCKIVDMIQE	224
		:: ::	
Db	211	DSGGPILVNCNLSGIIISWGSPCCGSDSPGVYTNINCRILDMIKK	254

```

RESULT 8
US-09-386-642-13
; Sequence 13, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with Homo sapien serine protease catalytic domain
US-09-386-642-13

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	Query Match	53.4%;	Score 671.5;	DB 4;	Length 288;	
	Best local similarity	51.6%;	Pred. No 2.6e-63;			
	Matches	116;	Conservative	42;	Mismatches	64;
					Indels	3;
					Gaps	3.
OY	1	I I K G F E C - K P H S O P W A L F E K T R L L C G A T L L I A B R M L T T A A H C L P R Y V I H L G O H N L O K E	59			
Db	52	I V G Y I N L E P H S O P W A L F Q G O O L L L G G V L Y G N E V L T A A H C K K P Y T V R L G D H S L Q N K	111			
OY	60	E G C G O T T A T E S P H P G F N N S L P K K D R N D I M L Y K M A S P V I T M A V R L T L S S R C Y T A G T	119			
Db	112	: : I P P E L E P P V O S I P H P C T N S S - D V E D N H D I M L L Q L R D Q A S L G S K V K P I S I A D R C T O P Q	170			
OY	120	S C L I S G S T S S P Q L R L P H T L R C A N I T I I E H O K C E N A V P G N I T D T M C A S V O E G G K D S C Q	179			
Db	171	K C F V S G G V T A S P R E N P P D L I N C A E V K I F P Q K C E D A V P Q I T G M W C A G S S K A - D I C Q	229			
OY	180	G D S G C P L V C N S L O G I T S M G Q D P C A I R R K B E V Y T R K V C K Y U W I O E	224			
Db	230	G D S G S P L V C D A L G I T S M G S D P C G R D R C P E V Y T N I R K Y D I M M K	274			

## RESULT 9

US-09-205-258	1150	Application US/09205258
Sequence	1150,	
Patent No.	6525174	
GENERAL INFORMATION:		
APPLICANT:	Young et al.,	
TITLE OF INVENTION:	207 Human Secreted Proteins	
FILE REFERENCE:	P2007P1	
CURRENT APPLICATION NUMBER:	US/09/205,258	
CURRENT FILING DATE:	1998-12-04	
EARLIER APPLICATION NUMBER:	FCT/US98/11422	
EARLIER FILING DATE:	1998-06-04	
EARLIER APPLICATION NUMBER:	60/048,885	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/049,375	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,881	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,880	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,896	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/049,020	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,876	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,895	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,884	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,894	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,971	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,964	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,882	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,899	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,893	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,900	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,901	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,892	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,915	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/049,019	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,970	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,972	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/049,374	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,917	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,949	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,974	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,883	
EARLIER FILING DATE:	1997-06-06	
EARLIER APPLICATION NUMBER:	60/048,897	
EARLIER FILING DATE:	1997-06-06	

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; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1150
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-1150

Query Match      51.7%; Score 651; DB 4; Length 228;
Best Local Similarity 91.7%; Pred. No. 2,8e-61;
Matches 121; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      1 IIKGFCKPHSOWOALFEKTRILCGATLIAPRWLLTAHCLKPRYIVHLGSHNLQKEE 60
         ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      4 IIKGFCKLHSOWOALFEKTRILCGATLIAPRWLLTAHCLKPRYIVHLGSHNLQKEE 63

QY      61 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKMA SPVSITWAVPLTSSRCVTAGTS 120
         ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      64 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKMA SPVSITWAVPLTSSRCVTAGTS 123

QY      121 CLISGNGSTSSP 132
         |
Db      124 CSFPAGARPPD 135

RESULT 10
US-09-205-258-1149
; Sequence 1149, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
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; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
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; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
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; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1149
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-1149

Query Match      51.7%; Score 651; DB 4; Length 246;
Best Local Similarity 91.7%; Pred. No. 3.1e-61;
Matches 121; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      1 IIKGFCKPHSOWOALFEKTRILCGATLIAPRWLLTAHCLKPRYIVHLGSHNLQKEE 60
         ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
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OY		61	GCEQRTTETSPHGFNNSLPNKDRNDIMLVKMASPVSITWVAPPLTLSSCVTAGTS	120
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OY		121	CLISGWGSTSSP	132
DB		142	CSFPAGAAPDP	153

  

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RESULT 11
US-09-996-243-309
; Sequence 309, Application US/09996243
Patent No. 6478825
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC13
CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/087759
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PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021

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75	PRIOR FILING DATE: 1998-06-19

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5	PRIOR APPLICATION NUMBER: 60/090252
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59	PRIOR APPLICATION NUMBER: 60/091633
60	PRIOR FILING DATE: 1998-07-02
61	PRIOR APPLICATION NUMBER: 60/091978
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63	PRIOR APPLICATION NUMBER: 60/091982
64	PRIOR FILING DATE: 1998-07-07
65	PRIOR APPLICATION NUMBER: 60/092182
66	PRIOR FILING DATE: 1998-07-09

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Db      67  IINGSDCHNHTQWQAALLLRPNQLYCGAVLHPHQMILTAHCKKVFVRVLGHYSLSPV 126
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QY      119  TSLISGMGSTSSPOLRLPHLTRCANTITLIEQCKEANAPEGNITDVMACSVDBGCDSC 178
      183  TKELVSGWGTSTKSPVHFPRKVLQCLNTISVLSQKCEDAPYPOIDITMFCAG-DKAGRSDC 241
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QY      179  QGGSGEPLVCNOSLOGIISMGODPAITRRKPEVYKVCAYDYMDIETMKNN 229
      242  QGSGSGEPLVCNOSLOGIISWMDYPCARRPRREVITNLCKFTKMLQETIIQAN 292
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US-08-824-874-1
Sequence 1, Application US/08824874
Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filled Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
type: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KERANOTO2
CLONE: 820694
US-08-824-874-1
Query Match: 47.5%; Score 597.5; DB 2; Length 268;
Best Local Similarity 49.1%; Pred No. 1,7e-55;
Matches 110; Conservative 39; Mismatches 68; Indels 7; Gaps 4
QY 7 CKPHSQWQALFEKTRLLCGATLLAPRLWLLTAACHSLKPRYLVIAGQHNLOK-EEGCEQT 65
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Db 50 CFP-SGQAAALLRRNOLYCGAVLVNPMQLLTAACHSKKVFYALGHYSLSPYEGSQGM 108
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Db 109 FQGVGKIPRIGS---HGHSNDMLTKLRNRIRPTKDVRIWVSCHSCATKCLVSG 164
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; Sequence 4, Application US/08790137
; Patent No. 5840871
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,137
; FILING DATE: Filed Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0195 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 55527
;
US-08-790-137-4
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Query Match 47.0%; Score 591.5; DB 2; Length 263;
Best Local Similarity 44.5%; Pred. No. 7.2e-55;
Matches 106; Conservative 44; Mismatches 79; Indels 9; Gaps 2;
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Db 25 IIGFNCENKNSQPMWAVYRFARYOCGVLLDANWVLTAAHCYNDKYQVWLGRNNREDE 84
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QY 61 GCEQTRATSESPFGNNSLPNKDH-----RNDIMVKMASPSITWAVRPLTSS 112
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QY 113 RCVTACTSCLISGSGSTS-SPQLRPLTLNCANITIEHCKENAYPGNITDTWVCASVQ 171
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QY 172 EGGKSDSCQSDSGPPLVCNOSLOGIISMGDPCAITRKPGVYTVKCKYVDMIOETMKN 229
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Search completed: October 15, 2003, 20:59:17  
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